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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 ; Search time 13.8672 seconds
(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191

Perfect score: 240
Sequence: 1 ALPARGLDHIENILSYLDA.....ALVCKEYRVTSOGMLMKK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq 101002:*

1: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
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11: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
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13: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
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18: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
20: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240	100.0	76	AAU98095	Human beta TrCP (b)
2	240	100.0	219	AAU98087	Human beta TrCP (b)
3	240	100.0	448	AAAB48289	Beta-TrCP, N/SKP2.C
4	240	100.0	569	AAAY24054	A human beta-trans
5	240	100.0	569	AAAB12812	Mouse ubiquitin 11
6	240	100.0	569	AAAB12813	Human beta-transdu
7	240	100.0	569	AAAY66697	Human beta-TrCP.
8	240	100.0	569	AAAY63041	F-box protein FBP-
9	240	100.0	569	AAAY83250	F-box protein FBP-
10	240	100.0	569	AAAY83254	F-box protein FBP1

11	240	100.0	569	21	AAAY44249	Human cell signal1
12	240	100.0	569	22	AAAB48298	Human ZF11 protein
13	240	100.0	579	22	AAAB78583	Human protein SEQ
14	240	100.0	590	22	AAAB00847	Human bone marrow
15	240	100.0	605	22	AAAB78582	Human protein SEQ
16	240	100.0	608	22	AAAB00960	Human bone marrow
17	240	100.0	632	22	AAAB78584	Human protein SEQ
18	240	100.0	654	22	AAAB79566	Human protein SEQ
19	240	100.0	654	22	AAAB79567	Human protein SEQ
20	240	100.0	654	22	AAAB79568	Human protein SEQ
21	237	98.8	517	16	AAAB85852	WD-40 domain-contg
22	236	98.3	45	21	AAAB12811	Ubiquitin ligase S
23	233	97.1	45	21	AAAB8276	SKP2-like protein
24	231	96.2	43	21	AAAB3048	F-box motif of FBP
25	226	94.2	42	20	AAE02249	F-box motif of FBP
26	226	94.2	42	22	AAE08021	Human DNA repair a
27	210	87.5	542	22	AAAB6942	Human E3 ubiquitin
28	210	87.5	542	21	AAAB79127	Human protein SEQ
29	210	87.5	542	22	AAAB40208	Human polypeptide
30	210	87.5	542	22	AAAB41994	Drosophila melanog
31	210	87.5	550	22	AAAB59857	Human protein SEQ
32	188	78.3	510	22	AAAB80111	Human protein Met3
33	178	74.2	138	22	AAAB80111	F-box motif of FBP
34	91	37.9	640	21	AAAB83252	F-box motif of FBP
35	83	34.6	39	21	AAAB3066	Human ORFX ORF38
36	83	34.6	483	21	AAAB40624	F-box protein FBP-
37	83	34.6	483	21	AAAB3087	Human ZF24 protein
38	83	34.6	483	22	AAAB8305	Drosophila melanog
39	82	34.2	464	22	AAAB64154	F-box structure pr
40	81	33.8	592	22	AAAB6507	Human ZF13 protein
41	80	33.3	108	22	AAAB48299	F-box protein FBP-
42	78	32.5	197	21	AAAB83079	Human ovarian anti
43	77	32.1	270	23	ABPA1293	Novel human diagno
44	77	32.1	472	22	ABG04396	Human ORFX ORF815
45	77	32.1	496	21	ABAB1051	

ALIGNMENTS

RESULT 1	AAU98095	standard; Protein; 76 AA.
ID	AAU98095	
AC	AAU98095	
XX		
DT	24-SEP-2002	(first entry)
XX		
DE	Human beta TrCP (bTrCP) mutant protein #1.	
XX		
KW	Human: beta TrCP; bTrCP; protein-protein interaction complex; Ras SFI;	
KW	drug screening; selected interacting domain; SID; tumour; gene therapy;	
KW	cytostatic; mutant; muten.	
XX		
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 1	/note="Wild-type N-terminus (residues 1-143 of AAU98087)
FT		have been deleted"
PN	WO200250261-A2.	
XX		
PD	27-JUN-2002.	
XX		
PF	18-DEC-2001; 2001WO-EP15414.	
XX		
PR	18-DEC-2000; 2000US-256276P.	
XX		
PA	(HYBR-) HYBRIGENTS.	
XX		
PA	(INRM) INST NAT SANTE & RECH MEDICALE.	
XX		

PI Legrain P, Benarous R, Blot G, Lassot I;
 XX WPI; 2002-508795/54.

XX Protein-protein complexes for screening drugs or agents that modulate
 PT interaction of proteins, e.g. for identifying the Selected Interacting
 PR Domains (SID), comprises interaction between beta-TrCP and Ras SFI -
 XX
 XX Example 9; Page -; 84pp; English.

CC The present invention relates to a new complex of protein-protein
 CC interaction between betaTrCP (not defined in specification) and Ras SFI.
 CC The protein-protein complex of the invention is useful for screening
 CC drugs or agents that modulate interaction of proteins. In particular,
 CC the protein complex is useful for identifying the Selected Interacting
 CC Domains (SID). The modulating compounds detected can be used for
 CC treating tumours. The polynucleotides encoding the protein complex may
 CC be used in gene therapy. The present amino acid sequence represents
 CC human beta TrCP (bTrCP) mutant protein #1, as described in the methods
 CC of the invention.
 CC Note: This sequence is not shown in the specification but is derived from
 CC the wild-type human bTrCP sequence (AAU98087) shown on page 47 of the
 CC specification.
 XX
 SQ Sequence 76 AA;

Query Match 100.0%; Score 240; DB 23; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 ALPARGLDHIAENILSYLDKSLCAAEIYCKEYRVTSIDGMLMK 45
 DB 4 ALPARGLDHIAENILSYLDKSLCAAEIYCKEYRVTSIDGMLMK 48

RESULT 2
 AAU98087
 ID AAU98087 standard; Protein; 219 AA.

AC AAU98087;

DT 24-SEP-2002 (first entry)

DE Human beta TrCP (bTrCP) bait protein sequence.

XX Human; beta TrCP; bTrCP; protein-protein interaction complex; Ras SFI;
 KW drug screening; selected interacting domain; SID; tumour; gene therapy;
 KW bait protein; cytostatic.

XX Homo sapiens.

PN MO200250261-A2.

FD 27-JUN-2002.

PF 18-DEC-2001; 2001MO-EP15414.

PR 18-DEC-2000; 2000US-256276P.

PA (HYBR-) HYBRIGENICS.

PA (INRM) INSR NAT SANTE & RECH MEDICALE.

PI Legrain P, Benarous R, Blot G, Lassot I;

XX WPI; 2002-508795/54.

DR N-PSDB; ABR6903.

PT Protein-protein complexes for screening drugs or agents that modulate
 PT interaction of proteins, e.g. for identifying the Selected Interacting
 XX Domains (SID), comprises interaction between beta-TrCP and Ras SFI -
 PS
 XX Claim 1; Page 47; 84pp; English.

CC The present invention relates to a new complex of protein-protein
 CC interaction between betaTrCP (not defined in specification) and Ras SFI.
 CC The protein-protein complex of the invention is useful for screening
 CC drugs or agents that modulate interaction of proteins. In particular,
 CC the protein complex is useful for identifying the Selected Interacting
 CC Domains (SID). The modulating compounds detected can be used for
 CC treating tumours. The polynucleotides encoding the protein complex may
 CC be used in gene therapy. The present amino acid sequence represents the
 CC human beta TrCP (bTrCP) protein that was used in the methods of the
 CC invention as a bait protein.
 XX
 SQ Sequence 219 AA;

Query Match 100.0%; Score 240; DB 23; Length 219;
 Best Local Similarity 100.0%; Pred. No. 3.0e-23;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 ALPARGLDHIAENILSYLDKSLCAAEIYCKEYRVTSIDGMLMK 45
 DB 147 ALPARGLDHIAENILSYLDKSLCAAEIYCKEYRVTSIDGMLMK 191

RESULT 3

ID AAB48289 standard; Protein; 448 AA.

AC AAB48289;

DT 02-APR-2001 (first entry)

DE Beta-TrCP.N/SKP2.C protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.

OS Synthetic.

PN MO200075184-A1.

PD 14-DEC-2000.

PF 05-JUN-2000; 2000MO-US15449.

PR 04-JUN-1999; 99US-0137494.

PA (UYVA) UNIV YALE.

PI Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

DR N-PSDB; AAC84601.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 XX proteins 1, 2 and cullin/CDC53 proteins -

PS Claim 5; Page 109-111; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.

SQ Sequence 448 AA;

Query Match 100.0%; Score 240; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 8.1e-23;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPARGIDHIAENILSYLDAKSLCAELVCKEWMYRVTSQGLMKK 45
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ALPARGIDHIAENILSYLDAKSLCAELVCKEWMYRVTSQGLMKK 165

RESULT 4
 AAY24054
 ID AAY24054 standard; Protein; 569 AA.

AC AAY24054;

XX 30-SEP-1999 (first entry)

DE A human beta-transducin repeat containing protein.

KM Beta-transducin repeat containing protein; beta-Trcp; Skrip.
 KM proteosome degradation pathway; Vpu protein; beta-catenin;
 KM human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;
 KM ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
 KM antiviral; antitumour; cell cycle regulation; protein degradation;
 KM and anti-inflammatory; osteo-articular inflammation; acute inflammation;
 KM tumour necrosis factor.

OS Homo sapiens.

XX Location/Qualifiers

PH Key 147..191

FT Region /note="F box sequence"

FT Region 259..292

FT Region /note="WD motif"

FT Region 304..332

FT Region /note="WD motif"

FT Region 343..372

FT Region /note="WD motif"

FT Region 387..415

FT Region /note="WD motif"

FT Region 427..455

FT Region /note="WD motif"

FT Region 467..492

FT Region /note="WD motif"

FT Region 516..544

FT Region /note="WD motif"

XX WO938969-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-FR00196.

XX 09-DEC-1998; 98FR-0015545.

XX 30-JAN-1998; 98FR-0001100.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (INSP) INST PASTEUR.

XX Azenana Seisdedos F, Benarous R, Concorde J, Durand H;
 PI Kroll M, Margotlin F;

XX WPI: 1999-469329/39.

XX N-PSDB; AAX86501.

PT New human beta-transducin repeat containing protein and its
 PT fragments useful as, or to screen for, antiviral, antitumour,
 PT anti-inflammatory and anti-Alzheimer's agents

PS Claim 1; Page 60-61; 71pp; French.

CC The present sequence represents a human beta-transducin repeat containing

CC protein (beta-Trcp). The protein directs proteins to the proteosome

CC degradation pathways. The protein is able to interact with the Vpu

CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins

CC Ikappab or beta-catenin (bc) and/or protein Skrip. The protein controls
 CC ubiquitinylation of phosphorylated proteins and thus their targeting to
 CC proteosomes for degradation. Depending on whether the process is
 CC inhibited or promoted, the result may be delayed breakdown of CD4 (in
 CC cases of HIV-1 infection); increased degradation of mutant bc in tumour
 CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
 CC patients. The beta-Trcp protein, and its active peptide fragments, or its
 CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
 CC antitumour agents that disrupt cell cycle regulation or protein
 CC degradation in human tumour cells, and anti-inflammatory agents that
 CC disrupt activation by NFkappab. Fragments of the protein are also
 CC useful for treating osteo-articular inflammation or acute inflammation
 CC associated with release of tumour necrosis factor.

XX Sequence 569 AA;

XX Query Match 100.0%; Score 240; DB 20; Length 569;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-22;

XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPARGIDHIAENILSYLDAKSLCAELVCKEWMYRVTSQGLMKK 45
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 147 ALPARGIDHIAENILSYLDAKSLCAELVCKEWMYRVTSQGLMKK 191

RESULT 5

XX AAB12812 standard; Protein; 569 AA.

XX AAB12812;

XX 27-NOV-2000 (first entry)

XX Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

XX Ubiquitin ligase SCF complex; F-box protein; ubiquitinylation; Ikappab;

XX beta-catenin; Skrip; Cull; F-box motif; WD40 repeat motif; FWD1;

XX gene therapy; colon cancer; beta-transducin repeat containing protein;

XX beta-Trcp.

XX Mus musculus.

XX JP2000166542-A.

XX 20-JUN-2000.

XX 02-DEC-1998; 98JP-0343437.

XX 02-DEC-1998; 98JP-0343437.

XX (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

XX WPI: 2000-485550/43.

XX N-PSDB; AAB13131.

XX F-box protein of ubiquitin ligase SCF complex which promotes the

XX ubiquitinylation of Ikappab or beta-catenin

XX Claim 2; Page 9-10; 19pp; Japanese.

XX The present invention describes an F-box motif protein of ubiquitin

XX ligase SCF complex which promotes the ubiquitinylation of Ikappab or

XX beta-catenin and is constituted by Skp1 protein, Cull protein and a

XX complex (SCF complex) of F-box protein containing F-box motif and WD40

XX repeat motif and has the amino acid sequence of 45 residues (AAB12811)

XX or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin

XX ligase FWD1 protein) and (AAB12813, which is human beta-transducin

XX repeat containing protein (beta-Trcp)). The F-box protein can be used for

XX the gene therapy of colon cancer by being recombined to a virus vector.

XX Sequence 569 AA;

Query Match 100.0%; Score 240; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1,1e-22;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 45
 DB 147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 191

RESULT 6
 AAB12813

ID AAB12813 standard; protein; 569 AA.

AC AAB12813;

DT 27-NOV-2000 (first entry)

DE Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.

KW Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-TrCP.

OS Homo sapiens.

PN JP200016542-A.

PD 20-JUN-2000.

PF 02-DEC-1998; 98JP-0343437.

PR 02-DEC-1998; 98JP-0343437.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR WPI: 2000-485550/43.

DR N-PSDB; AAA73132.

PT F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin

PS Claim 3; Page 10-12; 19pp; Japanese.

CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and a
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FWD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.

SQ Sequence 569 AA;

Query Match 100.0%; Score 240; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1,1e-22;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 45
 DB 147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 191

RESULT 7

ID AAY96697 standard; protein; 569 AA.

AC AAY96697;

DT 26-SEP-2000 (first entry)

DE Human beta-TrCP.

KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
 KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
 KW anti-inflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.

PN WO200034447-A2.

PD 15-JUN-2000.

PF 10-DEC-1999; 99WO-US29371.

PR 10-DEC-1998; 98US-0210060.

PA (SIGN-) SIGNAL PHARM INC.
 (YISS) YISSUM RES & DEV CO.

PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A,
 PI Layon I, Yaron A;

DR WPI: 2000-431294/37.

DR N-PSDB; AAA51229.

PT Polypeptide enhancing phosphorylated Ikappab ubiquitination useful for
 PT treating disorder associated with NF-kappa-B activation e.g. cancer,
 PT comprising amino acid sequence of human E3 ubiquitin ligase or its
 PT variant

PS Claim 21; Page 72-74; 77pp; English.

CC Human beta-TrCP, an F-box/WD protein family member, has been shown to
 CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
 CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
 CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
 CC degradation via the ubiquitin pathway is useful for identifying
 CC modulators of this process for use in treating diseases associated with
 CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
 CC the F-box results in a protein that functions as a dominant negative
 CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a
 CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
 CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
 CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
 CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
 CC inflammatory diseases, autoimmune diseases, cancer and viral infections.

SQ Sequence 569 AA;

Query Match 100.0%; Score 240; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1,1e-22;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 45
 DB 147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSIDGMIMRK 191

RESULT 8

ID AAY83041 standard; protein; 569 AA.

AC AAY83041;

DT 16-AUG-2000 (first entry)

DE F-box protein FBP-1.

KW F-box protein: FBP; diagnosis; treatment; screening; agonist;
 KW antagonist; proliferative disorder; differentiative disorder;
 KW breast cancer; prostate cancer; ovarian cancer; cancer;
 KW small cell lung carcinoma; immune disorder; cardiovascular disorder;
 KW inflammatory disorder; human.

XX OS Homo sapiens.
 XX PA WO200012679-A1.
 XX PN 09-MAR-2000.
 XX PD 27-AUG-1999; 99WO-US19560.
 XX PF 28-AUG-1998; 98US-0098355.
 XX PR 03-FEB-1999; 99US-0118568.
 XX PR 15-MAR-1999; 99US-0124449.
 XX PA (UNIV) UNIV NEW YORK STATE.
 XX PI Chlaur DS, Pagano M, Latres E;
 XX DR WPI: 2000-256635/22.
 XX DR N-PSDB; AA293350.
 XX PT Novel nucleic acid for screening compounds useful for treating
 XX PT proliferative and differentiative disorders such as cancer and immune
 XX PT disorders comprises sequences encoding ubiquitin ligases
 XX PS Disclosure: Figure 3a; 245pp; English.
 XX CC Nucleic acids encoding substrate-targeting subunits of ubiquitin
 XX CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 XX CC of proliferative and differentiated related disorders by measuring
 XX CC FBP gene expression. Cells expressing such proteins or
 XX CC their fragments are useful for screening compounds. The compounds
 XX CC are agonists or antagonists, which are useful for treating a,
 XX CC proliferative or differentiative disorder in a mammal, such as
 XX CC breast, ovarian and prostate cancer and small cell lung carcinoma
 XX CC and also major opportunistic infections, immune disorders,
 XX CC cardiovascular diseases and inflammatory disorders. FBP protein,
 XX CC analogs, derivatives and their subsequences, anti-FBP antibodies
 XX CC are also useful in diagnosis of the disorders.
 XX SO Sequence 569 AA;
 XX
 Query Match 100.0%; Score 240; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1,1e-22;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 45
 DB 147 ALPARGLDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 191
 RESULT 9
 AA83250
 ID AA83250 standard; Protein: 569 AA.
 XX
 AC AA83250;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE F-box protein hBetarCP.
 XX
 OS Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 XX KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 XX human.
 XX
 OS Homo sapiens.
 XX
 PN WO200022110-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23705.
 XX

PR 09-OCT-1998; 98US-0103787.
 XX (HARD) HARVARD COLLEGE.
 XX PI Zhou P, Howley P;
 XX DR WPI: 2000-317970/27.
 XX DR N-PSDB; AA293710.
 XX PT Targeting degradation of polypeptide useful for treating cancer and
 XX PT other proliferative disorders, involves conjugating polypeptide with
 XX PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 XX PT compound
 XX PS Claim 9; Page 171; 185pp; English.
 XX
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.
 XX SO Sequence 569 AA;
 XX
 Query Match 100.0%; Score 240; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1,1e-22;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 45
 DB 147 ALPARGLDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 191
 RESULT 10
 AA83254
 ID AA83254 standard; Protein: 569 AA.
 XX
 AC AA83254;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE F-box protein FWDLP.
 XX
 OS Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 XX KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 XX mouse; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200022110-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23705.
 XX
 PR 09-OCT-1998; 98US-0103787.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Zhou P, Howley P;

	Query Match	100.0%	Score 240;	DB 21;	Length 569;
	Best Local Similarity	100.0%	Preu. No. 1.le-22;		
	Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ALPARGDHTAENITLSYIDAKSISCAAEIYCKWYRVISDGLMKR	45		
DB	147	ALPARGDHTAENITLSYIDAKSISCAAEIYCKWYRVISDGLMKR	191		

RESULT	11
AAV44249	
ID	AAV44249 standard; Protein; 569 AA.
XX	
AC	AAV44249;
XX	
DT	28-FEB-2000 (first entry)
XX	
DE	Human cell signalling protein-12.
XX	
KW	Cell signalling protein-12; CSRG-12; cell proliferation;
KW	Inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS
XX	arteriosclerosis; Addison's disease; multiple sclerosis.
OS	Homo sapiens.
XX	

	Location/Qualifiers
FT FT FT	Modified-site 19 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 39 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 91 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 109 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 162 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 266 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 288 /note= "Potential phosphorylation site"
FT FT FT	Modified-site 38 /note= "Potential phosphorylation site"

FT	Modified-site	376	/note= "Potential phosphorylation site"
FT	Modified-site	381	/note= "Potential phosphorylation site"
FT	Modified-site	411	/note= "Potential phosphorylation site"
FT	Modified-site	418	/note= "Potential phosphorylation site"
FT	Modified-site	451	/note= "Potential phosphorylation site"
FT	Modified-site	514	/note= "Potential phosphorylation site"
FT	Modified-site	519	/note= "Potential phosphorylation site"
FT	Modified-site	535	/note= "Potential phosphorylation site"
FT	Modified-site	536	/note= "Potential phosphorylation site"
FT	Modified-site	17	/note= "Potential phosphorylation site"
FT	Modified-site	77	/note= "Potential glycosylation site"
FT	Modified-site	416	/note= "Potential glycosylation site"
FT	Modified-site	320..334	/note= "Potential glycosylation site"
FT	Region	360..374	/label= Signature_sequence
FT	Region	403..417	/label= Signature_sequence
FT	Region	443..457	/label= Signature_sequence
FT	Region	483..497	/label= Signature_sequence
FT	Region	532..546	/label= Signature_sequence
PN	W0958558-A2.		
XX	18-NOV-1999.		
XX	13-MAY-1999;	99MO-US10567.	
PR	13-MAY-1998;	98US-0085343.	
XX	26-AUG-1998;	98US-0098010.	
PA	(INCY-) INCYTE PHARM INC.		
PI	Bandman O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C;		
PI	Baughn MR, Yang J;		
DR	WPI: 2000-086432/07.		
DR	N-PDSB; AA29233.		
XX	Human cell signaling proteins useful for, e.g. diagnosing cell		
PT	proliferative and inflammatory disorders		
PS	Claim 1; Page 77-78; 90pp; English.		
XX			
CC	The present sequence is cell signalling protein-12 (CSIGP-12) encoded		
CC	by cDNA obtained from Incyte clone 3239149 of COLAUCT01 library. It is		
CC	expressed in musculoskeletal, gastrointestinal and nervous tissues and		
CC	found to be homologous to beta-transducin repeats containing		
CC	protein. Fragments of CSIGP encoding nucleic acid can be used as		
CC	hybridisation probe for detecting CSIGP related sequences or allelic		
CC	variants. Recombinant CSIGP can be produced in host cells by transforming		
CC	them with genetically engineered vectors. Agonists or antagonists can be		
CC	used in the treatment of cell proliferative and inflammatory disorders		
CC	associated with decreased or increased CSIGP expression. CSIGP is used in		
CC	like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory		
CC	disorders like AIDS, Addison's disease, multiple sclerosis, etc.		
XX			

SQ Sequence 569 AA;
Query Match 100.0%; Score 240; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 45;
147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 191

Db 147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 191

RESULT 12
AAB48298
ID AAB48298 standard; protein; 569 AA.
XX
AC AAB48298;
XX
DT 02-APR-2001 (first entry)
XX
DE Human ZF11 protein.
XX
KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytostatic.
XX
OS Homo sapiens.
XX
PN MO200075184-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-US15449.
XX
PR 04-JUN-1999; 99US-0137494.
XX
PI (UYA) UNIV YALE.
XX
PI Zhang H, Tsvetkov LM, Kondo T;
XX
DR WPI: 2001-061703/07.
XX
DR N-PSDB: AAC84610.
XX
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins -
XX
PS Claim 3; Page 130-132; 162pp; English.
XX
CC The invention relates to methods of altering the polypeptide levels in a
CC cell, using proteins selected from S-phase kinase associated proteins 1
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC cullin/CDC53 family of proteins). The method is useful for altering the
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC that modulate interactions between SKP and target proteins are useful for
CC treating tumours.
XX
SQ Sequence 569 AA;
Query Match 100.0%; Score 240; DB 22; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 45
147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 191

Db 147 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 191

RESULT 13
AAM78583
ID AAM78583 standard; protein; 579 AA.
XX
AC AAM78583;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1245.
XX
KW Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Zhang Y, Ren F, Chen R, Wang ZM;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
XX
DR N-PSDB: AAK51716.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3504-3505; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 579 AA;
Query Match 100.0%; Score 240; DB 22; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 45
157 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 201

Db 157 ALPARGLDHIAENILSYLDAKSLCAAEIVCKEMRYVTSQGLMKK 201

RESULT 14
AAM00847
ID AAM00847 standard; protein; 590 AA.
XX
AC AAM00847;
XX

```

XX 01-OCT-2001 (first entry)
DT
XX
DE Human bone marrow protein, SEQ ID NO: 210.
XX
KW Human; bone marrow; antiinflammatory; cyostatic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
XX
OS Homo sapiens.
XX
PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000MO-US34960.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 30-NOV-2000; 2000US-0250583.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Drmanac RT;
XX
DR WPI: 2001-488707/53.
DR N-PSDB: AAH89966.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT for treating e.g. cancer and immune deficiency disorders -
XX
PS Claim 10; Page 354-355; 648bp; English.
XX
CC The present sequence is one of 251 novel human polypeptides encoded
CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, or may result from a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one
CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.
XX
SQ Sequence 590 AA;

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Query Match 100.0%; Score 240; DB 22; Length 590;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALPARGDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 45
Db 168 ALPARGDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 212

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RESULT 15
ID AAM78582 standard; Protein: 605 AA.
XX
AC AAM78582;

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XX 06-NOV-2001 (first entry)
DT
XX
DE Human protein SEQ ID NO 1244.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZM;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB: AAK51715.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3503-3504; 6221bp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 605 AA;

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Query Match 100.0%; Score 240; DB 22; Length 605;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ALPARGDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 45
Db 183 ALPARGDHIAENILSYLDAKSLCAELVCKEWRVTSQGLMKK 227

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Search completed: April 11, 2003, 11:48:12
Job time : 14.8672 secs

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Fri Apr 11 13:31:07 2003

us-09-601-168b-2_copy_147_191.rai

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 4.65895 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191
Perfect score: 240
Sequence: 1 ALPARGLDHIAENILSYDLA.....AEVCKEWYRTSDGMLMK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237	98.8	517	1	US-08-190-802A-30 Sequence 30, Appl
2	237	98.8	517	4	US-08-477-346-30 Sequence 30, Appl
3	237	98.8	517	4	US-08-473-089-30 Sequence 30, Appl
4	237	98.8	517	4	US-08-487-072A-30 Sequence 30, Appl
5	226	94.2	42	4	US-09-172-841-1 Sequence 1, Appl
6	91	37.9	640	4	US-09-177-165A-30 Sequence 30, Appl
7	77	32.1	519	4	US-09-172-841-55 Sequence 37, Appl
8	73	30.4	38	4	US-09-172-841-37 Sequence 4, Appl
9	72.5	30.2	435	2	US-08-531-439B-4 Sequence 13, Appl
10	69	28.7	38	4	US-09-172-841-13 Sequence 13, Appl
11	68	28.3	33	4	US-09-172-841-29 Sequence 29, Appl
12	67	27.9	33	4	US-09-172-841-39 Sequence 39, Appl
13	65.5	27.3	35	4	US-09-172-841-19 Sequence 19, Appl
14	65	27.1	38	4	US-09-172-841-33 Sequence 33, Appl
15	64	26.7	38	4	US-09-172-841-15 Sequence 15, Appl
16	64	26.7	78	4	US-08-905-223-416 Sequence 416, Appl
17	63.5	26.5	35	4	US-09-172-841-21 Sequence 21, Appl
18	61	25.4	456	4	US-09-172-841-51 Sequence 51, Appl
19	58	24.2	38	4	US-09-172-841-3 Sequence 3, Appl
20	57	23.8	38	4	US-08-944-483-46 Sequence 47, Appl
21	57	23.8	234	4	US-08-944-483-46 Sequence 27, Appl
22	56	23.3	40	4	US-09-172-841-27 Sequence 15, Appl
23	53.5	22.3	321	4	US-09-166-350-15 Sequence 23, Appl
24	52	21.7	38	4	US-09-172-841-23 Sequence 41, Appl
25	51.5	21.5	43	4	US-09-172-841-41 Sequence 12, Appl
26	51	21.2	120	4	US-09-173-151A-12 Sequence 147, Appl
27	51	21.2	182	1	US-08-127-954-147 Sequence 147, Appl

28	51	21.2	216	4	US-08-914-375C-19 Sequence 19, Appl
29	51	21.2	324	1	US-08-597-236-10 Sequence 10, Appl
30	51	21.2	406	4	US-08-746-682A-10 Sequence 10, Appl
31	51	21.2	324	4	US-09-171-699-4 Sequence 4, Appl
32	51	21.2	406	5	PCT-US94-02107-2 Sequence 14, Appl
33	51	21.2	610	4	US-09-173-151A-14 Sequence 16, Appl
34	51	21.2	614	4	US-09-173-151A-16 Sequence 16, Appl
35	51	21.2	701	2	US-08-533-669A-16 Sequence 16, Appl
36	51	21.2	701	4	US-09-183-861-16 Sequence 14, Appl
37	51	21.2	701	4	US-09-022-765-16 Sequence 14, Appl
38	50.5	21.0	106	2	US-08-820-825-14 Sequence 14, Appl
39	50.5	21.0	106	4	US-09-307-817-14 Sequence 14, Appl
40	50.5	21.0	106	4	US-09-734-036-14 Sequence 2, Appl
41	50.5	21.0	107	1	US-08-409-731A-2 Sequence 2, Appl
42	50.5	21.0	107	2	US-08-470-298B-2 Sequence 2, Appl
43	50.5	21.0	107	2	US-09-023-073A-2 Sequence 2, Appl
44	50.5	21.0	107	4	US-09-361-737-2 Sequence 57, Appl
45	50.5	20.8	39	4	US-09-172-841-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESS: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabbio, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-190-802A-30

Query Match 98.8%, Score 237, DB 1, Length 517;
Best local Similarity 97.8%, Pred. No. 4.3e-24;
Matches 44, Conservative 1, Mismatches 0, Gaps 0;

Db 112 ALPARGDHAENILSYLDAKSLCSAEVCKEYRVTSDGMLMK 156

RESULT 2

US-08-477-346-30
Sequence 30, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeol
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match 98.8%; Score 237; DB 4; Length 517;
Best Local Similarity 97.8%; Pred. No. 4.3e-24;
Matches 44; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGDHAENILSYLDAKSLCSAEVCKEYRVTSDGMLMK 45
Db 112 ALPARGDHAENILSYLDAKSLCSAEVCKEYRVTSDGMLMK 156

RESULT 3

US-08-473-089-30
Sequence 30, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeol
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 98.8%; Score 237; DB 4; Length 517;
Best Local Similarity 97.8%; Pred. No. 4.3e-24;
Matches 44; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGDHAENILSYLDAKSLCSAEVCKEYRVTSDGMLMK 45
Db 112 ALPARGDHAENILSYLDAKSLCSAEVCKEYRVTSDGMLMK 156

RESULT 4

US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeol
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0753 30:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match          98.8%; Score 237; DB 4; Length 517;
Best Local Similarity 97.8%; Pred. No. 4,3e-24;
Matches 44; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRVTSQGLMK 45
DB 112 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRVTSQGLMK 156

RESULT 5
US-09-172-841-1
; Sequence 1, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-1

Query Match          94.2%; Score 226; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPARGLDHIAENILSYLDAKSLCAELVCKEYRVTSQGLMK 43
DB 1 LPARGLDHIAENILSYLDAKSLCAELVCKEYRVTSQGLMK 42

RESULT 6
US-09-177-165A-30
; Sequence 30, Application US/09177165A
; Patent No. 6426205
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; FILE REFERENCE: 11757.10US01
; CURRENT APPLICATION NUMBER: US/09/177,165A
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 640

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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

Query Match          37.9%; Score 91; DB 4; Length 640;
Best Local Similarity 50.0%; Pred. No. 0.00033;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 ILSTYDAKSLCAELVCKEYRVTSQGLMK 43
DB 195 ILSTYDCQSLCNAQVCKRMKQLADDDRW 224

RESULT 7
US-09-172-841-55
; Sequence 55, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-55

Query Match          32.1%; Score 77; DB 4; Length 519;
Best Local Similarity 34.9%; Pred. No. 0.02;
Matches 15; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

QY 6 GLDHIAE----NLSTYDAKSLCAELVCKEYRVTSQGLMK 44
DB 32 GLTHLPPEVWLSTFYLNPQLRCQSVSKMSQLTKTGLMK 74

RESULT 8
US-09-172-841-37
; Sequence 37, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-37

Query Match          30.4%; Score 73; DB 4; Length 38;
Best Local Similarity 53.3%; Pred. No. 0.003;
Matches 16; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 14 ILSTYDAKSLCAELVCKEYRVTSQGLMK 43
DB 9 ILSTYDAVSLQAQVNRKNNMELASDVLW 38

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RESULT 9

US-08-531-439B-4
Sequence 4, Application US/08531439B
Patent No. 5981702

GENERAL INFORMATION:

APPLICANT: Zhang, Hui
APPLICANT: Beach, David
TITLE OF INVENTION: Cyclin/CDK Associated Proteins,
and Uses Related Thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE:

Foley, Hoag & Elliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/531,439B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-006.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-531-439B-4

Query Match

Best Local Similarity 30.2%; Score 72.5; DB 2; Length 435;
Matches 14; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

QY 23 LCAAEI---VCKEMYVTSQGMWK 44
DB 124 LCLPELKVSGCKRWYLADESLWQ 150

RESULT 10

US-09-172-841-13
Sequence 13, Application US/09172841
Patent No. 6232081

GENERAL INFORMATION:

APPLICANT: Harper, Jeffrey W.
APPLICANT: Ellledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13
US-09-172-841-13
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens

Query Match

Best Local Similarity 28.7%; Score 69; DB 4; Length 38;
Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Matches 12; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 13 NILSLDAKSLCAAEIYCKEMYRVTSQGMW 43
DB 8 SIFSILNPQLCRCSQVSMKWSQLTKGSLW 38

RESULT 11

US-09-172-841-29
Sequence 29, Application US/09172841
Patent No. 6232081

GENERAL INFORMATION:

APPLICANT: Harper, Jeffrey W.
APPLICANT: Ellledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 33
TYPE: PRT
ORGANISM: Mus musculus
US-09-172-841-29

Query Match
Best Local Similarity 28.3%; Score 68; DB 4; Length 33;
Matches 15; Conservative 2; Mismatches 11; Indels 4; Gaps 1;

QY 2 LPARGLDHIAENILSYLDAKSLCAAEIYCKEW 33
DB 1 LPA---LITKIFSQLDIRSICRASLTGRSW 28

RESULT 12

US-09-172-841-39
Sequence 39, Application US/09172841
Patent No. 6232081

GENERAL INFORMATION:

APPLICANT: Harper, Jeffrey W.
APPLICANT: Ellledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 38
TYPE: PRT
ORGANISM: Mus musculus
US-09-172-841-39

Query Match
Best Local Similarity 27.9%; Score 67; DB 4; Length 38;
Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 10 IAEHILSYLDAKSLCAAEIYCKEMYRVTSQGMW 43
DB 5 ILVKILSYLDAVTLVCGVSRFRYHLADNDLIW 38

RESULT 13

US-09-172-841-19
Sequence 19, Application US/09172841
Patent No. 6232081

GENERAL INFORMATION:

APPLICANT: Harper, Jeffrey W.

APPLICANT: Ellledge, Stephen J.
 TITLE OF INVENTION: F-BOX PROTEINS AND GENES
 FILE REFERENCE: BCM-03510
 CURRENT APPLICATION NUMBER: US/09/172,841
 CURRENT FILING DATE: 1998-10-15
 EARLIER APPLICATION NUMBER: 08/951,621
 EARLIER FILING DATE: 1997-10-16
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO: 19
 LENGTH: 35
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-172-841-19

Query Match 27.3%; Score 65.5; DB 4; Length 35r
 Best Local Similarity 46.7%; Pred. No. 0.029; 9; Indels 3; Gaps 1;
 Matches 14; Conservative 4; Mismatches 9;

OY 14 ILISYDAKSLCAAEIYCKEYRVTSDGMLW 43
 DB 9 ILISYLAATDCLASCY---MODLANDELLW 35

RESULT 14
 US-09-172-841-33
 Sequence 33; Application US/09172841
 Patent No. 6232081
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeffrey W.
 APPLICANT: Ellledge, Stephen J.
 TITLE OF INVENTION: F-BOX PROTEINS AND GENES
 FILE REFERENCE: BCM-03510
 CURRENT APPLICATION NUMBER: US/09/172,841
 EARLIER APPLICATION NUMBER: 08/951,621
 EARLIER FILING DATE: 1998-10-15
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO: 33
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-172-841-33

Query Match 27.1%; Score 65; DB 4; Length 38;
 Best Local Similarity 36.1%; Pred. No. 0.037; 18; Indels 0; Gaps 0;
 Matches 13; Conservative 5; Mismatches 18;

OY 8 DHTAENILSYLDAKSLCAAEIYCKEYRVTSDGMLW 43
 DB 3 DSIYVQIFILSLGPADYLAAGLVCRQWQAVSRDEFILW 38

RESULT 15
 US-09-172-841-15
 Sequence 15; Application US/09172841
 Patent No. 6232081
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeffrey W.
 APPLICANT: Ellledge, Stephen J.
 TITLE OF INVENTION: F-BOX PROTEINS AND GENES
 FILE REFERENCE: BCM-03510
 CURRENT APPLICATION NUMBER: US/09/172,841
 CURRENT FILING DATE: 1998-10-15
 EARLIER APPLICATION NUMBER: 08/951,621
 EARLIER FILING DATE: 1997-10-16
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Mus musculus

US-09-172-841-15

Query Match 26.7%; Score 64; DB 4; Length 38;
 Best Local Similarity 35.5%; Pred. No. 0.05; 14; Indels 0; Gaps 0;
 Matches 11; Conservative 6; Mismatches 14;

OY 13 NILSYLDAKSLCAAEIYCKEYRVTSDGMLW 43
 DB 8 SIFSILNPDELRCRCQSVTRKMSQIAKTGSLW 38

Search completed: April 10, 2003, 12:51:17
 Job time : 6.65895 secs

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GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 4.60414 Seconds
(Without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191

Perfect score: 240

Sequence: 1 ALPARGLDHIENILSYLDA.....AEVCKEYRVTSIDGMLMK 45

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Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	240	100.0	219	9 US-10-023-530-2	Sequence 2, Appli
2	240	100.0	569	9 US-10-038-010-8	Sequence 8, Appli
3	240	100.0	569	12 US-10-042-417-2	Sequence 2, Appli
4	231	96.2	43	12 US-10-042-417-15	Sequence 15, Appli
5	210	87.5	265	9 US-10-116-016-30	Sequence 30, Appli
6	210	87.5	265	10 US-09-764-848-30	Sequence 30, Appli
7	91	37.9	9	9 US-10-060-019-30	Sequence 30, Appli
8	83	34.6	39	12 US-10-042-417-71	Sequence 71, Appli
9	83	34.6	483	12 US-10-042-417-48	Sequence 48, Appli
10	79	32.9	678	10 US-09-801-368-314	Sequence 314, App
11	78	32.5	197	12 US-10-042-417-32	Sequence 32, Appli
12	77	32.1	590	12 US-10-042-417-52	Sequence 52, Appli
13	77	31.7	39	12 US-10-042-417-64	Sequence 64, Appli
14	74	30.8	39	12 US-10-042-417-73	Sequence 73, Appli
15	72.5	30.2	39	12 US-10-042-417-22	Sequence 22, Appli
16	70	29.2	540	9 US-09-213-888-7	Sequence 7, Appli
17	70	29.2	540	9 US-09-213-888-10	Sequence 10, Appli
18	70	29.2	540	9 US-09-328-877A-7	Sequence 7, Appli
19	70	29.2	540	9 US-09-328-877A-10	Sequence 10, Appli

20	70	29.2	545	9 US-09-213-888-6	Sequence 6, Appli
21	70	29.2	545	9 US-09-328-877A-6	Sequence 6, Appli
22	70	29.2	553	9 US-09-213-888-5	Sequence 5, Appli
23	70	29.2	553	9 US-09-328-877A-5	Sequence 5, Appli
24	70	29.2	559	9 US-09-213-888-9	Sequence 9, Appli
25	70	29.2	559	9 US-09-328-877A-9	Sequence 9, Appli
26	70	29.2	589	9 US-09-213-888-8	Sequence 8, Appli
27	70	29.2	589	9 US-09-328-877A-8	Sequence 8, Appli
28	70	29.2	592	9 US-09-213-888-4	Sequence 4, Appli
29	70	29.2	592	9 US-09-328-877A-4	Sequence 4, Appli
30	70	29.2	626	9 US-09-213-888-21	Sequence 21, Appli
31	70	29.2	626	9 US-09-328-877A-21	Sequence 21, Appli
32	70	29.2	627	9 US-09-213-888-3	Sequence 3, Appli
33	70	29.2	627	9 US-09-328-877A-3	Sequence 3, Appli
34	70	29.2	666	9 US-09-213-888-27	Sequence 27, Appli
35	70	29.2	666	9 US-09-328-877A-27	Sequence 27, Appli
36	70	29.2	669	9 US-09-213-888-25	Sequence 25, Appli
37	70	29.2	669	9 US-09-328-877A-25	Sequence 25, Appli
38	66.5	27.7	36	12 US-10-042-417-61	Sequence 61, Appli
39	66.5	27.7	319	9 US-10-028-072-134	Sequence 134, App
40	66.5	27.7	319	9 US-10-121-049-134	Sequence 134, App
41	66.5	27.7	319	9 US-10-123-904-134	Sequence 134, App
42	66.5	27.7	319	9 US-10-140-470-134	Sequence 134, App
43	66.5	27.7	319	9 US-10-175-746-134	Sequence 134, App
44	66.5	27.7	319	9 US-10-176-918-134	Sequence 134, App
45	66.5	27.7	319	9 US-10-176-921-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-10-023-530-2
Sequence 2, Application US/10023530
Publication No. US20030007956A1
GENERAL INFORMATION:
APPLICANT: LEBERAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BIOT, Guillaume
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TRCP
FILE REFERENCE: B4717A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: BetaTRCP
LOCATION: (1)..(219)
OTHER INFORMATION: F-box protein
US-10-023-530-2

Query Match Score 240; DB 9; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.2e-25;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIENILSYLDAKSLCAAEVCKEYRVTSIDGMLMK 45
DB 147 ALPARGLDHIENILSYLDAKSLCAAEVCKEYRVTSIDGMLMK 191
RESULT 2
US-10-038-010-8
Sequence 8, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS

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APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta-TICP1
LOCATION: (1)..(569)
OTHER INFORMATION:
US-10-038-010-8
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Query Match
Best local Similarity 100.0%; Score 240; DB 9; Length 569;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 45
DB 147 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 191
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RESULT 3
US-10-042-417-2
Sequence 2, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
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APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2
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Query Match
Best local Similarity 100.0%; Score 240; DB 12; Length 569;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 45
DB 147 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 191
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RESULT 4
US-10-042-417-15
Sequence 15, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
```

```
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 15
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-15
```

```
Query Match
Best local Similarity 96.2%; Score 231; DB 12; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 LPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 44
DB 1 LPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 43
```

```
RESULT 5
US-10-116-016-30
```

```
Sequence 30, Application US/10116016
Publication No. US20030054379A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT208C1
CURRENT APPLICATION NUMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-016-30
```

```
Query Match
Best local Similarity 87.5%; Score 210; DB 9; Length 265;
Matches 39; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 45
DB 115 ALPARGDHTAENILSYLDARSLCAELVCKEWMYRVTSDGMLMK 159
```

```
RESULT 6
US-09-764-848-30
```

```
Sequence 30, Application US/09764848
Patent No. US2002007270A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT208
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-848-30
```

```
Query Match
Best local Similarity 87.5%; Score 210; DB 10; Length 265;
Matches 39; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 ALPARGDHTAENILSYLDAKSLCAELVCKEWMYRVTSDGMLMK 45
DB 115 ALPARGDHTAENILSYLDARSLCAELVCKEWMYRVTSDGMLMK 159
```

```
RESULT 7
US-10-060-019-30
```

```
; Sequence 30, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-060-019-30

Query Match          37.9%; Score 91; DB 9; Length 640;
Best Local Similarity 50.0%; Pred. No. 0.00023;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 ILSTYDAKSLCAAEIYCKEYRYVTSQGLMK 43
Db 195 ILSTYDCOSLCNATRVCKKMKLADDDRNV 224

RESULT 8
US-10-042-417-71
; Sequence 71, Application US/10042417
; Patent No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-71

Query Match          34.6%; Score 83; DB 12; Length 39;
Best Local Similarity 37.8%; Pred. No. 0.00012;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 8 DHTAENILSTYDAKSLCAAEIYCKEYRYVTSQGLMK 44
Db 3 DHTSWOIFSELPNOLCRCARVCRRWYNLAMDRLMK 39

RESULT 9
US-10-042-417-48
; Sequence 48, Application US/10042417
; Patent No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
```

```
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-48

Query Match          34.6%; Score 83; DB 12; Length 483;
Best Local Similarity 37.8%; Pred. No. 0.0021;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 8 DHTAENILSTYDAKSLCAAEIYCKEYRYVTSQGLMK 44
Db 111 DHTSWOIFSELPNOLCRCARVCRRWYNLAMDRLMK 147

RESULT 10
US-09-801-368-314
; Sequence 314, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 314
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-801-368-314

Query Match          32.9%; Score 79; DB 10; Length 678;
Best Local Similarity 40.0%; Pred. No. 0.011;
Matches 18; Conservative 5; Mismatches 18; Indels 4; Gaps 1;

QY 1 ALPARGIDHTAENILSTYDAKSLCAAEIYCKEYRYVTSQGLMK 45
Db 183 ALP-----PEIAFKILCYLDTTSLCKASOVSRGNRLADDDVYVHR 223

RESULT 11
US-10-042-417-32
; Sequence 32, Application US/10042417
; Patent No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
```

;; CURRENT FILING DATE: 2002-01-07
;; PRIOR APPLICATION NUMBER: 60/260,179
;; PRIOR FILING DATE: 2001-01-5
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 32
;; LENGTH: 197
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-042-417-32

Query Match 32.5%; Score 78; DB 12; Length 197;
Best Local Similarity 39.5%; Pred. No. 0.0037;
Matches 15; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

Oy 8 DHAENILSYLDKSKCAAEVCKEYRYTSDGMLMK 45
Db 146 DEVYVKTFSTLEODLCRAVCCKRSESLANDPNLMKR 183
| : |||| : ||| ||| : : ||| :
US-10-042-417-52

;; Sequence 52, Application US/10042417
;; Patent No. US20020123082A1
;; GENERAL INFORMATION:
;; APPLICANT: Pagano, M.
;; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
;; FILE REFERENCE: 5914-090-999
;; CURRENT APPLICATION NUMBER: US/10/042,417
;; CURRENT FILING DATE: 2002-01-07
;; PRIOR APPLICATION NUMBER: 60/260,179
;; PRIOR FILING DATE: 2001-01-5
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 52
;; LENGTH: 590
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: all Xaa positions
;; OTHER INFORMATION: Xaa-unknown amino acid residue
US-10-042-417-52

Query Match 32.1%; Score 77; DB 12; Length 590;
Best Local Similarity 34.9%; Pred. No. 0.018;
Matches 15; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Oy 6 GLDHIAE---NILSYLDKSKCAAEVCKEYRYTSDGMLMK 44
Db 48 GITHLPEVVMISFYINPELRCRCQSVSMKWSQITKTSIMK 90
| : |||| : ||| ||| : : ||| :
US-10-042-417-64

;; Sequence 64, Application US/10042417
;; Patent No. US20020123082A1
;; GENERAL INFORMATION:
;; APPLICANT: Pagano, M.
;; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
;; FILE REFERENCE: 5914-090-999
;; CURRENT APPLICATION NUMBER: US/10/042,417
;; CURRENT FILING DATE: 2002-01-07
;; PRIOR APPLICATION NUMBER: 60/260,179
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 64
;; LENGTH: 39
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-10-042-417-64

Query Match 31.7%; Score 76; DB 12; Length 39;
Best Local Similarity 40.5%; Pred. No. 0.0011;
Matches 15; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 8 DHAENILSYLDKSKCAAEVCKEYRYTSDGMLMK 44
Db 3 DEVYVKTFSTLEODLCRAVCCKRSESLANDPNLMK 39
| : |||| : ||| ||| : : ||| :
US-10-042-417-73

;; Sequence 73, Application US/10042417
;; Patent No. US20020123082A1
;; GENERAL INFORMATION:
;; APPLICANT: Pagano, M.
;; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
;; FILE REFERENCE: 5914-090-999
;; CURRENT APPLICATION NUMBER: US/10/042,417
;; CURRENT FILING DATE: 2002-01-07
;; PRIOR APPLICATION NUMBER: 60/260,179
;; PRIOR FILING DATE: 2001-01-5
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 73
;; LENGTH: 39
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-042-417-73

Query Match 30.8%; Score 74; DB 12; Length 39;
Best Local Similarity 40.6%; Pred. No. 0.002;
Matches 13; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 13 NILSYLDKSKCAAEVCKEYRYTSDGMLMK 44
Db 8 SIFSLNPELRCRCQSVSMKWSQITKTSIMK 39
| : |||| : ||| ||| : : ||| :
US-10-042-417-22

;; Sequence 22, Application US/10042417
;; Patent No. US20020123082A1
;; GENERAL INFORMATION:
;; APPLICANT: Pagano, M.
;; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
;; FILE REFERENCE: 5914-090-999
;; CURRENT APPLICATION NUMBER: US/10/042,417
;; CURRENT FILING DATE: 2002-01-07
;; PRIOR APPLICATION NUMBER: 60/260,179
;; PRIOR FILING DATE: 2001-01-5
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 22
;; LENGTH: 39
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-042-417-22

Query Match 30.2%; Score 72.5; DB 12; Length 39;
Best Local Similarity 51.9%; Pred. No. 0.0033;
Matches 14; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

Oy 23 LCAAEV---VCKEYRYTSDGMLMK 44
Db 13 LCLPELKVSGVCKRWRYLADSESLMQ 39
| : |||| : ||| ||| : : ||| :
US-10-042-417-11

Search completed: April 10, 2003, 13:16:42
Job time : 4.60414 secs

, Fri Apr 11 13:31:07 2003

us-09-601-168b-2_copy_147_191.rapb

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 5.20706 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191

Perfect score: 240
Sequence: 1 ALPARGLDHIAENILSYLDA.....AEVCKEYRYVTSQGLMKK 45

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237	98.8	518	2 B48088	beta-transducin re
2	91	37.9	640	2 S49932	MET30 protein - ye
3	88	36.7	605	2 T38932	probable sulfur me
4	81.5	34.0	662	2 T50319	hypothetical F-box
5	80.5	33.5	775	2 T45136	WD repeat protein
6	79	32.9	506	2 T50211	WD repeat protein
7	78	32.5	197	2 G88523	truncated hypotet
8	78	32.5	489	2 S44609	hypothetical prote
9	75.5	31.5	614	2 T32441	hypothetical prote
10	75	31.2	419	2 T09902	hypothetical prote
11	74	30.8	151	2 T09884	hypothetical prote
12	72.5	30.2	435	2 T39171	hypothetical prote
13	70.5	29.4	592	2 T52139	cyclin A/CDK2-asso
14	68.5	28.5	449	2 B85069	LRR-containing F-b
15	68	28.3	324	2 B85069	hypothetical prote
16	66	27.5	304	2 G85068	hypothetical prote
17	66	27.1	411	2 T47951	hypothetical prote
18	62	25.8	418	2 T16410	hypothetical prote
19	62	25.8	431	2 T06019	sulfur controller
20	62	25.8	650	2 T46660	hypothetical prote
21	61	25.4	382	2 T45851	hypothetical prote
22	61	25.4	934	2 T05201	F-box protein FBL2
23	60	25.0	276	2 T52349	probable regulator
24	59.5	24.8	463	2 T39987	FLK23.7 protein -
25	59.5	24.8	577	2 B86261	hypothetical prote
26	59	24.6	141	2 S30832	N7-like protein [i
27	59	24.6	302	2 F83068	N7-like protein [i
28	59	24.6	307	2 A85069	hypothetical prote
29	59	24.6	701	2 T16607	hypothetical prote

30	58.5	24.4	160	2 F86283	protein T15D22.6 [
31	58.5	24.4	561	2 H86423	hypothetical prote
32	58	24.2	76	2 C43559	homeotic protein R
33	57.5	24.0	465	2 D96567	F6D8.13 (imported)
34	57	23.8	122	2 T08915	hypothetical prote
35	57	23.8	262	1 A31372	granzyme A (EC 3.4
36	57	23.8	269	2 T16487	hypothetical prote
37	57	23.8	279	2 G96545	hypothetical prote
38	57	23.8	384	2 G84482	hypothetical prote
39	57	23.8	384	2 T49128	hypothetical prote
40	57	23.8	554	2 AD1572	propanediol dehydr
41	57	23.8	554	2 A11218	hypothetical prote
42	56	23.3	475	2 T47778	hypothetical prote
43	55	22.9	188	2 C97438	conserved hypotet
44	55	22.9	188	2 AF2656	hypothetical prote
45	55	22.9	346	2 T45748	hypothetical prote

ALIGNMENTS

RESULT 1
B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trop
C:Species: Xenopus laevis (African clawed frog)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spewak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A>Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; MUID:9330289; PMID:8393141
A:Accession: B48088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SP>
A:Cross-references: GB:M98268; NID:9295542; PID:NAA02810.1; PID:9295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
E:431-462/Domain: WD repeat homology <WD1>

Query Match 98.8% Score 237; DB 2; Length 518;
Best Local Similarity 97.8%; Pred. No. 2; le-23;
Matches 44; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 45
Db 112 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 156

RESULT 2
S49932
MET30 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein Y19905.02; protein Y11046w
C:Species: Saccharomyces cerevisiae
C>Date: 26-May-1993 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
C:Accession: S49932; S43750
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, December 1994
A:Reference number: S49932
A:Accession: S49932
A:Molecule type: DNA
A:Residues: 1-640 <CODE>
A:Cross-references: GB:Z47047; EMBL:Z46861; NID:9603997; PID:9763300; MIPS:Y11046w
R:Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
A:Reference number: S43750
A:Accession: S43750
A:Molecule type: DNA
A:Residues: 1-60, '1', 62-640 <THO>
A:Cross-references: EMBL:L26505; NID:9432493; PID:9432494
C:Genetics: SOD:MET30
A:Gene: SOD:MET30

A:Cross-references: SGD:S0001308; MIPS:YIL046w
 A:Map position: 9L
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:298-329/Domain: WD repeat homology <WD1>
 F:338-369/Domain: WD repeat homology <WD2>
 F:374-409/Domain: WD repeat homology <WD3>
 F:417-450/Domain: WD repeat homology <WD4>

Query Match 37.9%; Score 91; DB 2; Length 640;
 Best Local Similarity 50.0%; Pred. No. 0.00058;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 ILSTLDKSLCAAEIYCKEYRVTSDGMW 43
 DB 195 ILSTLDKSLCAAEIYCKEYRVTSDGMW 224

RESULT 3

T38932

probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000

C:Accession: T38932
 R:Padcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, April 1997

A:Reference number: 221818
 A:Accession: T38932

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-605 <BAD>
 A:Cross-references: EMBL:Z94864; PIDN:CA08168.1; GSPDB:GN00066; SPDB:SPAC57A10.05C

A:Experimental source: strain 972h-; cosmid c57A10
 C:Genetics:
 A:Gene: SPDB:SPAC57A10.05C
 A:Map position: 1

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 36.7%; Score 88; DB 2; Length 605;
 Best Local Similarity 44.4%; Pred. No. 0.0014;
 Matches 16; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 10 IAENILSYLDKSLCAAEIYCKEYRVTSDGMW 45
 DB 117 ISFRILSFLDARSLCAQAVSKHWKRLADDDYVHR 152

RESULT 4

T50319

hypothetical F-box domain protein [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C:Accession: T50319
 R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Gallibert, F.
 submitted to the EMBL Data Library, January 2000

A:Reference number: 225061
 A:Accession: T50319

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-662 <MCD>
 A:Cross-references: EMBL:AL136536; PIDN:CA06450.1; GSPDB:GN00067; SPDB:SPAC1703.06

A:Experimental source: strain 972h(-); cosmid c1703
 C:Genetics:
 A:Gene: SPDB:SPAC1703.06
 A:Map position: 2

A:Introns: 37/1

Query Match 34.0%; Score 81.5; DB 2; Length 662;
 Best Local Similarity 30.8%; Pred. No. 0.011;
 Matches 16; Conservative 9; Mismatches 12; Indels 15; Gaps 1;

QY 8 DHIEN-----ILSYLDKSLCAAEIYCKEYRVTSDGMW 44
 DB 21 DHSSNNTNRTVNLNPKKIIILIFSPFLDPRSLSLACCTCKYMKRLSDLSMR 72

RESULT 5

T45136

WD repeat protein popl [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000

C:Accession: T45136; T40157
 R:Kohnmi, K.; Toda, T.
 submitted to the EMBL Data Library, September 1996

A:Description: fission yeast WD repeat protein popl is involved in maintenance of plo
 A:Reference number: 222925

A:Accession: T45136
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-775 <KOM>

A:Cross-references: EMBL:Y08391; PIDN:CA069671.1
 A:Experimental source: strain h-972

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1998

A:Reference number: 221842
 A:Accession: T40157

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-775 <WOO>
 A:Cross-references: EMBL:AL022103; PIDN:CA017898.1; GSPDB:GN00067; SPDB:SPAC2G2.18

A:Experimental source: strain 972h-; cosmid c262
 C:Genetics:
 A:Gene: SPAC2G2.18
 A:Map position: 2

A:Note: popl+

Query Match 33.5%; Score 80.5; DB 2; Length 775;
 Best Local Similarity 47.2%; Pred. No. 0.017;
 Matches 17; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 10 IAENILSYLDKSLCAAEIYCKEYR-VTSDGMW 44
 DB 308 ITNLVLTFLDAPSLCAVSOVSHMYKLVSSNEELW 343

RESULT 6
 T50211

WD repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000

C:Accession: T50211
 R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.

submitted to the EMBL Data Library, January 2000
 A:Reference number: 225046

A:Accession: T50211
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-506 <MCD>

A:Cross-references: EMBL:AL136538; PIDN:CA06464.1; GSPDB:GN00066; SPDB:SPAC30.05
 A:Experimental source: strain 972h(-); cosmid c30

C:Genetics:
 A:Gene: SPAC29E.01; SPDB:SPAC30.05
 A:Map position: 1

A:Introns: 43/1; 74/3
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 32.9%; Score 79; DB 2; Length 506;
 Best Local Similarity 35.1%; Pred. No. 0.018;
 Matches 13; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 8 DHIENILSYLDKSLCAAEIYCKEYRVTSDGMW 44
 DB 78 BEVSLRVFSYLDQDLCKCKMLSKRWKRLLEDPGIWK 114

RESULT 7
 G88523

truncated hypothetical protein C02F5.7 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Nov-2001
C:Accession: G88523
R:Anonymous: The *C. elegans* Sequencing Consortium.
Science 282, 2012-2018, 1996
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genoume.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published extra appeared in Science 283, 35, 1999; and
A:Accession: G88523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:chr_III; PIDN:AAB59171.1; PID:g156212; GSPDB:GN00021
A:Note: putative
C:Genetics:
A:Map position: 3

Query Match	32.5%;	Score 78;	DB 2;	Length 197;
Best Local Similarity	37.5%;	Pred. No. 0.0089;		
Matches 12; Conservative	8;	Mismatches 12;	Indels 0;	Gaps 0

```

OY      14  ILSLDAKSLCAELVCKEWMRYVTSDCMLMK 45
          : : | | | : | | : | | : | :
Db      68  VFSFLDTKALCRSAQVCRSMSTLALDGSNWR 99

```

RESULT 8

hypothetical protein C02F5.7 - *Caenorhabditis elegans*
N:Contains: hypothetical protein C30A5.1
N:Species: *Caenorhabditis elegans*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C:Accession: S44609; S44774
R:Anderson, K.
Submitted to the EMBL data library, May 1993
A:Description: Sequence of the *C. elegans* cosmid C02F5.
A:Reference number: S44603
A:Accession: S44609
A:Molecule type: DNA
A:Residues: 1-189 <AND>
A:Cross-references: EMBL:L14745; NID:g289607; PID:g289614
A:Experimental source: cosmid C02F5
R:Anderson, K.
Submitted to the EMBL Data Library, February 1993
A:Description: Sequence of the *C. elegans* cosmid C30A5.

A:Accession: Q5M4774
A:Molecule_type: DNA
A:Residues: 1-197 <ANNN>
A:Cross-references: EMBL:U10990; NID:g156211; PID:g156212
A:Experimental_source:csmsd C30A5
A:Note: designated as C30A5.1 protein
A:GeneIds: 3973
A:Interons: 67/2, 197/2; 264/3; 431/3
A:1-197/Product: hypothetical protein C30A5.1 #status predicted <CPX>

Query Match	32.5%	Score 78;	DB 2;	Length 489;
Best Local Similarity	37.5%;	Pred. No. 0.023;		
Matches 12;	Conservative	8;	Mismatches 12;	Indels 0;
			Gaps	0;

```
QY      14 ILSYLDAKSLCAELVCKEWRVTS DGLMKK 45  
       :|:|||||:|::|:|:|:  
Db     68 VFSELDFTKALCRSAQVCRSNLSILALDGSNWQR 99
```

RESULT 9

T09902
hypothetical protein T22a6.220 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: T09902

R: Brevan, M.; Zimmermann, W.; Gruenewald, A.; Mamut, R.; Bancroft, I.; Mewes, H.W. et al. submitted to the Protein Sequence Database, June 1999
A: Reference number: Z16896
A: Accession: T09902
A: Molecule type: DNA
A: Residues: 1-614 <BEV>
A: Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP: T22A6.220
A: Experimental source: cultivar Columbia; BAC clone T22A6
C: Genetics:
A: Gene: ATSP: T22A6.220
A: Map position: 4
A: Introns: 192/2; 358/3

Query Match	31.58;	Score 75.5;	DB 2;	Length 614;
Best Local Similarity	37.28;	Pred. No. 0.062;		
Matches 16; Conservative	9;	Mismatches 13;	Indels 5;	Gaps 2

QY 3 PARGLDIAENILSLDKASLC---AAELVCKEKRWRTSGML 42
|::||:|::| | |||:||||-
Db 42 PDHVLLENLNVLPFLTSR--CDRNAVSIVCRSMIRVEAQLRL 82

RESULT 10
833441

hypodermal protein T28B4.1 - *Caenorhabditis elegans*
132441
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T32441
R:Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T28B4.
A:Reference number: Z21168
A:Accession: T32441
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-419 <ML>
A:Cross-references: EMBL:AF026206; PIDD:AA87162.1; GSPDB:GN00028; CESP:T28B4.1
A:Experimental source: strain Bristol NZ; clone T28B4
C:Genetics
A:Gene: CESP:T28B4.1
A:Map position: X
A:Introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Query Match:	31.2%	Score 75:	DB 2:	Length 419:
Best Local Similarity:	44.7%	Pred. No. 0.049:		
Matches 17: Conservative	4:	Mismatches 15:	Indels 2:	Gaps 2:
OY	8	PHIAENILSYIDAKSLCAELVYCKEWMYRTSDG:MLMK	44	
		: : : : : : : : : : : : : : :		
DB	54	DKVLDDIFQYILSPKQINDVGLVCKRW:RYVSQNRLMLMK	90	

RESULT 11
T09884

C/Accession: T09884
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 04-Mar-2000
C/Species: Arabidopsis thaliana (mouse ear cress)
C/Accession: T09884

C/Accession: U03004
C/Author: Ribeyan, M.; Zimmermann, W.; Gruenelisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.
C/Title: submitted to the Protein Sequence Database, June 1999

Submitted to the Protein Data Bank
A; Reference number: 2I6896
A; Accession: T09884

A; accession: 102004
A; molecule type: DNA
A; residues: 1-151 <BEV>

A; residues: 1-121; 227-237
A; Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6
A; Experimental source: cultivar Columbia; BAC clone T22A6

A;Gene: ATSP:T22A6.40

A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical protein T22A6.40

Query Match 30.88; Score 74; DB 2; Length 151;

Best Local Similarity 32.6%; Pred. No. 0.023

QY 6 GLDHAEN----ILSYDAKSLCAELVCKEMYRTSDGMLWK 44
| :: || :: ||| : | | | : | ||:
Db 31 GFSNLDENVYEVLLKHVDAKTLAMSSCVSKIWHKTAQDERLWE 73

C:Accession: I39171
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C:Species: Homo sapiens (man)
C:cyclin A/cdk2-associated p45 - human

A;Gene: Skp2
C;Keywords: cell cycle control

A;Cross-References: EMBL:U33761; NID:g995825; PIDN:AAC50242.1; PID:g995826
C;Genetics:

QY 23 LCAAE-----VCKEYRYTSDGMLWK 44
 11 11 11 11 11 11
 Db 124 LCLPELKVSGVCKRWYRLASDESLWQ 150

Unk:containing F-box protein [imported] - Arabidopsis thaliana
 M:Alternate names: hypothenoidal protein At2g39940
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 16-Feb-2001
 C:Accession: T521319; C84823

A;status:preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-592 <XIE>
A;Cross-references: EMBL:AF036340. EMBL:AF037400.1
A;Residues: 1-592 <XIE>

A;Residues: 1-592 <Sto>
A;Cross-references: GB:AE002093; NID:g2088647; PIDD:AAB95279.1; GSPDB:GN0135
C;Genetics:
A;Gene: COIL1, At2g39940
A;Map position: 2

Query Match	29.48;	Score 70.5;	DB 2;	Length 592;
Best Local Similarity	32.48;	Pred. No. 0.28;		
Matches	11;	Conservative	12;	Mismatches 10;
				Indels 1;
				Gaps 1

D_b QY 7 LDHIAENILSYL-DAKSLCAELVCKEWMRYRTSD 39
:
17 VDDVIEQVMITYITDPKDRDSASLVCRWFKIDSE 50

hypothetical protein Atg405500 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: B85069

A:Cross-references: GR:NC_001268; NID:g7267310; PIDN:CAB81092.1; GSPDB:CN00140
C:Genetics:
A:Gene: AT4g05500
A:Map position: 4

QY 2 LPARGDHIAEINILSYLDA-KSLCAELVCKEYRYVTS DGMILMK 45
 ||: : || | : | : ||: || | : ||: |
 Db 184 LPSK----LTSSILRLGALIELQNAQVKCKRWHRYCKDPSMRK 224

C:Accession: E84505
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change

A:Cross-references: GB:AE002093; NID:g4586069, PIDD:AA02586.1, GSPDB:GN00139
A:Gene: At2g13130
A:Map position: 2
C:Genetics:

Query	Match	Similarity	Score	DB	Length
Best Local	28.3%	39.5%	68	2	324
Matches	15	Conservative	4	Mismatches	19
				Indels	0
				Gaps	0

Search completed: April 10, 2003, 13:22:59
Job time : 7.20706 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 3.2386.Seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191

Perfect score: 240
Sequence: 1 ALPARGDHTAENILSTYLA.....AEVCKEWRVTSQGLMKK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240	100.0	605	1	09Y297 homo sapien
2	237	98.8	518	1	FWIA_HUMAN
3	210	87.5	542	1	TRCB_XENLA
4	91	37.9	640	1	09ukb1 homo sapien
5	88	36.7	605	1	MT30_YEAST
6	81.5	34.0	662	1	POPI_SCHPO
7	80.5	33.5	775	1	POPI_SCHPO
8	79	32.9	506	1	POPI_SCHPO
9	79	32.9	506	1	POPI_SCHPO
10	78	32.5	461	1	YKK7_CAEEL
11	77	32.1	684	1	CC4_CANAL
12	66.5	27.7	319	1	FBX8_HUMAN
13	64.5	26.9	412	1	FBX8_MOUSE
14	64	26.7	412	1	FBX8_MOUSE
15	62	25.8	650	1	SC02_NEUCR
16	61	25.4	410	1	FBM4_MOUSE
17	59	24.6	141	1	YEFS_YEAST
18	59	24.6	522	1	FBX7_HUMAN
19	59	24.6	551	1	FBX7_HUMAN
20	59	24.6	551	1	FBX7_HUMAN
21	59	24.6	551	1	FBX7_HUMAN
22	58	24.2	76	1	GRM4_RAT
23	57	23.8	262	1	GRM4_HUMAN
24	55	22.9	422	1	FBM2_HUMAN
25	53.5	22.3	447	1	FBX9_HUMAN
26	53.5	22.3	500	1	YDAK_YEAST
27	53.5	22.3	593	1	YDAK_YEAST
28	53	22.1	318	1	MTF2_HUMAN
29	52	21.7	263	1	TRUA_BACHD
30	52	21.7	263	1	TRUA_BACHD
31	52	21.7	447	1	YLB_PSEPU
32	51.5	21.5	295	1	BAG5_HUMAN
33	51.5	21.5	332	1	FBX2_HUMAN

34	51	21.2	491	1	VIE1_HCMVA	P13202 human cytom
35	51	21.2	491	1	VIE1_HCMVA	P03169 human cytom
36	51	21.2	701	1	HS83_LEIAM	P27741 leishmania
37	51	21.2	727	1	VR22_CAEEL	009639 caenorhabd1
38	50	20.8	242	1	YBUB_PSEAE	09hw11 pseudomonas
39	50	20.8	382	1	V382_ASEFL5	P26712 african swi
40	50	20.8	493	1	V100_STRPN	097p44 streptococ
41	50	20.8	664	1	TRX7_CAEEL	023467 caenorhabd1
42	49.5	20.6	517	1	VGLG_VSVJO	P04882 vesicular s
43	49	20.4	668	1	YMI8_YEAST	004511 saccharomyc
44	48.5	20.2	134	1	RET5_HUMAN	P82980 homo sapien
45	48.5	20.2	254	1	ADH_DROCK	000670 drosophila

ALIGNMENTS

RESULT 1	FWIA_HUMAN	STANDARD:	PRT:	605 AA.
AC	09Y297: 09Y213:			
DT	16-OCT-2001 (rel. 40, Created)			
DT	16-OCT-2001 (rel. 40, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TRCP)			
DE	(E3RS1kappab) (pikappabalpha-E3 receptor subunit).			
GN	FBXWIA OR FBWIA OR FBXW1 OR FBXW2 OR FBXW3			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=90075339; PubMed=9859996;			
RA	Varon A., Hatzubel A., Davis M., Lavon I., Amit S., Manning A.M.,			
RA	Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;			
RT	"Identification of the receptor component of the IkappaBalpha-			
RL	ubiquitin ligase."			
RL	Nature 396:590-594(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Lymphoid;			
RX	MEDLINE=98325370; PubMed=9660940;			
RA	Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,			
RA	Thomas D., Strebel K., Benarous R.;			
RT	"A novel human WD protein, h-beta TRCP, that interacts with HIV-1 Vpu			
RL	connects CD4 to the ER degradation pathway through an F-box motif."			
RL	Mol. Cell 1:565-574(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=20003060; PubMed=10531035;			
RA	Cenciarelli C., Chlaud D.S., Guardavaccaro D., Parks W., Vidal M.,			
RA	Pagano M.;			
RT	"Identification of a family of human F-box proteins."			
RL	Curr. Biol. 9:1177-1179(1999).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=99145464; PubMed=990852;			
RA	Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,			
RA	Harper J.W.;			
RT	"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically			
RT	with phosphorylated destruction motifs in I-kappa-B-alpha and			
RT	beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."			
RL	Genes Dev. 13:270-283(1999).			
CC	- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA			
CC	(PIKAPPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR			
CC	UBQUITINATION AND DEGRADATION.			
CC	- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.			
CC	- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	- FUNCTIONAL PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2: ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING.			
CC	- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.			
CC	- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			

```

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DR EMBL: AF101784; AAD08702.1; -
DR EMBL: Y14153; CA74572.1; -
DR EMBL: AF129530; AAF04464.1; -
DR Genew: HGNC:1144; BTRC.
DR MIM: 603482; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
KW DOMAIN 190 228 F-BOX.
FT REPEAT 301 338 WD 1.
FT REPEAT 341 378 WD 2.
FT REPEAT 381 418 WD 3.
FT REPEAT 424 461 WD 4.
FT REPEAT 464 503 WD 5.
FT REPEAT 505 541 WD 6.
FT REPEAT 553 590 WD 7.
FT VARSPLIC 17 52 MISSING (IN ISOPFORM 2).
SQ SEQUENCE 605 AA; 68866 MW; 4C67F3B7E400FD37 CRC64;

Query Match
Best Local Similarity 100.0%; Score 240; DB 1; Length 605;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 45
Db 183 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 227

RESULT 2
TROB_XENLA STANDARD; PRT; 518 AA.
AC Q91854; P70037; P70038;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-TrCP (beta-transducin repeat-containing protein).
GN FBXW1 OR BTRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9330289; PubMed=8393141;
RA Spevak W., Kelper B.D., Stratowa C., Castanon M.J.;
RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
RT anaphase are rescued by Xenopus CDNA's encoding N-ras or a protein
RT with beta-transducin repeats.";
RL Mol. Cell. Biol. 13:4953-4966(1993).
RN [2]
RP SEQUENCE OF 302-518 FROM N.A.
RX MEDLINE=97109804; PubMed=8952061;
RA Hudson J.W., Alarcon V.B., Elinson R.P.;

```

```

RT "identification of new localized RNAs in the Xenopus oocyte by
RT differential display PCR.";
RL Dev. Genet. 19:190-198(1996).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
CC MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
CC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
CC NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
CC TADPOLE EMBRYO.
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
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DR EMBL: M98268; AAA02810.1; -
DR EMBL: U63921; AAB49671.1; -
DR EMBL: U63922; AAB49672.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Ubl conjugation pathway; Repeat; WD repeat.
KW DOMAIN 119 157 F-BOX.
FT REPEAT 230 258 WD 1.
FT REPEAT 270 298 WD 2.
FT REPEAT 310 338 WD 3.
FT REPEAT 353 381 WD 4.
FT REPEAT 393 421 WD 5.
FT REPEAT 433 461 WD 6.
FT REPEAT 482 510 WD 7.
FT REPEAT 504 534 WD 8.
FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
SQ SEQUENCE 518 AA; 59507 MW; 2A52EC19028127F3 CRC64;

Query Match
Best Local Similarity 98.8%; Score 237; DB 1; Length 518;
Matches 44; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 45
Db 112 ALPARGLDHIAENILSYLDAKSLCAELVCKEYRYVTSQGLMKK 156

RESULT 3
FWIB_HUMAN STANDARD; PRT; 542 AA.
AC Q9UKB1; Q9Y4C6; Q9P2S8; Q9P2S9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP2).
GN FBXW1B OR FWIB1B OR BTRCP2 OR KIAA0696.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20003060; PubMed=10531035;
 RA Genciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Fetal lung;
 RX MEDLINE=20160458; PubMed=10694485;
 RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katoh M.;
 RT "Molecular cloning and genomic structure of the betatrop2 gene on
 RT chromosome 5q35.1.";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A, B AND C (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: AF176022; AAF04528.1; -;
 DR EMBL: AB033279; BAA92329.1; -;
 DR EMBL: AB033280; BAA92330.1; -;
 DR EMBL: AB033281; BAA92331.1; -;
 DR EMBL: AB014596; BAA31671.1; ALT_INT.
 DR Genew: HGNC:13607; FBXW1B.
 DR MIM: 605651; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; PBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Ubl conjugation pathway: Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 129 167 F-BOX.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPLIC 16 49 MISSING (IN ISOFORM A).

FT VARSPLIC 16 48 CSVPSRLMIGCANLVESMCALSCLOSPSYRCL -> NTSV
 FT SEQUENCE 542 AA; 62090 MW; 7CD40087EFAA5C8A CRC64;
 SQ MEDONDESEPKKTLW (IN ISOFORM B).
 Query Match 87.5%; Score 210; DB 1; Length 542;
 Best Local Similarity 86.7%; Pred. No. 8.8e-21;
 Matches 39; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 1 ALPARGLDHIAENILSTYDAKSLCAELVCKEWMYRVSIDGMLMKR 45
 DB 122 ALPEGLDHIENILSTYDAKSLCAELVCKEWMYRVSIDGMLMKR 166
 RESULT 4
 MT30_YEAST STANDARD; PRT; 640 AA.
 ID MT30_YEAST
 AC P39014.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MET30 protein.
 GN MET30 OR YIL046W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180-1A;
 RX MEDLINE=96069360; PubMed=8524217;
 RA Thomas D., Kuras L., Barbey R., Cherest H., Blaiseau P.L.,
 RA Surdin-Kerjan Y.;
 RT "Met30p, a yeast transcriptional inhibitor that responds to S-
 RT adenosylmethionine, is an essential protein with WD40 repeats.";
 RL Mol. Cell. Biol. 15:6526-6534(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Barrall B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentsel S., Hamlyn N., Hornell T.S., Hunt S., Jagels K., Jones M.,
 RA Louis F., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Rajadream M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BIOSYNTHESIS
 CC GENES EXPRESSION.
 CC -1- SUBUNIT: SEEMS TO INTERACT WITH MET4.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE MET30/SCOMB/SCON-2 FAMILY OF WD-REPEAT
 CC PROTEINS.
 CC -----
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 CC -----
 DR EMBL: Z46861; CAAB6905.1; -;
 DR EMBL: L26505; AAA96717.1; -;
 DR SGD: S0001308; MET30.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS50181; FBOX; 1.

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DR PROSITE: PS00678; WD_REPEATS.1; 4.
DR PROSITE: PS50082; WD_REPEATS.2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION.1.
KW Transcription regulation; Methionine biosynthesis;
KW Cysteine biosynthesis; Repeat; WD repeat.
FT DOMAIN 181 227 F-BOX.
FT REPEAT 300 328 WD 1.
FT REPEAT 340 368 WD 2.
FT REPEAT 380 408 WD 3.
FT REPEAT 419 449 WD 4.
FT REPEAT 461 499 WD 5.
FT REPEAT 509 538 WD 6.
FT REPEAT 550 578 WD 7.
FT REPEAT 607 635 WD 8 (POTENTIAL).
FT CONFLICT 61 61 M -> I (IN REF. 1).
SQ SEQUENCE 640 AA; 72835 MW; 5135D4BCA2E1EB97 CRC64;

Query Match 37.9%; Score 91; DB 1; Length 640;
Best Local Similarity 50.0%; Pred. No. 0.00014;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 ILSYLDKSLCAELVCKEYRVTSQGLM 43
Db 195 ILSYLDKSLCAELVCKEYRVTSQGLM 224

RESULT 5
POFA_SCHPO STANDARD; PRT; 605 AA.
ID POFA_SCHPO
AC P87053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof1 (Skp1-binding protein 1).
GN POF1 OR SBP1 OR SPAC57A10.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Katayama S., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RL fission yeast.";
RN Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson S., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicakeert G., Aert R., Robben J., Gymnopoulos B.,
RA Welter J., Vastreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

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RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL; AB032410; BAA84528.1; -
DR EMBL; Z64864; CAB08168.1; -
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPOTEINRPT.
DR PRODOM; PD000018; WD40; 5.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50078; WD_REPEATS.1; 2.
DR PROSITE; PS50082; WD_REPEATS.2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION.1.
KW Ub1 conjugation; Repeat; WD repeat.
FT DOMAIN 107 153 F-BOX.
FT REPEAT 271 299 WD 1.
FT REPEAT 311 339 WD 2.
FT REPEAT 350 379 WD 3.
FT REPEAT 390 420 WD 4.
FT REPEAT 432 460 WD 5.
FT REPEAT 472 500 WD 6.
FT REPEAT 510 538 WD 7.
SQ SEQUENCE 605 AA; 67110 MW; 7118C9379EC5C1F0 CRC64;

Query Match 36.7%; Score 88; DB 1; Length 605;
Best Local Similarity 44.4%; Pred. No. 0.00034;
Matches 16; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 10 IAEIILSYLDKSLCAELVCKEYRVTSQGLM 45
Db 117 ISFRIISFLDARSLCAAOVSKMKELADDDVIWHR 152

RESULT 6
POFA_SCHPO STANDARD; PRT; 662 AA.
ID POFA_SCHPO
AC Q9P7W4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof10 (Skp1-binding protein 2).
GN POF10 OR SBP2 OR SPBC1703.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RX MEDLINE=21678905; PubMed=11820777;
RA Ikebe C., Komihama K.-I., Toda T., Nakayama K.-I.;
RT "Isolation and characterization of a novel F-box protein Pof10 in
RL fission yeast.";

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RL Biochem. Biophys. Res. Commun. 290:1399-1407(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Grymoprez B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN1-F-BOX) PROTEIN LIGASE COMPLEX
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 CC
 CC EMBL: AB061725; BAB55636.1;
 DR EMBL: AL136536; CAB66450.1;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR003903; UJM.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 1.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
 DR PROSITE: PS50082; WD_REPEATS_2; 1.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Ubl conjugation: Repeat: WD repeat.
 FT DOMAIN 28 74 F-BOX.
 FT REPEAT 215 260 WD 1.
 FT REPEAT 263 302 WD 2.
 FT REPEAT 429 468 WD 3.
 SO SEQUENCE 662 AA; 74205 MW; 44061C20A61F602C CRC64;
 Query Match 34.0%; Score 81.5; DB 1; Length 662;
 Best Local Similarity 30.8%; Pred. No. 0.0029;
 Matches 16; Conservative 9; Mismatches 12; Indels 15; Gaps 1;
 OY 8 DHIAEN-----ILSYLAKSLCAELVCKEWEKRVTSIDMLWK 44
 DB 21 DHSNNNTNTVNLKREKILLIFFLDPRSLLSAOCCTCKYMKKLISDDLMSR 72

RESULT 7
 POP1_SCHPO
 ID POP1_SCHPO STANDARD; PRT; 775 AA.
 AC P87060;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE WD-repeat protein pop1.
 GN POP1 OR SPBC262.18.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-97347242; PubMed-9203581;
 RA Komianam K., Toda T.;
 RT "Fission yeast WD-repeat protein pop1 regulates genome ploidy through
 RT ubiquitin proteasome-mediated degradation of the CDK inhibitor Rum1
 RT and the S-phase initiator Cdc18.";
 RL Genes Dev. 11:1548-1560(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Grymoprez B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 RN [3]
 RP SUBUNIT.
 RC STRAIN-972;
 RX MEDLINE-99144318; PubMed-990507;
 RA Komianam K.-I., Ochotorena I., Toda T.;
 RT "Two F-box/WD-repeat proteins Pop1 and Pop2 form hetero- and homo-
 RT complexes together with cullin-1 in fission yeast SCF (Skip-cullin-1-
 RT F-box) ubiquitin ligase.";
 RL Genes Cells 3:721-735(1998).
 CC -1- FUNCTION: Involved in maintenance of ploidy through proteasome
 CC dependent degradation of CDK inhibitor rum1 and S-phase initiator
 CC cdc18. Functions as a recognition factor for rum1 and cdc18, which
 CC are subsequently ubiquitinated and targeted to the 26S proteasome
 CC for degradation.
 CC -1- SUBUNIT: Homodimer and heterodimer with pop2. Binds to pool and
 CC cdc18.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC

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DR EMBL: Y08391; CAA69671.1; -
 DR EMBL: AL022103; CAA17898.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 3.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS; 1; 3.
 DR PROSITE: PS00682; WD_REPEATS; 2; 4.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 DR Repeat; WD repeat.
 FT DOMAIN 298 345 F-BOX.
 FT REPEAT 444 472 WD 1.
 FT REPEAT 484 538 WD 2.
 FT REPEAT 575 603 WD 3.
 FT REPEAT 615 645 WD 4.
 FT REPEAT 657 687 WD 5.
 SQ SEQUENCE 775 AA; 87816 MW; B06EDBA46553EEC1 CRC64;

Query Match 33.5%; Score 80.5; DB 1; Length 775;
 Best Local Similarity 47.2%; Pred. No. 0.0046;
 Matches 17; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 10 IAEINILSTLDKSLCAELVCKEYR-VTSDGMLWK 44
 DB 308 ITNLVLTLDAPSLCAVSGVSHHWKLYVSNDELWK 343

RESULT 8
 SCOP_SCHPO STANDARD; PRT; 506 AA.
 AC 009655; Q9P7V1; -
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein pof1.
 GN POF1 OR SPAC2956.01 OR SPAC30.05.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI_TaxID=4896;
 [1]
 RP SEQUENCE FROM N.A.
 RA Harrison C.L., Toda T.;
 RT "Systematic genome-wide analysis of F-box protein-encoding genes in
 RT fission yeast."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RP STRAIN-972;
 RC MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Squoroos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolkehart G., Aert R., Robben J., Glynnoprez B.,
 RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzner E., Moestl D., Hilbert H.,
 RA Borzym K., Zimmermann W., Wedler H., Wambolt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Ielaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas R., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Dague R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovskii G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).

CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
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DR EMBL: AB061694; BAB55543.1; -
 DR EMBL: AL136538; CAB66464.1; -
 DR EMBL: Z66525; CAA91423.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 3.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 8.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS; 1; 3.
 DR PROSITE: PS00682; WD_REPEATS; 2; 6.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 DR Repeat; WD repeat.
 FT DOMAIN 70 116 F-BOX.
 FT REPEAT 219 236 WD 1.
 FT REPEAT 259 298 WD 2.
 FT REPEAT 301 338 WD 3.
 FT REPEAT 345 386 WD 4.
 FT REPEAT 388 426 WD 5.
 FT REPEAT 427 464 WD 6.
 FT REPEAT 468 505 WD 7.
 SQ SEQUENCE 506 AA; 58257 MW; CEF34DAEFBC2E10 CRC64;

Query Match 32.9%; Score 79; DB 1; Length 506;
 Best Local Similarity 35.1%; Pred. No. 0.0047;
 Matches 13; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 8 DHAENILSTLDKSLCAELVCKEYR-VTSDGMLWK 44
 DB 78 EEVSLRFVSYLDIDLCCKIMSKRMLLEDPGIWK 114

RESULT 9
 SCOP_EMENT STANDARD; PRT; 678 AA.
 ID SCOP_EMENT
 AC 000659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sulfur metabolite repression control protein.
 GN SCONB OR MAPBI.

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OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_Taxid=5072;
RN [1]
RP SEQUENCE FROM N.A.
RA Natorff R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
CC REPRESSION.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON 2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U21220; AAC15905.1;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Transcription regulation Repeat; WD repeat.
KW DOMAIN 178 224 F-BOX.
FT REPEAT 347 375 WD 1.
FT REPEAT 387 415 WD 2.
FT REPEAT 427 455 WD 3.
FT REPEAT 466 496 WD 4.
FT REPEAT 508 543 WD 5.
FT REPEAT 553 595 WD 6.
FT REPEAT 607 635 WD 7.
FT REPEAT 647 675 WD 8.
SQ SEQUENCE 678 AA; 76070 MW; D840D452E37B4C53 CRC64;

Query Match 32.9%; Score 79; DB 1; Length 678;
Best Local Similarity 40.0%; Pred. No. 0.0064;
Matches 18; Conservative 5; Mismatches 18; Indels 4; Gaps 1;

OY 1 ALPARGLDHIAENIIISYDAKSLCAELVCKEWMYRTSDGMLMK 45
DB 183 ALP-----PEIAFKILICYLDTSTLCASOVSRGMRALADDVWHR 223

RESULT 10
YK77_CABEL
ID YK77_CABEL STANDARD; PRT; 461 AA.
AC P34284;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical F-box/LRR-repeat protein C02F5.7 in chromosome III.
GN C02F5.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Bristol N2;

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RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smaiden N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Wilkinson-Sproat J.,
RA Waterston J., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL: L14745; AAA27922.2;
DR PIR: S44609; S44609.
DR WormPep: C02F5.7; CE24780.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00646; F-box; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00370; LRR; 5.
DR PROSITE: PS50181; FBOX; 1.
DR Hypothetical protein; Repeat; Leucine-rich repeat.
KW DOMAIN 54 100 F-BOX.
FT REPEAT 122 147 LRR 1.
FT REPEAT 148 173 LRR 2.
FT REPEAT 174 199 LRR 3.
FT REPEAT 200 225 LRR 4.
FT REPEAT 226 251 LRR 5.
FT REPEAT 252 277 LRR 6.
FT REPEAT 278 303 LRR 7.
FT REPEAT 304 329 LRR 8.
FT REPEAT 330 355 LRR 9.
FT REPEAT 356 381 LRR 10.
FT REPEAT 408 433 LRR 11.
SQ SEQUENCE 461 AA; 51552 MW; BB28C98A5CA7B1D5 CRC64;

Query Match 32.5%; Score 78; DB 1; Length 461;
Best Local Similarity 37.5%; Pred. No. 0.0058;
Matches 12; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 14 ILSYDAKSLCAELVCKEWMYRTSDGMLMK 45
DB 68 VESFLDTKALCRSAQVCSWILADGSMOR 99

RESULT 11
CC4_CANAL
ID CC4_CANAL STANDARD; PRT; 684 AA.
AC P53699;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell division control protein 4.
GN CDC4.
OS Candida albicans (Yeast).

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CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SG126;
 RA Shieh J.C., White A.M., Rosamond J.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
 CC REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM THE
 CC POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
 CC DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
 CC VARIOUS ASPECTS OF SPOGULATION. REQUIRED FOR HTAI-HTBI LOCUS
 CC TRANSCRIPTION ACTIVATION (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 DR EMBL; X96763; CAA65538.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 1.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS50082; WD_REPEATS_2; 4.
 DR PROSITE: PS50284; WD_REPEATS_REGION; 1.
 DR Cell division; Mitosis; Sporulation; Repeat; WD repeat.
 KW DOMAIN 212 258
 FT REPEAT 322 351 WD 1.
 FT REPEAT 363 391 WD 2.
 FT REPEAT 403 431 WD 3.
 FT REPEAT 442 468 WD 4 (POTENTIAL).
 FT REPEAT 478 506 WD 5.
 FT REPEAT 519 549 WD 6.
 FT REPEAT 561 589 WD 7.
 SQ SEQUENCE 684 AA; 76090 MW; 3DD65DB31293B107 CRC64;
 Query Match 32.1%; Score 77; DB 1; Length 684;
 Best Local Similarity 38.9%; Pred. No. 0.012;
 Matches 14; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 OY 10 IAEILSYLDASLCALVCKEYRVTSQGLMK 45
 Db 222 VTKMLSYLDYKTLTSLVAQVCKKMDIINNPTWIK 257
 RESULT 12
 FBX8_HUMAN
 ID FBX8_HUMAN STANDARD; PRT; 319 AA.
 AC Q9NRD0; Q9NRD5; Q9URC4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box only protein 8 (F-box/SEC7 protein FBS) (DC10).
 GN FBX8 OR FBX8 OR FBS.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chiar D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20399565; PubMed=10945468;
 RA Liyin G.P., Riialand M., Pigeon C., Guen Gullouzo C.;
 RT "CDNA cloning and expression analysis of new members of the mammalian
 RT F-box protein family.";
 RL Genomics 67:40-47(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Li Y., Peng Y., Qian B., Zhang Z., Han Z., Fu G., Chen Z.;
 RT "Novel genes expressed in human dentritic cell.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY PROMOTE GUANINE-NUCLEOTIDE EXCHANGE ON AN ARF.
 CC PROMOTES THE ACTIVATION OF ARF THROUGH REPLACEMENT OF GDP WITH
 CC GTP (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SEC7 DOMAIN.
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 CC -----
 DR EMBL; AF174596; AAF04517.1; ALT_INIT.
 DR EMBL; AF233224; AAF67154.1; -
 DR EMBL; AF201932; AAF86868.1; -
 DR EMBL; BC014679; AAH14679.1; -
 DR HSSP; Q99418; IPBV.
 DR GeneW; HGNC:13587; FBX08.
 DR MIM; 605649; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR000904; SEC7.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF01369; SEC7; 1.
 DR SMART: SM00222; SEC7; 1.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS50190; SEC7; 1.
 KW Guanine-nucleotide releasing factor.
 FT DOMAIN 68 111
 FT DOMAIN 146 276 SEC7.
 FT CONFLICT 119 119 C->W (IN REF. 3).
 FT CONFLICT 135 135 L->V (IN REF. 3).
 SQ SEQUENCE 319 AA; 37068 MW; 125D6DB57CA7C79 CRC64;
 Query Match 27.7%; Score 66.5; DB 1; Length 319;
 Best Local Similarity 45.2%; Pred. No. 0.14;
 Matches 14; Conservative 5; Mismatches 9; Indels 3; Gaps 1;
 OY 14 ILSYLDASLCALVCKEYRVTSQGLMK 44
 Db 82 ILSYLDATDCLASCV---WDLANDELLMO 109
 RESULT 13
 FBX8_MOUSE
 ID FBX8_MOUSE STANDARD; PRT; 319 AA.
 AC Q90ZM3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE F-box only protein 8.
GN FBX08 OR FBX8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20003061; PubMed=10511037;
RA Winston J.T., Koepf D.M., Zhu C., Ellledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
CC -1- FUNCTION: MAY PROMOTE GUANINE-NUCLEOTIDE EXCHANGE ON AN ARF.
CC PROMOTES THE ACTIVATION OF ARF THROUGH REPLACEMENT OF GDP WITH
CC GTP (POTENTIAL).
CC -1- TISSUE SPECIFICITY: High expression in brain, heart, kidney,
CC liver, lung, skeletal muscle, testis, and day-7 embryos.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SEC7 DOMAIN.
CC -----
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CC -----
CC EMBL: AF176527; AAF09136.1; -.
CC DR HSSP: Q99418; 1PBV.
CC DR MGD: MG1:1354696; FBX08.
CC DR InterPro: IPR001810; F-box.
CC DR InterPro: IPR000904; Sec7.
CC DR Pfam: PF00646; F-box; 1.
CC DR Pfam: PF01369; Sec7; 1.
CC DR SMART: SM00222; Sec7; 1.
CC DR PROSITE: PS50181; FBOX; 1.
CC DR PROSITE: PS50190; SEC7; 1.
CC KW Guanine-nucleotide releasing factor.
CC FT DOMAIN 68 111 F-BOX.
CC FT DOMAIN 146 276 SEC7.
CC SQ SEQUENCE 319 AA; 36982 MW; F961BC04AFLB3A3D CRC64;

Query Match 26.9%; Score 64.5; DB 1; Length 319;
Best Local Similarity 45.2%; Pred. No. 0.26;
Matches 14; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

OY 14 ILSYDAKSLCAELVCKEYRYVTS DGLMK 44
DB 82 ILSYLNAIDILCLASCV--WDLANDLMLQ 109

RESULT 14
FBW4_HUMAN STANDARD; PRT; 412 AA.
AC P57775; Q961M6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein 4 (Dactylin).
GN FBXW4 OR FBW4 OR SHPM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99335360; PubMed=10405324;
RA Iankiev P., Kilpatrick M.W., Dealy C., Koshner R., Korenberg J.R.,
RA Chen X.N., Tsipouras P.;
RT "A novel human gene encoding an F-box/WD40 containing protein maps in
RT the SHPM3 critical region on 10q24."
RL Biochem. Biophys. Res. Commun. 261:64-70(1999).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20399565; PubMed=10945468;
RA Llyin G.P., Riialand M., Pigeon C., Guigen-Guillouzo C.;
RT "CDNA cloning and expression analysis of new members of the mammalian
RT F-box protein family."
RL Genomics 67:40-47(2000).
RN [3]
RP SEQUENCE OF 121-412 FROM N.A.
RC TISSUE=pancreas;
RA Strusberg R.;
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PROBABLY RECOGNIZE AND BINDS TO SOME PHOSPHORYLATED
CC PROTEINS AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION. LIKELY
CC TO BE INVOLVED IN KEY SIGNALING PATHWAYS CRUCIAL FOR NORMAL LIMB
CC DEVELOPMENT.
CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY, LUNG AND LIVER.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
CC EMBL: AF281859; AAG22739.1; -.
CC DR EMBL: BC007380; AAH07380.1; -.
CC DR Genew: HGNC:10847; SHPM3.
CC DR MIM: 600095; -.
CC DR InterPro: IPR001680; F-box.
CC DR InterPro: IPR001810; WD40.
CC DR Pfam: PF00400; WD40; 4.
CC DR Pfam: PF00646; F-box; 1.
CC DR SMART: SM00256; FBOX; 1.
CC DR SMART: SM00320; WD40; 5.
CC DR PROSITE: PS50181; FBOX; 1.
CC DR PROSITE: PS00678; WD-REPEATS; 1; FALSE_NEG.
CC DR PROSITE: PS50082; WD-REPEATS; 2; 1.
CC DR PROSITE: PS50294; WD-REPEATS_REGION; 1.
CC KW Developmental protein; DB1 conjugation pathway; Repeat; WD repeat.
CC FT DOMAIN 25 71 F-BOX.
CC FT REPEAT 161 198 WD 1.
CC FT REPEAT 200 237 WD 2.
CC FT REPEAT 291 329 WD 3.
CC FT REPEAT 335 374 WD 4.
CC FT REPEAT 363 363 L -> P (IN REF. 3).
CC SQ SEQUENCE 412 AA; 46337 MW; 36C175FDE30D283B CRC64;

Query Match 26.7%; Score 64; DB 1; Length 412;
Best Local Similarity 37.3%; Pred. No. 0.4;
Matches 19; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 1 ALPARG--LDHIAENIL-----SYLDAKSLCAELVCKEYRYVTS DGLMK 45
DB 20 ARPAGAGRLMRLPEELLILICSYLDMRALRLAQLAGYCWLRPFISCDLWLR 70

RESULT 15
SC02_NEUCR STANDARD; PRT; 650 AA.
ID SC02_NEUCR
AC 001277;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfur controller-2 (SCON2).
GN SCON-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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OC Sordariiales; Sordariaceae; Neurospora.
OX NCHI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=95241499; PubMed=7724564;
RA Kumar A., Paletta J.V.;
RT "The sulfur controller-2 negative regulatory gene of Neurospora
RL crassa encodes a protein with beta-transducin repeats.";
CC proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
CC -1- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONE/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17251; AAA68968.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00296; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Transcription regulation; Repeat; WD repeat.
FT DOMAIN 124 170
FT REPEAT 292 320 WD 1.
FT REPEAT 332 360 WD 2.
FT REPEAT 372 400 WD 3.
FT REPEAT 411 441 WD 4.
FT REPEAT 453 488 WD 5.
FT REPEAT 528 564 WD 6.
FT REPEAT 576 604 WD 7.
FT REPEAT 616 644 WD 8.
SQ SEQUENCE 650 AA; 72189 MW; 7473859C99F1B028 CRC64;

Query Match 25.8%; Score 62; DB 1; Length 650;
Best Local Similarity 32.6%; Pred. No. 1.2;
Matches 14; Conservative 6; Mismatches 19; Indels 4; Gaps 1;

QY 1 ALPARGIDHIAENILSYDAKSLCAAEIVCKEYRYVTSQGLM 43
   ||| :| ||| | | | | | :|
Db 129 ALPV---ELAQKVLCLDTVSLTKAAQVSQRMRTLADSDAVM 167

```

Search completed: April 10, 2003, 13:19:32
 Job time : 4.23386 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 : Search time 10.6334 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_147_191
Perfect score: 240
Sequence: 1 ALPARGIDHTAENILSYLDA.....AELVCKEYRWISDGMWK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	240	100.0	569	11	Q92159	Q92159 mus musculu
2	240	100.0	569	11	Q90U15	Q90U15 mus musculu
3	236	98.3	569	11	Q91G17	Q91G17 mus musculu
4	216	90.0	62	13	Q80UN7	Q80UN7 xenopus lae
5	210	87.5	563	11	Q923H0	Q923H0 mus musculu
6	188	78.3	510	5	Q9VDE3	Q9VDE3 drosophila
7	184	76.7	510	5	Q44382	Q44382 drosophila
8	83.5	34.8	619	10	Q91TX2	Q91TX2 arabidopsis
9	83	34.6	483	4	Q94926	Q94926 homo sapien
10	83	34.6	491	4	Q90UT9	Q90UT9 homo sapien
11	82	34.2	464	5	Q9V605	Q9V605 drosophila
12	80	33.2	144	11	Q902N2	Q902N2 mus musculu
13	78	32.5	197	4	Q9UKC2	Q9UKC2 homo sapien
14	78	32.5	466	5	Q8T3G0	Q8T3G0 caenorhabdi
15	78	32.5	511	5	Q8T0K1	Q8T0K1 drosophila
16	77.5	32.3	635	10	Q9A0H6	Q9A0H6 populus tre

17	77	32.1	474	4	Q9UK66	Q9UK66 homo sapien
18	77	32.1	496	4	Q9Y2K7	Q9Y2K7 homo sapien
19	77	32.1	535	4	Q9UKC8	Q9UKC8 homo sapien
20	77	32.1	636	4	Q9XN22	Q9XN22 homo sapien
21	77	32.1	674	4	Q9P010	Q9P010 homo sapien
22	77	32.1	690	4	Q90UT7	Q90UT7 homo sapien
23	77	32.1	691	4	Q9P0X5	Q9P0X5 homo sapien
24	77	32.1	694	4	Q9UKA1	Q9UKA1 homo sapien
25	77	32.1	757	4	Q9H7H5	Q9H7H5 homo sapien
26	77	32.1	1182	5	Q9VH60	Q9VH60 drosophila
27	77	32.1	1326	5	Q9VZFA	Q9VZFA drosophila
28	75.5	31.5	614	10	Q9STV5	Q9STV5 arabidopsis
29	75.5	31.5	623	10	Q8RM08	Q8RM08 arabidopsis
30	75	31.2	157	10	Q91UB6	Q91UB6 caenorhabdi
31	75	31.2	518	5	Q968Y8	Q968Y8 caenorhabdi
32	75	31.2	535	5	Q968Y7	Q968Y7 caenorhabdi
33	74	30.8	151	10	Q9STX3	Q9STX3 arabidopsis
34	74	30.8	192	4	Q90HT1	Q90HT1 homo sapien
35	74	30.8	253	13	Q91B68	Q91B68 brachydanio
36	74	30.8	392	13	Q91BH3	Q91BH3 brachydanio
37	74	30.8	359	10	Q9VAK7	Q9VAK7 drosophila
38	73	30.4	389	5	Q9VGV4	Q9VGV4 arabidopsis
39	72.5	30.2	410	4	Q9BV69	Q9BV69 homo sapien
40	72.5	30.2	424	4	Q8T021	Q8T021 homo sapien
41	72.5	30.2	435	4	Q13309	Q13309 homo sapien
42	72.5	30.2	442	4	Q8T020	Q8T020 homo sapien
43	72	30.0	135	10	Q91U04	Q91U04 arabidopsis
44	71	29.6	573	11	Q9QXW2	Q9QXW2 mus musculu
45	70.5	29.4	592	10	Q04197	Q04197 arabidopsis

ALIGNMENTS

RESULT 1
ID Q92159 PRELIMINARY: PRT: 569 AA.
AC Q92159;
DC 01-MAY-1999 (TREMUREL. 10, Created)
DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)
DE Beta-transducin repeat containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed-9990853;
RA Spencer E., Jiang J., Chen Z.,
RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
Slimb/beta-Trcp.";
RT Genes Dev. 13:284-294(1999).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF112979; AAD04181.1;
DR MGD; MGI:1338871; BTRC.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA: 65047 MW: BC7C7A44815BD96 CRC64:
Query Match 100.0%; score 240; DB 11; Length 569;

Best Local Similarity 100.0%; Pred. No. 3,1e-25;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 45
DB 147 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 191

RESULT 2
OY0015 PRELIMINARY; PRT; 569 AA.
ID OY0015;
AC OY0015;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE ubiquitin ligase FWD1 (Beta-transducin repeat containing protein)
DE (F-box WD40 repeat protein 1).
GN BTRC OR FBXW1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199275; PubMed=10097128;
RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
RA Nakayama K.,
RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a
RT ubiquitin ligase SKP1/Cul 1/F-box protein FWD1.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99075339; PubMed=9859996;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.,
RT "Identification of the receptor component of the IkappaBalpha-
RT ubiquitin ligase.";
RL Nature 396:590-594(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21601157; PubMed=11735228;
RA Maryama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA Nakayama K.,
RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
RT Caenorhabditis elegans SEL-10.";
RL Genomics 78:214-222(2001).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF081887; AAD1775.1; -;
DR EMBL: AF099932; AAD08701.1; -;
DR EMBL: BC003989; AAH03989.1; -;
DR EMBL: AF391190; AAL40929.1; -;
DR EMBL: AF391178; AAL40929.1; JOINED.
DR EMBL: AF391179; AAL40929.1; JOINED.
DR EMBL: AF391180; AAL40929.1; JOINED.
DR EMBL: AF391181; AAL40929.1; JOINED.
DR EMBL: AF391182; AAL40929.1; JOINED.
DR EMBL: AF391183; AAL40929.1; JOINED.
DR EMBL: AF391184; AAL40929.1; JOINED.
DR EMBL: AF391185; AAL40929.1; JOINED.
DR EMBL: AF391186; AAL40929.1; JOINED.
DR EMBL: AF391187; AAL40929.1; JOINED.
DR EMBL: AF391188; AAL40929.1; JOINED.
DR EMBL: AF391189; AAL40929.1; JOINED.
DR MGD: MGI:1338871; Btrc.
DR InterPro: IPR001810; F-box.
DR Pfam: PF00646; F-box; 1.

DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW ligase; Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65209 MW; 6C7D6544815B2296 CRC64;

Query Match
Best Local Similarity 100.0%; Score 240; DB 11; Length 569;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 45
DB 147 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 191

RESULT 3
OYR1G7 PRELIMINARY; PRT; 569 AA.
ID OYR1G7
AC OYR1G7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Beta-transducin repeat-containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF110396; AAD41025.1; -;
DR MGD: MGI:1338871; Btrc.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65209 MW; 6C7D6544815B2296 CRC64;

Query Match
Best Local Similarity 98.8%; Score 236; DB 11; Length 569;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 45
DB 147 ALPARGLDHIAENILSYLDAKSLCAAEVCKEYRVTSDDGMLMK 191

RESULT 4
OYR0N7 PRELIMINARY; PRT; 62 AA.
ID OYR0N7;
AC OYR0N7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Beta-Trip protein (Fragment).

GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Carnevall F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ballarino M.;
 RL "Analisi strutturale e funzionale del gene beta-TRCP in Xenopus laevis";
 RL Thesis (2001),
 RL Department of Genetics and Molecular Biology Charles Darwin,
 RL University of Rome La Sapienza, Rome, Italy.
 DR EMBL, AJ428934; CAD21911.1; -.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PS50181; FBOX; 1.
 FT NON_TER
 FT 1 62
 FT 62 62
 SEQUENCE 62 AA: 7299 MW: A735E62CA442C02 CRC64;

Query Match 90.0%; Score 216; DB 13; Length 62;
 Best Local Similarity 95.2%; Pred. No. 5.4e-23;
 Matches 40; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ARGLDHIAENITSLYDAKSLCAELVCKEMRYVTSQGLMKK 45
 DB 1 ARGLDHIAENITSLYDAKSLCAELVCKEMRYVTSQGLMKK 42

RESULT 5
 O923H0 PRELIMINARY: PRT: 563 AA.
 AC O923H0:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE F-box/WD40 repeat-containing protein HOS.
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Bhalla N., Heter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
 RT "Mouse homolog of HOS (mHOS) is overexpressed in skin tumors and
 RT implicated in constitutive activation of NF-kappaB";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL, AF038079; AAK72095.1; -.
 DR MGD: MG1:2144023; Fbxw1b.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; F-box; 1.
 DR Pfam: PF00446; F-box; 1.
 DR ProDom: PD000018; WD40; 4.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS500982; WD_REPEATS_2; 7
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Repeat; WD repeat.
 SQ SEQUENCE 563 AA: 64741 MW: 9AB562F3FF5E3496 CRC64;

Query Match 87.5%; Score 210; DB 11; Length 563;
 Best Local Similarity 86.7%; Pred. No. 5.2e-21;

Matches 39; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALPARGLDHIAENITSLYDAKSLCAELVCKEMRYVTSQGLMKK 45
 DB 143 ALPARGLDHIAENITSLYDAKSLCAELVCKEMRYVTSQGLMKK 187

RESULT 6
 O9VDE3 PRELIMINARY: PRT: 510 AA.
 ID O9VDE3:
 AC O9VDE3:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SLMB protein (SLMB).
 GN SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Chame M., Pfeiffer B.D.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Plamkoc C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
 RA Dodson K., Dou P.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 RA Jajuel M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jia L., Kallish F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matell B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY, AND IMAGINAL DISC;
 RC MEDLINE=20245299; PubMed=10781936;
 RT Miletich I., Limbourg-Bouchon B.;
 RT "Drosophila null slmb clones transiently deregulate Hedgehog-
 RT independent transcription of wingless in all limb discs, and induce
 RT decapentaplegic transcription linked to imaginal disc regeneration";
 RT Mech. Dev. 93:15-26(2000).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL: AE003733; AAF55853.1; -
 DR EMBL: AF222924; AAF63214.1; -
 DR EMBL: AF222923; AAF63213.1; -
 DR FlyBase: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00256; F-box; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; F-box; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58952 MW; F4D5DF126F58A012 CRC64;

Query Match 78.3%; Score 188; DB 5; Length 510;
 Best Local Similarity 79.5%; Pred. No. 5.9e-18;
 Matches 35; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 LPARGDHIENILSYDANSICAAELVCKEWRVTSQGMIMKK 45
 DB 92 LPKIGLDHIGENILSYDAESLSKSELVCKEWMRLVISEGMIMKK 135

RESULT 7
 ID 044382 PRELIMINARY; PRT; 510 AA.
 AC 044382;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE SLMB.
 GN SLMB OR SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121115; PubMed=9461217;
 RA Jiang J., Struhl G.;
 RT Regulation of the Hedgehog and Wingless signalling pathways by the F-box/WD40-repeat protein Slmb.
 RL Nature 391:493-496(1998).
 CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF032878; AAC38852.1; -
 DR FlyBase: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00256; F-box; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58952 MW; DB0243D3730A5E8 CRC64;

Query Match 76.7%; Score 184; DB 5; Length 510;
 Best Local Similarity 77.3%; Pred. No. 2.2e-17;
 Matches 34; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 LPARGDHIENILSYDANSICAAELVCKEWRVTSQGMIMKK 45
 DB 92 LPKIGLDHIGENILSYDAESLSKSELVCKEWMRLVISEGMIMKK 135

RESULT 8
 ID 09LTX2 PRELIMINARY; PRT; 619 AA.
 AC 09LTX2;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Transport inhibitor response 1 protein (At5g49980/K9P8_12).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty p1 and TrAC clones."
 RT DNA Res. 7:31-63(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.D., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB024032; BAA97019.1; -
 DR EMBL: AY056431; AAL08287.1; -
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 SQ SEQUENCE 619 AA; 69316 MW; D0614AF071EB4PD2 CRC64;

Query Match 34.8%; Score 83.5; DB 10; Length 619;
 Best Local Similarity 45.9%; Pred. No. 0.0043;
 Matches 17; Conservative 8; Mismatches 7; Indels 5; Gaps 2;

OY 3 PARGDHIENILSYDANSICAAELVCKEWRV 36
 DB 51 PDHVLNVLNVLQFLDSR--CDRNAASLVCKSMWRV 85

RESULT 9
 ID 094926 PRELIMINARY; PRT; 483 AA.
 AC 094926;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE KIA0840 protein (Fragment).
 GN KIA0840 OR FBL7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code

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RT for large proteins in vitro."
RL DNA Res. 5:355-364(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20003060; PubMed=10531035;
RA Cenciarelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RT Pagano M.;
RT "Identification of a family of human F-box proteins."
RL Curr. Biol. 9:1177-1179(1999).
DR EMBL: AB020647; BAA74863.1; -
DR EMBL: AF174593; AAF04514.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00370; LRR; 1.
DR PROSITE: PSS0181; FBOX; 1.
DR NONTER
SQ SEQUENCE 483 AA; 53773 MW; AEC3991439E396EF CRC64;

Query Match 34.6%; Score 83; DB 4; Length 483;
Best Local Similarity 37.8%; Pred. No. 0.0037;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 8 DHIAENILSYDAKSLCAELVCKEYRVTSDGMLMK 44
DB 111 DHSWQIFSFLEPTNOLCRCAVRCRRMYNLAMPRLMR 147

RESULT 10
Q9UT9 PRELIMINARY; PRT; 491 AA.
AC Q9UT9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE F-box protein FBL6.
GN FBL6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20399565; PubMed=10945468;
RA Liyin G.P., Rialland M., Pigeon C., Gugen-Guilouzo C.;
RT "cDNA Cloning and Expression Analysis of New Members of the Mammalian
RT F-box Protein Family."
RL Genomics 67:40-47(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liyin G.P.;
RT "F-box protein FBL6 containing leucine-rich repeats."
RT Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF199356; AAF09248.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00370; LRR; 1.
DR PROSITE: PSS0181; FBOX; 1.
SQ SEQUENCE 491 AA; 54574 MW; A70C092A4E7A8C69 CRC64;

Query Match 34.6%; Score 83; DB 4; Length 491;
Best Local Similarity 37.8%; Pred. No. 0.0038;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 8 DHIAENILSYDAKSLCAELVCKEYRVTSDGMLMK 44
DB 119 DHSWQIFSFLEPTNOLCRCAVRCRRMYNLAMPRLMR 155

RESULT 11

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Q9V605
ID Q9V605 PRELIMINARY; PRT; 464 AA.
AC Q9V605;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE CG9003 protein.
GN CG9003.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Blandard D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpis G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Styrcas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-T., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003625; AAF58635.1; -
DR FlyBase: FBgn003639; CG9003.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00560; LRR; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00370; LRR; 9.
DR PROSITE: PSS0181; FBOX; 1.
SQ SEQUENCE 464 AA; 51606 MW; 18B0C987BCD20B41 CRC64;

Query Match 34.2%; Score 82; DB 5; Length 464;
Best Local Similarity 46.9%; Pred. No. 0.0049;
Matches 15; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 14 ILSYDAKSLCAELVCKEYRVTSDGMLMK 45

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Db 64 VFSYLDVVSICRCAGVCKYNNVIALDSSWOK 95

RESULT 12
Q90ZLN2

ID Q90ZLN2 PRELIMINARY; PRT; 144 AA.

AC Q90ZLN2; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

GN FBX012.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Winston J.T., Elledge S.J., Harper W.;

RT "A family of mammalian F-box proteins.";

RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF176528; AAF09137.1; -

DR MGD: MG1:1354703; FBX012.

DR InterPro: IPR001810; F-box.

DR Pfam: PF00646; F-box; 1.

DR SMART: SM00256; FBOX; 1.

DR PROSITE: PS50181; FBOX; 1.

FT NON_TER 1

SQ SEQUENCE 144 AA; 17265 MW; C02H7CC36348AEDA CRC64;

Query Match 33.3%; Score 80; DB 11; Length 144;

Best Local Similarity 53.1%; Pred. No. 0.0024;

Matches 17; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 14 ILSTYLDKSLCAELVCKEYRVTSDGMLMK 45

Db 17 ILSTYLDAYSLQAQYVKNMNELASSDVLMRK 48

RESULT 13

ID Q90KC2 PRELIMINARY; PRT; 197 AA.

AC Q90KC2; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

GN F-box protein FBX11 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20003060; PubMed=10531035;

RA Cenciarelli C., Chiur D.S., Guardavaccaro D., Parks W., Vidal M.,

RT "Identification of a family of human F-box proteins.";

RL Curr. Biol. 9:1177-1179(1999).

DR EMBL: AF174599; AAF04520.1; -

DR InterPro: IPR003267; F-box.

DR InterPro: IPR001810; F-box.

DR Pfam: PF00646; F-box; 1.

DR PRINTS: PR01217; PRICHEXTENS.

DR PRINTS: PR00021; PROTRICH.

DR SMART: SM00256; FBOX; 1.

DR PROSITE: PS50181; FBOX; 1.

FT NON_TER 1

SQ SEQUENCE 197 AA; 22336 MW; F8C37A23510924D0 CRC64;

Query Match 32.5%; Score 78; DB 4; Length 197;

Best Local Similarity 39.5%; Pred. No. 0.0066;

Matches 15; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 8 DHIAENILSYLDKSLCAELVCKEYRVTSDGMLMK 45

Db 146 DEVVLKIFSYLLEDDICRACVCKRFSLELANDPNLMRK 183

RESULT 14

ID 08T3G0 PRELIMINARY; PRT; 466 AA.

AC 08T3G0; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN C02F5.7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditidae;

OC Rhabdilitidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-BRISTOL N2;

RC MEDLINE=99069613; PubMed=9851916;

DR Waterston R.;

RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-BRISTOL N2;

RC Anderson K.;

RT "The sequence of C. elegans cosmid C02F5.";

RL Submitted (May-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Waterston R.;

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: L14745; AAM15540.1; -

DR KW Hypothetical protein.

SQ SEQUENCE 466 AA; 52064 MW; 05BCEB2AA606E15F CRC64;

Query Match 32.5%; Score 78; DB 5; Length 466;

Best Local Similarity 37.5%; Pred. No. 0.018;

Matches 12; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 14 ILSTYLDKSLCAELVCKEYRVTSDGMLMK 45

Db 68 VFSYLDTRKALCRSAQVCRSWSIALDSSNMQR 99

RESULT 15

ID 08T0K1 PRELIMINARY; PRT; 511 AA.

AC 08T0K1; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN CG20184P.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

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XX Example 5: Page 80-82; 351pp; English.
 PS
 CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.

SQ Sequence 517 AA;

Query Match 100.0%; Score 186; DB 16; Length 517;
 Best Local Similarity 100.0%; Pred. No. 3e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIW 34
 ||||||||||||||||||||||||||||||||
 DB 224 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIW 257

RESULT 2
 ID AAY24054
 AAY24054 standard; Protein: 569 AA.

AC AAY24054;

DT 30-SEP-1999 (first entry)

DE A human beta-transducin repeat containing protein.

XX
 KW Beta-transducin repeat containing protein; beta-Trcp; Skp1p;
 KW Proteasome degradation pathway; Vpu protein; beta-catenin;
 KW human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;
 KW ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
 KW antiviral; antitumour; cell cycle regulation; protein degradation;
 KW and anti-inflammatory; osteo-articular inflammation; acute inflammation;
 KW tumour necrosis factor.

XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 147..191

FT /note= "F box sequence"

FT Region 259..292

FT /note= "WD motif"

FT Region 304..332

FT /note= "WD motif"

FT Region 343..372

FT /note= "WD motif"

FT Region 387..415

FT /note= "WD motif"

FT Region 427..455

FT /note= "WD motif"

FT Region 467..492

FT /note= "WD motif"

FT 516..544

FT /note= "WD motif"

XX WO9938969-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-FR00196.

XX 09-DEC-1998; 98FR-0015545.

PR 30-JAN-1998; 98FR-0001100.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR.

PI Atenzana Selsdesos F, Benarous R, Concordet J, Durand H;

PI Kroll M, Margotlin F,

DR WPI: 1999-469329/39.

DR N-PSDB; AAX86501.

PT New human beta-transducin repeat containing protein and its

PT fragments useful as, or to screen for, antiviral, antitumour,

PT anti-inflammatory and anti-Alzheimer's agents

PS Claim 1: Page 60-61; 71pp; French.

XX The present sequence represents a human beta-transducin repeat containing
 CC protein (beta-trcp). The protein directs proteins to the proteasome
 CC degradation pathways. The protein is able to interact with the Vpu
 CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
 CC Ikappab or beta-catenin (bc) and/or protein Skp1p. The protein controls
 CC ubiquitinylation of phosphorylated proteins and thus their targeting to
 CC proteasomes for degradation. Depending on whether the process is
 CC inhibited or promoted, the result may be delayed breakdown of CD4 (in
 CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
 CC activity of NFkappab) and increased degradation of mutant bc in tumour
 CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
 CC patients. The beta-Trcp protein, and its active peptide fragments, or its
 CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
 CC antitumour agents that disrupt cell cycle regulation or protein
 CC degradation in human tumour cells, and anti-inflammatory agents that
 CC disrupt activation by NFkappab. Fragments of the protein are also
 CC useful for treating osteo-articular inflammation or acute inflammation
 CC associated with release of tumour necrosis factor.

SQ Sequence 569 AA;

Query Match 100.0%; Score 186; DB 20; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIW 34
 ||||||||||||||||||||||||||||||||
 DB 259 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIW 292

RESULT 3

ID AAB12812
 AAB12812 standard; protein: 569 AA.

AC AAB12812;

DT 27-NOV-2000 (first entry)

DE Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

XX Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-Trcp.

XX Mus musculus.

XX JP2000166542-A.

XX 20-JUN-2000.

XX 02-DEC-1998; 98JP-0343437.

XX 02-DEC-1998; 98JP-0343437.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JTGODAN.


```

XX  WPI: 2000-485550/43.
DR  N-PSDB: AAA73131.
XX
XX  F-box protein of ubiquitin ligase SCF complex which promotes the
PT  ubiquitination of IkappaB or beta-catenin
XX
XX  Claim 2; Page 9-10; 19pp; Japanese.
PS
XX  The present invention describes an F-box motif protein of ubiquitin
CC  ligase SCF complex which promotes the ubiquitination of IkappaB or
CC  beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
CC  complex (SCF complex) of F-box protein containing F-box motif and Wp40
CC  repeat motif and has the amino acid sequence of 45 residues (AAB12811)
CC  or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
CC  ligase FWD1 protein) and (AAB12813, which is human beta-transducin
CC  repeat containing protein (beta-TrCP)). The F-box protein can be used for
CC  the gene therapy of colon cancer by being recombined to a virus vector.
XX
XX  Sequence 569 AA:
SQ
XX
XX  Query Match 100.0%; Score 186; DB 21; Length 569;
XX  Best Local Similarity 100.0%; Pred. No. 3,4e-18;
XX  Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 RHCRSETSKGYCLOYDQKIVSGLRDNTIKIW 34
XX  |||||||||||||||||||||||||||||||
Db 259 RHCRSETSKGYCLOYDQKIVSGLRDNTIKIW 292

RESULT 4
AAB12813
ID AAB12813 standard; protein; 569 AA.
XX
XX  AAB12813:
XX
XX  27-NOV-2000 (first entry)
XX
XX  Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
DE
XX  ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB;
KM  beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
KM  gene therapy; colon cancer; beta-transducin repeat containing protein;
KM  beta-TrCP.
XX
XX  Homo sapiens.
OS
XX
XX  JP200016542-A.
XX
XX  20-JUN-2000.
XX
XX  02-DEC-1998; 98JP-0343437.
XX
XX  02-DEC-1998; 98JP-0343437.
XX
XX  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX  WPI: 2000-485550/43.
DR  N-PSDB: AAA73132.
XX
XX  F-box protein of ubiquitin ligase SCF complex which promotes the
PT  ubiquitination of IkappaB or beta-catenin
XX
XX  Claim 3; Page 10-12; 19pp; Japanese.
XX
XX  The present invention describes an F-box motif protein of ubiquitin
CC  ligase SCF complex which promotes the ubiquitination of IkappaB or
CC  beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
CC  complex (SCF complex) of F-box protein containing F-box motif and Wp40
CC  repeat motif and has the amino acid sequence of 45 residues (AAB12811)
CC  or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
CC  ligase FWD1 protein) and (AAB12813, which is human beta-transducin
CC  repeat containing protein (beta-TrCP)). The F-box protein can be used for

```

```

CC  the gene therapy of colon cancer by being recombined to a virus vector.
XX
XX  Sequence 569 AA:
SQ
XX
XX  Query Match 100.0%; Score 186; DB 21; Length 569;
XX  Best Local Similarity 100.0%; Pred. No. 3,4e-18;
XX  Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 RHCRSETSKGYCLOYDQKIVSGLRDNTIKIW 34
XX  |||||||||||||||||||||||||||||||
Db 259 RHCRSETSKGYCLOYDQKIVSGLRDNTIKIW 292

RESULT 5
AAI96697
ID AAI96697 standard; protein; 569 AA.
XX
XX  AAI96697:
XX
XX  26-SEP-2000 (first entry)
XX
XX  Human beta-TrCP.
DE
XX  E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KM  nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KM  anti-inflammatory; immunosuppressive; cytostatic.
XX
XX  Homo sapiens.
OS
XX
XX  WO200034447-A2.
XX
XX  15-JUN-2000.
XX
XX  10-DEC-1999; 99WO-US29371.
XX
XX  10-DEC-1998; 98US-0210060.
XX
XX  (SIGN-) SIGNAL PHARM INC.
PA  (YISS) YISSOM RES & DEV CO.
XX
XX  Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
PI  Lavon I, Yaron A;
XX
XX  WPI: 2000-431294/37.
XX
XX  N-PSDB: AAA51229.
XX
XX  polypeptide enhancing phosphorylated IkappaB ubiquitination useful for
PT  treating disorder associated with NF-kappaB activation e.g. cancer,
PT  comprising amino acid sequence of human E3 ubiquitin ligase or its
PT  variant
XX
XX  Claim 21; Page 72-74; 77pp; English.
XX
XX  Human beta-TrCP, an F-box/WD protein family member, has been shown to
CC  have homology to human E3 ubiquitin ligase (E3). E3 enhances
CC  ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
CC  nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
CC  degradation via the ubiquitin pathway is useful for identifying
CC  modulators of this process for use in treating diseases associated with
CC  activation of NF-kappa-B. In vitro analysis suggests that deletion of
CC  the F-box results in a protein that functions as a dominant negative
CC  molecule in vivo. Transient over-expression of delta-beta-TrCP (a
CC  deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
CC  in stimulated Jurkat cells, resulting in accumulation of phosphorylated
CC  I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
CC  inflammatory diseases, autoimmune diseases, cancer and viral infections.
CC
XX  Sequence 569 AA:
SQ
XX
XX  Query Match 100.0%; Score 186; DB 21; Length 569;
XX  Best Local Similarity 100.0%; Pred. No. 3,4e-18;
XX  Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 34
 Db 259 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 292

RESULT 6
 AA83041

ID AAY83041 standard; Protein: 569 AA.

AC AAY83041;

DT 16-AUG-2000 (first entry)

DE F-box protein FBP-1.

XX F-box protein: FBP; diagnosis; treatment; screening; agonist;

KW antagonist; proliferative disorder; differentiative disorder;

KW breast cancer; prostate cancer; ovarian cancer; cancer;

KW small cell lung carcinoma; immune disorder; cardiovascular disorder;

XX inflammatory disorder; human.

OS Homo sapiens.

PN WO200012679-A1.

PD 09-MAR-2000.

PF 27-AUG-1999; 99WO-US19560.

PR 28-AUG-1998; 98US-0098355.

PR 03-FEB-1999; 98US-0118568.

PR 15-MAR-1999; 99US-0124449.

PA (UYNV) UNIV NEW YORK STATE.

PI Chlaur DS, Pagano M, Latres E;

DR WPI: 2000-256635/22.

DR N-PSDB: AA293350.

PT Novel nucleic acid for screening compounds useful for treating
 proliferative and differentiative disorders such as cancer and immune
 disorders comprises sequences encoding ubiquitin ligases

PS Disclosure: Figure 3a; 245pp; English.

CC Nucleic acids encoding substrate-targeting subunits of ubiquitin
 CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 CC of proliferative and differentiated related disorders by measuring
 CC FBP gene expression. Cells expressing such proteins or
 CC their fragments are useful for screening compounds. The compounds
 CC are agonists or antagonists, which are useful for treating a
 CC proliferative or differentiative disorder in a mammal such as
 CC breast, ovarian and prostate cancer and small cell lung carcinoma
 CC and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein,
 CC analogs, derivatives and their subsequences, anti-FBP antibodies
 CC are also useful in diagnosis of the disorders.

XX Sequence 569 AA;

Query Match 100.0%; Score 186; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3,4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 34
 Db 259 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 292

RESULT 7
 AA83250

ID AAY83250 standard; Protein: 569 AA.

AC AAY83250;

DT 16-AUG-2000 (first entry)

DE F-box protein hBetrCP.

XX Ubiquitin ligase; SCF: F-box protein; targeted degradation;

KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;

KW oncoprotein; Huntington's disease; gene knockout; delivery systems;

XX human.

OS Homo sapiens.

PN WO200022110-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23705.

PR 09-OCT-1998; 98US-0103787.

PA (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR WPI: 2000-317970/27.

DR N-PSDB: AA293710.

PT Targeting degradation of polypeptide useful for treating cancer and
 other proliferative disorders, involves conjugating polypeptide with
 ubiquitin protein ligase or inhibiting ubiquitination using organic
 compound

PS Claim 9; Page 171; 185pp; English.

CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

XX Sequence 569 AA;

Query Match 100.0%; Score 186; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3,4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 34
 Db 259 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 292

RESULT 8
 AA83254

ID AAY83254 standard; Protein: 569 AA.

AC AAY83254;

DT 16-AUG-2000 (first entry)

DR N-PSDB; AA229233.
 XX
 CC Human cell signalling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders
 XX
 PS Claim 1; Page 77-78; 90pp; English.
 XX
 CC The present sequence is cell signalling protein-12 (CSIGP-12) encoded
 CC by cDNA obtained from Incyte clone 3239149 of COLAUC701 library. It is
 CC expressed in musculoskeletal, gastrointestinal and nervous tissues and is
 CC found to be homologous to beta-transducin repeats containing
 CC protein. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC them with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 XX
 SQ Sequence 569 AA;

Query Match 100.0%; Score 186; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3,4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCLOYDDQKIVSGLRNTTIK 34
 ||||||||||||||||||||||||||||
 DB 259 RHCRSETSKGYCLOYDDQKIVSGLRNTTIK 292

RESULT 10
 AAB48298
 ID AAB48298 standard; Protein: 569 AA.
 XX
 AC AAB48298;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human ZF11 protein.
 XX

KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytosolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200075184-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000WO-US15449.
 XX
 PR 04-JUN-1999; 99US-0137494.
 XX
 PA (UYVA) UNIT YALE.
 XX
 PI Zhang H, Tsvetkov IM, Kondo T;
 XX
 DR WPI; 2001-061703/07.
 DR N-PSDB; AAC84610.
 XX
 XX

Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 XX
 PS Claim 3; Page 130-132; 162pp; English.

The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the

CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 XX
 SQ Sequence 569 AA;

Query Match 100.0%; Score 186; DB 22; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3,4e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCLOYDDQKIVSGLRNTTIK 34
 ||||||||||||||||||||||||||||
 DB 259 RHCRSETSKGYCLOYDDQKIVSGLRNTTIK 292

RESULT 11
 AAM78583
 ID AAM78583 standard; Protein: 579 AA.
 XX
 AC AAM78583;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1245.
 XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 XX
 PR 27-APR-2000; 2000US-0560875.
 XX
 PR 20-JUN-2000; 2000US-0598075.
 XX
 PR 19-JUL-2000; 2000US-0620325.
 XX
 PR 01-SEP-2000; 2000US-0654936.
 XX
 PR 15-SEP-2000; 2000US-0663561.
 XX
 PR 20-OCT-2000; 2000US-0693825.
 XX
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 XX
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 XX
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51716.
 XX
 XX

Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 PT
 XX
 PS Claim 20; Page 3504-3505; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and

CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK60020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 579 AA;

Query Match 100.0%; Score 186; DB 22; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3,5e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 34
 ||||||||||||||||||||||||||||||||||||
 Db 269 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 302

RESULT 12

AAK00847 ID AAK00847 standard; Protein; 590 AA.

XX AAK00847:

DT 01-OCT-2001 (first entry)

XX Human bone marrow protein, SEQ ID NO: 210.

XX Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
 XX antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 XX immunosuppressive; gene therapy; cytokine cell proliferation;
 XX cell differentiation modulator; immune disorder; infection; cancer;
 XX human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

OS Homo sapiens.

XX WO20015453-A2.

XX 26-JUL-2001.

XX 23-DEC-2000; 2000WO-US34960.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0634550.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 30-NOV-2000; 2000US-0250583.

XX (HYSE-) HYSEQ INC.

XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
 XX Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
 XX Zhao QA, Zhou P, Drmanac RT;

XX WPI: 2001-488707/53.

XX N-PSDB; AAK89966.

XX Novel bone-marrow-expressed polynucleotides and polypeptides, useful
 XX for treating e.g. cancer and immune deficiency disorders -

XX Claim 10; Page 354-355; 648pp; English.

CC The present sequence is one of 251 novel human polypeptides encoded
 CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
 CC polypeptide encoded by it are useful in the treatment of various
 CC immune deficiencies and disorders. The deficiencies and disorders may
 CC be genetic, may be caused by a viral (e.g. HIV) bacterial or fungal
 CC infection, or may result from an autoimmune disorder, a coagulation
 CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
 CC suppression of an inflammatory response or treatment of a nervous
 CC system disorder such as Alzheimer's disease. Detection of the presence
 CC or increased expression of the polynucleotide or the protein it

CC encodes is useful for the diagnosis and/or prognosis of one
 CC or more types of cancer. The polynucleotide and polypeptide can be
 CC used as nutritional sources or supplements and in the screening of
 CC chemical compounds as potential drugs.

XX Sequence 590 AA;

Query Match 100.0%; Score 186; DB 22; Length 590;
 Best Local Similarity 100.0%; Pred. No. 3,6e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 34
 ||||||||||||||||||||||||||||||||||||
 Db 280 RHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 313

RESULT 13

AAK78582 ID AAK78582 standard; Protein; 605 AA.

XX AAK78582:

DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1244.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 XX tissue growth factor; immunomodulatory; cancer; leukaemia;
 XX nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX 20-JUN-2000; 2000US-0598075.

XX 19-JUL-2000; 2000US-0620325.

XX 01-SEP-2000; 2000US-0654936.

XX 15-SEP-2000; 2000US-0663561.

XX 20-OCT-2000; 2000US-0693325.

XX 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 XX Zhao QA, Wang J, Werhman T, Ren F, Chen R, Wang ZW;
 XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI: 2001-476283/51.

XX N-PSDB; AAK51715.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 XX useful in diagnosis and gene therapy -

XX Claim 20; Page 3503-3504; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX

SO Sequence 605 AA;

Query Match 100.0%; Score 186; DB 22; Length 605;
 Best Local Similarity 100.0%; Pred. No. 3,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCLOYDDOKIVSGLRDNTIKIW 34
 Db 295 RHCRSETSKGYCLOYDDOKIVSGLRDNTIKIW 328

RESULT 14

AAM00960
 ID AAM00960 standard; Protein; 608 AA.

XX AAM00960;

DT 01-OCT-2001 (first entry)

DE Human bone marrow protein, SEQ ID NO: 436.

XX Human: bone marrow; antiinflammatory; cytostatic; neuroprotective;
 KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 KW immunosuppressive; gene therapy; cytokine cell proliferation;
 KW cell differentiation modulator; immune disorder; infection; cancer;
 KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
 XX
 OS Homo sapiens.

PN WO200153453-A2.

PD 26-JUL-2001.

PF 23-DEC-2000; 2000WO-US34960.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 30-NOV-2000; 2000US-0250583.

(HYSE-) HYSEQ INC.

PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y,
 PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Drmanac RT;

DR WPI: 2001-488707/53.

DR N-PSDB; AAK90079.

PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
 PT for treating e.g. cancer and immune deficiency disorders -

XX Claim 10; Page 523-524; 648pp; English.

XX The present sequence is one of 251 novel human polypeptides encoded
 CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
 CC polypeptide encoded by it are useful in the treatment of various
 CC immune deficiencies and disorders. The deficiencies and disorders may
 CC be genetic, or may result from a viral (e.g. HIV), bacterial or fungal
 CC infection, or may result from an autoimmune disorder, a coagulation
 CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
 CC suppression of an inflammatory response or treatment of a nervous
 CC system disorder such as Alzheimer's disease. Detection of a nervous
 CC or increased expression of the polynucleotide or the protein it
 CC encodes is useful for the diagnosis and/or prognosis of one

CC or more types of cancer. The polynucleotide and polypeptide can be
 CC used as nutritional sources or supplements and in the screening of
 CC chemical compounds as potential drugs.
 XX

SO Sequence 608 AA;

Query Match 100.0%; Score 186; DB 22; Length 608;
 Best Local Similarity 100.0%; Pred. No. 3,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCLOYDDOKIVSGLRDNTIKIW 34
 Db 298 RHCRSETSKGYCLOYDDOKIVSGLRDNTIKIW 331

RESULT 15

AAM78584
 ID AAM78584 standard; Protein; 632 AA.

XX AAM78584;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1246.

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

(HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI: 2001-476283/51.

DR N-PSDB; AAK51717.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -

XX Claim 20; Page 3505-3507; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 632 AA;

Query Match 100.0%; Score 186; DB 22; Length 632;
 Best Local Similarity 100.0%; Pred. No. 3.9e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGVYCYLOYDDOKIVSGLRDNTIKIW 34
 |||
 Db 322 RHCRSETSKGVYCYLOYDDOKIVSGLRDNTIKIW 355

Search completed: April 11, 2003, 11:48:13
 Job time : 11.4775 secs

... ..

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.5201 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168B-2_COPY_259_292

Perfect score: 186
Sequence: 1 RHCRSEKSGVYCLQYDDQKIVSGLRDNTIKIW 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	517	1 US-08-190-802A-30	Sequence 30, Appl
2	186	100.0	517	4 US-08-477-346-30	Sequence 30, Appl
3	186	100.0	517	4 US-08-473-089-30	Sequence 30, Appl
4	186	100.0	517	4 US-08-487-072A-30	Sequence 83, Appl
5	181	97.3	34	1 US-08-190-802A-83	Sequence 83, Appl
6	181	97.3	34	4 US-08-477-346-83	Sequence 83, Appl
7	181	97.3	34	4 US-08-473-089-83	Sequence 83, Appl
8	181	97.3	34	4 US-08-487-072A-83	Sequence 83, Appl
9	87	46.8	29	1 US-08-190-802A-87	Sequence 87, Appl
10	87	46.8	29	4 US-08-477-346-87	Sequence 87, Appl
11	87	46.8	29	4 US-08-473-089-87	Sequence 87, Appl
12	87	46.8	29	4 US-08-487-072A-87	Sequence 87, Appl
13	73	39.2	640	1 US-09-177-165A-30	Sequence 88, Appl
14	70	37.6	29	4 US-08-190-802A-88	Sequence 88, Appl
15	70	37.6	29	4 US-08-477-346-88	Sequence 88, Appl
16	70	37.6	29	4 US-08-473-089-88	Sequence 88, Appl
17	70	37.6	29	4 US-08-487-072A-88	Sequence 88, Appl
18	68.5	36.8	28	1 US-08-190-802A-84	Sequence 84, Appl
19	68.5	36.8	28	4 US-08-477-346-84	Sequence 84, Appl
20	68.5	36.8	28	4 US-08-473-089-84	Sequence 84, Appl
21	68.5	36.8	28	4 US-08-487-072A-84	Sequence 84, Appl
22	66	35.5	209	3 US-08-899-578-6	Sequence 6, Appl
23	66	35.5	587	3 US-08-899-578-2	Sequence 89, Appl
24	64	34.4	29	1 US-08-190-802A-89	Sequence 89, Appl
25	64	34.4	29	4 US-08-477-346-89	Sequence 89, Appl
26	64	34.4	29	4 US-08-473-089-89	Sequence 89, Appl
27	64	34.4	29	4 US-08-487-072A-89	Sequence 89, Appl

28	63	33.9	31	1	US-08-190-802A-71	Sequence 71, Appl
29	63	33.9	31	1	US-08-190-802A-102	Sequence 102, App
30	63	33.9	31	1	US-08-190-802A-130	Sequence 130, App
31	63	33.9	31	1	US-08-190-802A-174	Sequence 174, App
32	63	33.9	31	4	US-08-477-346-71	Sequence 71, Appl
33	63	33.9	31	4	US-08-477-346-102	Sequence 102, App
34	63	33.9	31	4	US-08-477-346-130	Sequence 130, App
35	63	33.9	31	4	US-08-477-346-174	Sequence 174, App
36	63	33.9	31	4	US-08-473-089-71	Sequence 71, Appl
37	63	33.9	31	4	US-08-473-089-102	Sequence 102, App
38	63	33.9	31	4	US-08-473-089-130	Sequence 130, App
39	63	33.9	31	4	US-08-473-089-174	Sequence 174, App
40	63	33.9	31	4	US-08-487-072A-71	Sequence 71, Appl
41	63	33.9	31	4	US-08-487-072A-102	Sequence 102, App
42	63	33.9	31	4	US-08-487-072A-130	Sequence 130, App
43	63	33.9	31	4	US-08-487-072A-174	Sequence 174, App
44	63	33.9	317	1	US-08-190-802A-27	Sequence 27, Appl
45	63	33.9	317	1	US-08-190-802A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-190-802A-30
Query Match 100.0%; Score 186; DB 1; Length 517;
Best Local Similarity 100.0%; Pred. No. 5.6e-19;
Matches 34; Conservative 0; Mismatches 0; Gaps 0;

Db 224 RHCRSETSGVYCLQYDDQKIVSGLRDNTIKIM 257

RESULT 2

US-08-477-346-30
Sequence 30, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match 100.0%; Score 186; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 5,6e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 RHCRSETSGVYCLQYDDQKIVSGLRDNTIKIM 257

RESULT 3

US-08-473-089-30
Sequence 30, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 100.0%; Score 186; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 5,6e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 RHCRSETSGVYCLQYDDQKIVSGLRDNTIKIM 257

RESULT 4

US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 100.0%; Score 186; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 5.6e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 34
DB 224 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 257

RESULT 5
US-08-190-802A-83
Sequence 83, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-190-802A-83

Query Match 97.3%; Score 181; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 34

DB 1 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 33

RESULT 6
US-08-477-346-83
Sequence 83, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-477-346-83

Query Match 97.3%; Score 181; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 34
DB 1 IHCRTSKGVYCLQYDDOKIVSGLRDNRTIKIW 33

RESULT 7
US-08-473-089-83
Sequence 83, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-473-089-83

Query Match
Best Local Similarity 97.3%; Score 181; DB 4; Length 34;
Matches 33; Conservative 100.0%; Pred. No. 1,1e-19;
Indels 0; Gaps 0;

Db 1 HCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 33

RESULT 8
US-08-487-072A-83
Sequence 83, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-487-072A-83

Query Match
Best Local Similarity 97.3%; Score 181; DB 4; Length 34;
Matches 33; Conservative 100.0%; Pred. No. 1,1e-19;
Indels 0; Gaps 0;

Db 1 HCRSETSKGVYCLQYDDQKIVSGLRDNTIKIM 33

RESULT 9
US-08-190-802A-87
Sequence 87, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rV, Fig. 13
US-08-190-802A-87

Query Match
Best Local Similarity 46.8%; Score 87; DB 1; Length 29;
Matches 14; Conservative 56.0%; Pred. No. 4,1e-06;
Indels 6; Mismatches 5; Gaps 0;

QY 10 KGVYCLQYDDQKIVSGLRDNTIKIM 34

Fri Apr 11 13:31:08 2003

us-09-601-168b-2_copy_259_292.rai

Page 5

Db 4 RGIACLOYRDRLVSGSSDNTIRLM 28

RESULT 10

US-08-477-346-87

Sequence 87, Application US/08477346

Patent No. 6262023

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: 08/487,072

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13

US-08-477-346-87

Query Match 46.8%; Score 87; DB 4; Length 29;

Best Local Similarity 56.0%; Pred. No. 4,1e-06;

Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 10 KGVYCLQYDDOKIVSGLRDNTIKIM 34

DB 4 RGIACLOYRDRLVSGSSDNTIRLM 28

RESULT 11

US-08-473-089-87

Sequence 87, Application US/08473089

Patent No. 6342368

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,072A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13

US-08-473-089-87

Query Match 46.8%; Score 87; DB 4; Length 29;

Best Local Similarity 56.0%; Pred. No. 4,1e-06;

Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 10 KGVYCLQYDDOKIVSGLRDNTIKIM 34

DB 4 RGIACLOYRDRLVSGSSDNTIRLM 28

RESULT 12

US-08-487-072A-87

Sequence 87, Application US/08487072A

Patent No. 6423684

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,072A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13

US-08-473-089-87

Query Match 46.8%; Score 87; DB 4; Length 29;

Best Local Similarity 56.0%; Pred. No. 4,1e-06;

Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 10 KGVYCLQYDDOKIVSGLRDNTIKIM 34

DB 4 RGIACLOYRDRLVSGSSDNTIRLM 28

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13

US-08-473-089-87

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-487-072A-87

Query Match 46.8%; Score 87; DB 4; Length 29;
Best Local Similarity 56.0%; Pred. No. 4,1e-06;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 10 KGVYCIQYDDQKIVSGIRNTIKIW 34
DB 4 RGACIQYRDLRVSSGSDMTIRLW 28

RESULT 13
US-09-177-165A-30
Sequence 30, Application US/09177165A
Patent No. 6426205
GENERAL INFORMATION:
APPLICANT: Tyers, Mike
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
FILE REFERENCE: 11757.10USU1
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

Query Match 39.2%; Score 73; DB 4; Length 640;
Best Local Similarity 46.2%; Pred. No. 0.018;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 9 SKGYCCIOYDDQKIVSGIRNTIKIW 34
DB 342 SDGVKLYFDKRLITIGSLDKTIRWV 367

RESULT 14
US-08-190-802A-88
Sequence 88, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
FILE REFERENCE: 11757.10USU1
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
NUMBER OF SEQ ID NOS: 265
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-190-802A-88

Query Match 37.6%; Score 70; DB 1; Length 29;
Best Local Similarity 47.8%; Pred. No. 0.0012;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 12 VYCIQYDDQKIVSGIRNTIKIW 34
DB 6 VCIQYDDQKIVSGIRNTIKIW 28

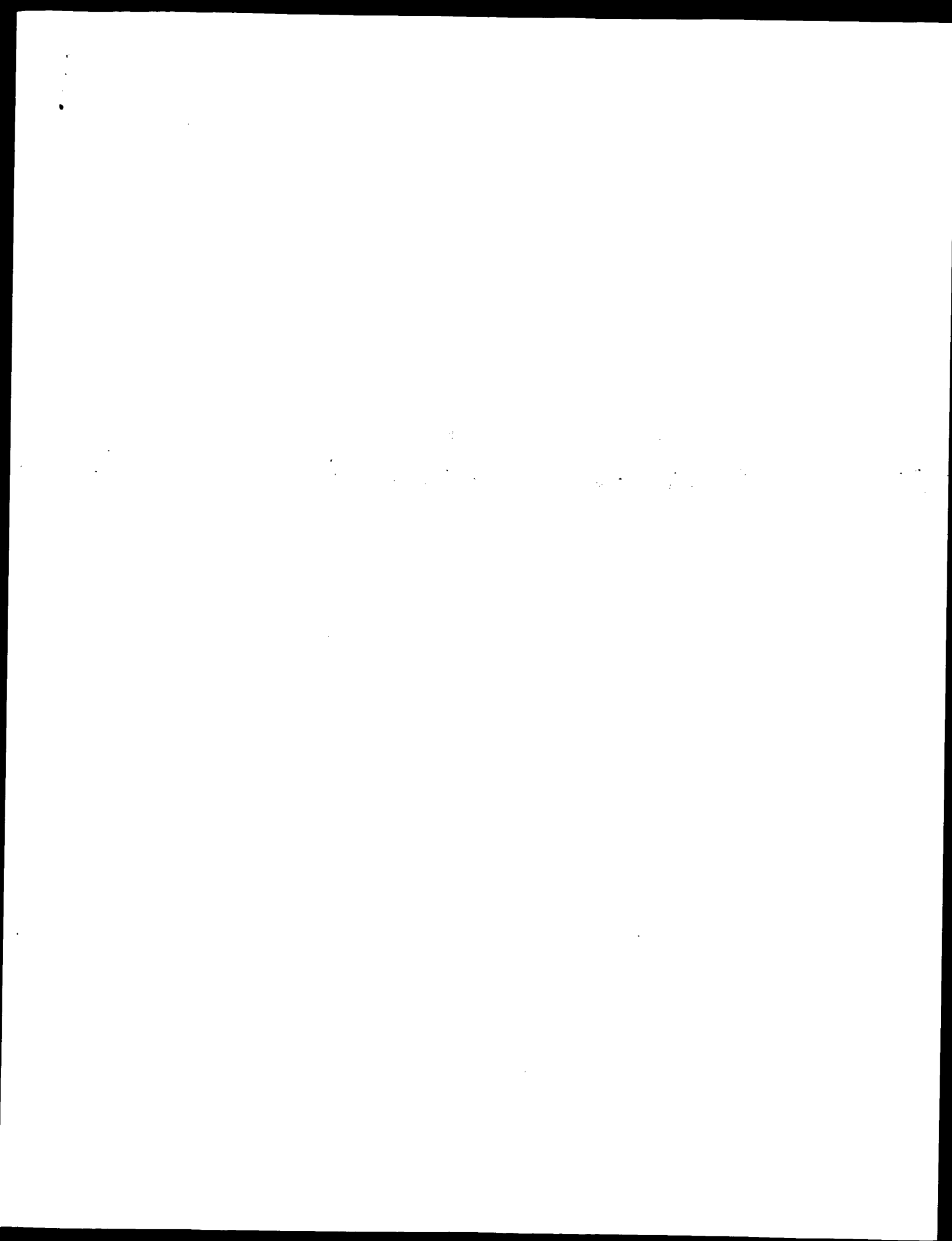
RESULT 15
US-08-477-346-88
Sequence 88, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
FILE REFERENCE: 11757.10USU1
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
NUMBER OF SEQ ID NOS: 265
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

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: INFORMATION FOR SEQ ID NO: 88:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 29 amino acids
:   TYPE: amino acid
:   TOPOLOGY: unknown
:   MOLECULE TYPE: peptide
:   HYPOTHETICAL: NO
:   ANTI-SENSE: NO
:   ORIGINAL SOURCE:
:     INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
: US-08-477-346-88
:
: Query Match      37.6%; Score 70; DB 4; Length 29;
: Best Local Similarity 47.8%; Pred. No. 0.0012;
: Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
:
: QY      12 VYCLQYDDQKIVSGLRDNTIKIW 34
:         | |::|::| | | | | | | |
: Db       6 VRCIRFDNKRIVSGAYDGKIKIW 28

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Search completed: April 10, 2003, 12:51:17
 Job time : 3.5201 secs



Fri Apr 11 13:31:08 2003

us-09-601-168b-2_copy_259_292.rapb

Page 1

GenCore version 5.1.4.P5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 3.47868 Seconds
(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_259_292

Perfect score: 186
Sequence: 1 RHCRSEKSGVYCYQYDDQKIVSGLRDNTIKIW 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	100.0	569	US-10-038-010-8	Sequence 8, Appli
2	186	100.0	569	US-10-042-417-2	Sequence 2, Appli
3	123	66.1	265	US-10-116-016-30	Sequence 30, Appli
4	123	66.1	265	US-09-764-848-30	Sequence 30, Appli
5	90	48.4	678	US-09-801-368-314	Sequence 314, App
6	73	39.2	640	US-10-060-019-30	Sequence 30, Appli
7	72	38.7	540	US-09-213-888-7	Sequence 7, Appli
8	72	38.7	540	US-09-213-888-10	Sequence 10, Appli
9	72	38.7	540	US-09-328-877A-7	Sequence 7, Appli
10	72	38.7	540	US-09-328-877A-10	Sequence 10, Appli
11	72	38.7	545	US-09-213-888-6	Sequence 6, Appli
12	72	38.7	545	US-09-328-877A-6	Sequence 6, Appli
13	72	38.7	553	US-09-213-888-5	Sequence 5, Appli
14	72	38.7	553	US-09-328-877A-5	Sequence 5, Appli
15	72	38.7	559	US-09-213-888-9	Sequence 9, Appli
16	72	38.7	559	US-09-328-877A-9	Sequence 9, Appli
17	72	38.7	589	US-09-213-888-8	Sequence 8, Appli
18	72	38.7	589	US-09-328-877A-8	Sequence 8, Appli
19	72	38.7	592	US-09-213-888-4	Sequence 4, Appli

20	72	38.7	592	US-09-328-877A-4	Sequence 4, Appli
21	72	38.7	626	US-09-213-888-21	Sequence 21, Appli
22	72	38.7	626	US-09-328-877A-21	Sequence 21, Appli
23	72	38.7	627	US-09-213-888-3	Sequence 3, Appli
24	72	38.7	627	US-09-328-877A-3	Sequence 3, Appli
25	72	38.7	666	US-09-213-888-27	Sequence 27, Appli
26	72	38.7	666	US-09-328-877A-27	Sequence 27, Appli
27	72	38.7	669	US-09-213-888-25	Sequence 25, Appli
28	72	38.7	669	US-09-328-877A-25	Sequence 25, Appli
29	63	33.9	114	US-09-796-692-1541	Sequence 1541, Ap
30	63	33.9	114	US-09-796-692-1895	Sequence 1895, Ap
31	63	33.9	316	US-09-828-310-12	Sequence 12, Appli
32	63	33.9	317	US-09-998-042-9	Sequence 9, Appli
33	63	33.9	1356	US-10-077-111-10	Sequence 10, Appli
34	63	33.9	422	US-10-042-417-4	Sequence 4, Appli
35	62	33.3	744	US-09-925-300-1347	Sequence 1347, Ap
36	61	32.8	732	US-09-832-292-12	Sequence 12, Appli
37	60	32.3	732	US-09-994-485-8	Sequence 8, Appli
38	60	32.3	190	US-10-016-447-4	Sequence 4, Appli
39	59.5	32.0	114	US-09-796-692-2023	Sequence 2023, Ap
40	59	31.7	114	US-10-083-357-1300	Sequence 1300, Ap
41	59	31.7	296	US-10-060-019-29	Sequence 29, Appli
42	59	31.7	779	US-09-832-292-10	Sequence 10, Appli
43	58	31.2	1146	US-09-994-485-6	Sequence 6, Appli
44	58	31.2	1146	US-09-994-485-6	Sequence 6, Appli
45	57	30.6	64	US-09-843-845-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-10-038-010-8
Sequence 8, Application US/10038010
Publication No. US2003040089A1
GENERAL INFORMATION:
APPLICANT: HBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038.010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta-trcp1
LOCATION: (1)-(569)
OTHER INFORMATION:
US-10-038-010-8

Query Match 100.0%; Score 186; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSEKSGVYCYQYDDQKIVSGLRDNTIKIW 34
Db 259 RHCRSEKSGVYCYQYDDQKIVSGLRDNTIKIW 292

RESULT 2
US-10-042-417-2
Sequence 2, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Paganon, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 186; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 34
Db 259 RHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIW 292

RESULT 3
US-10-116-016-30
Sequence 30, Application US/10116016
Publication No. US20030054379A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ08C1
CURRENT APPLICATION NUMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-016-30

Query Match 66.1%; Score 123; DB 9; Length 265;
Best Local Similarity 84.6%; Pred. No. 8e-10;
Matches 22; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHCRSETSKGVYCLQYDDOKIVSGLR 26
Db 225 RHCRSETSKGVYCLQYDDOKIVSGLR 250

RESULT 4
US-09-764-848-30
Sequence 30, Application US/09764848
Patent No. US2002007270A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ08
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-848-30

Query Match 66.1%; Score 123; DB 10; Length 265;
Best Local Similarity 84.6%; Pred. No. 8e-10;
Matches 22; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHCRSETSKGVYCLQYDDOKIVSGLR 26
Db 225 RHCRSETSKGVYCLQYDDOKIVSGLR 250

RESULT 5
US-09-801-368-314
Sequence 314, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 314
LENGTH: 678
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-801-368-314

Query Match 48.4%; Score 90; DB 10; Length 678;
Best Local Similarity 58.3%; Pred. No. 0.00011;
Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 11 GVCYCLQYDDOKIVSGLRDNTIKIW 34
Db 391 GVCYCLQYDDOKIVSGLRDNTIKIW 414

RESULT 6
US-10-060-019-30
Sequence 30, Application US/10060019
Publication No. US20030003564A1
GENERAL INFORMATION:
APPLICANT: Tyers, Mike
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
FILE REFERENCE: 11757.100S01
CURRENT APPLICATION NUMBER: US/10/060,019
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/177,165
PRIOR FILING DATE: 1998-10-22
Prior Application removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-060-019-30

Query Match 39.2%; Score 73; DB 9; Length 640;
Best Local Similarity 46.2%; Pred. No. 0.028;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 9 SKGYCLOYDDOKIVSGLRDNTIKIW 34
DB 342 SDGYKTYLFPDDRKLITGSLDKTIRW 367

RESULT 7
US-09-213-888-7
; Sequence 7, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 38.7%; Score 72; DB 9; Length 540;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDOKIVSGLRDNTIKIW 34
DB 217 ITCLOFGCNRIVSGSDNTLKW 239

RESULT 8
US-09-213-888-10
; Sequence 10, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-10

Query Match 38.7%; Score 72; DB 9; Length 540;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDOKIVSGLRDNTIKIW 34
DB 217 ITCLOFGCNRIVSGSDNTLKW 239

RESULT 9

US-09-328-877A-7
; Sequence 7, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-7

Query Match 38.7%; Score 72; DB 9; Length 540;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDOKIVSGLRDNTIKIW 34
DB 217 ITCLOFGCNRIVSGSDNTLKW 239

RESULT 10
US-09-328-877A-10
; Sequence 10, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-10

Query Match 38.7%; Score 72; DB 9; Length 540;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDOKIVSGLRDNTIKIW 34
DB 217 ITCLOFGCNRIVSGSDNTLKW 239

RESULT 11
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-6

Query Match 38.7%; Score 72; DB 9; Length 545;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDQKIVSGLRDNTIKIW 34
: |||: |||: |||: |||:
DB 222 ITCLQFCGNRIYSGSDNTLTKW 244

RESULT 12

US-09-328-877A-6
Sequence 6, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-6

Query Match 38.7%; Score 72; DB 9; Length 545;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDQKIVSGLRDNTIKIW 34
: |||: |||: |||: |||:
DB 222 ITCLQFCGNRIYSGSDNTLTKW 244

RESULT 13

US-09-213-888-5
Sequence 5, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-5

Query Match 38.7%; Score 72; DB 9; Length 553;

Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDQKIVSGLRDNTIKIW 34
: |||: |||: |||: |||:
DB 230 ITCLQFCGNRIYSGSDNTLTKW 252

RESULT 14

US-09-328-877A-5
Sequence 5, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match 38.7%; Score 72; DB 9; Length 553;
Best Local Similarity 52.2%; Pred. No. 0.032;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDQKIVSGLRDNTIKIW 34
: |||: |||: |||: |||:
DB 230 ITCLQFCGNRIYSGSDNTLTKW 252

RESULT 15

US-09-213-888-9
Sequence 9, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-9

Query Match 38.7%; Score 72; DB 9; Length 559;
Best Local Similarity 52.2%; Pred. No. 0.033;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCLQYDDQKIVSGLRDNTIKIW 34
: |||: |||: |||: |||:
DB 236 ITCLQFCGNRIYSGSDNTLTKW 258

Search completed: April 10, 2003, 13:16:43
J00 time : 4.47868 secs

GenCore version 5.1.4-P5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 : Search time 3.93423 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_259_292

Perfect score: 186
Sequence: 1 RHCRSETSKGYCLOYPDQKIVSGLRNTIKIW 34

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR:73:*
2: PIR:1:*
3: PIR:2:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	186	100.0	518	B48088	beta-transducin re
2	165	88.7	701	T16607	hypothetical prote
3	89	47.8	506	T50211	WD-repeat protein
4	85	45.7	605	T38932	probable sulfur me
5	82	44.1	650	T46660	sulfur controller
6	73	39.2	640	S49932	MET30 protein - ye
7	70	37.6	659	S38108	hypothetical prote
8	66	35.5	579	T22703	hypothetical prote
9	64	34.4	310	T43158	probable GRP-bindi
10	64	34.4	314	T43299	probable GRP-bindi
11	63.5	34.1	589	AG2400	WD-repeat protein
12	63	33.9	316	S57839	CP2 protein - Neu
13	63	33.9	317	A33928	GRP-binding protei
14	63	33.9	317	B33928	GRP-binding protei
15	63	33.9	317	S45054	GRP-binding regula
16	63	33.9	317	S38398	GRP-binding regula
17	63	33.9	317	A36986	activated protein
18	63	33.9	318	S11904	GRP-binding regula
19	63	33.9	349	AE2568	WD repeat protein
20	63	33.9	1356	T18521	beta transducin-II
21	62	33.3	267	S62507	hypothetical trp-a
22	62	33.3	422	A56640	CD4 repeat unit-c
23	62	33.3	1101	T26919	hypothetical prote
24	61	32.8	703	T43557	F-box/WD-repeat pr
25	61	32.8	906	S35342	Golgi-associated p
26	61	32.8	906	S35312	coatomeer complex
27	60.5	32.5	438	T45823	hypothetical prote
28	60.5	32.5	473	T33805	hypothetical prote
29	60.5	32.5	558	T40651	pre-mrna splicing

30	59.5	32.0	586	2	T38992	MD-40 repeat regul
31	59	31.7	325	2	T23309	hypothetical prote
32	59	31.7	779	2	S56245	cell division cont
33	59	31.7	1000	2	T21970	hypothetical prote
34	58	31.2	532	1	B34104	protein-tyrosine k
35	58	31.2	920	2	C96831	hypothetical prote
36	58	31.2	926	2	G96563	probable coatomeer
37	58	31.2	1146	2	A55532	myosin-heavy-chain
38	58	31.2	1893	2	T27762	hypothetical prote
39	57.5	30.9	336	2	T02300	hypothetical prote
40	57	30.6	290	2	T06784	GRP-binding regula
41	57	30.6	325	2	T09613	probable GTP-bindi
42	57	30.6	325	2	T09613	probable GTP-bindi
43	57	30.6	327	2	S48839	guanine nucleotide
44	57	30.6	334	2	T03764	protein RMD - rice
45	57	30.6	523	1	TVEVMT	protein-tyrosine k

ALIGNMENTS

RESULT 1

B48088 beta-transducin repeat-containing protein - African clawed frog

N:Alternate names: Beta-Trop C:Species: Xenopus laevis (African clawed frog)

C>Date: 26-May-1994 #sequence, revision 26-May-1994 #text-change 21-Jul-2000

C:Accession: B48088

R:Spewak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase

A:Reference number: A48088; MUID:9330289; PMID:8393141

A:Accession: B48088

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-518 <SP>

A:Cross-references: GB:M88268; NID:9295542; PIDN:AAA02810.1; PID:9295543

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

C:Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match

Best Local Similarity 100.0%; Pred. No. 5.9e-18;

Matches 34; Conservative 0; Mismatches 0; Indels 0;

QY 1 RHCRSETSKGYCLOYPDQKIVSGLRNTIKIW 34

Db 224 RHCRSETSKGYCLOYPDQKIVSGLRNTIKIW 257

RESULT 2

T16607 hypothetical protein K10B2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence, revision 20-Sep-1999 #text-change 20-Sep-1999

C:Accession: T16607

R:Miller, N. submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid K10B2.

A:Reference number: Z18545

A:Accession: T16607

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-701 <ML>

A:Cross-references: EMBL:U08730; NID:9860694; PID:9860695; PIDN:AAA6258.1; CESP:K10B

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:K10B2.1

A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3

Query Match

Best Local Similarity 88.7%; Score 165; DB 2; Length 701;

Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match 34.48; Score 64; DB 2; Length 310;

Query Match	34.18;	Score 63.5;	DB 2;	Length 589;
Best Local Similarity	44.88;	Pred. No. 0.78;		
Matches 13;	Conservative	6;	Mismatches	9;
			Indels	1;
			Gaps	1

OY 6 SETSKGYCQYDDQKIVSGLRDNTIKIM 34
 DB 345 TDVTRAI-ALTPDDQTLISGSADRTIKIM 372

RESULT 12

S57839
 C:Species: Neurospora crassa
 C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
 C/Accession: S57839
 R:Guillemot, F.; Krueger, D.; Sattlegger, E.; Hoffmann, B.; Ballario, P.; Kanan, M.; Bart
 Mol. Gen. Genet. 248, 162-173, 1995
 A>Title: The cpc-2 gene of Neurospora crassa encodes a protein entirely composed of WD-
 A/Reference number: S57839; MUID:95379761; PMID:7651339
 A/Accession: S57839
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-316 <MUE>
 A:Cross-references: EMBL:X81875; NID:971565; PIDN:CAA57460.1; PID:9971566
 C:Genetics:
 A:Introns: 14/3; 27/2; 69/3; 175/3
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:11-45/Domain: WD repeat homology <WD1>
 F:59-92/Domain: WD repeat homology <WD2>
 F:101-134/Domain: WD repeat homology <WD3>
 F:144-179/Domain: WD repeat homology <WD4>
 F:188-221/Domain: WD repeat homology <WD5>
 F:231-261/Domain: WD repeat homology <WD6>
 F:279-312/Domain: WD repeat homology <WD7>

Query Match 33.9%; Score 63; DB 2; Length 316;
 Best Local Similarity 64.7%; Pred. No. 0.48;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 18 DDOKIVSGLRDNTIKIM 34
 DB 116 DNRQIVSGSRDRTIKIM 132

RESULT 13

A33928
 C:Species: Gallus gallus (chicken)
 C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jul-2000
 C/Accession: A33928
 R:Guillemot, F.; Billault, A.; Auffray, C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4594-4598, 1989
 A>Title: Physical linkage of a guanine nucleotide-binding protein-related gene to the ch
 A/Reference number: A33928; MUID:89282817; PMID:2499885
 A/Accession: A33928
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-317 <GUI>
 A:Cross-references: GB:M24193; NID:9212293; PIDN:AAA50559.1; PID:9212294
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:11-45/Domain: WD repeat homology <WD1>
 F:59-92/Domain: WD repeat homology <WD2>
 F:101-134/Domain: WD repeat homology <WD3>
 F:144-179/Domain: WD repeat homology <WD4>
 F:188-221/Domain: WD repeat homology <WD5>
 F:231-261/Domain: WD repeat homology <WD6>
 F:279-312/Domain: WD repeat homology <WD7>

Query Match 33.9%; Score 63; DB 2; Length 317;
 Best Local Similarity 64.7%; Pred. No. 0.48;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 18 DDOKIVSGLRDNTIKIM 34
 DB 116 DNRQIVSGSRDRTIKIM 132

RESULT 14

B33928
 C:Species: Homo sapiens (man)
 C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 26-May-2000
 C/Accession: B33928
 R:Guillemot, F.; Billault, A.; Auffray, C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4594-4598, 1989
 A>Title: Physical linkage of a guanine nucleotide-binding protein-related gene to the
 A/Reference number: A33928; MUID:89282817; PMID:2499885
 A/Accession: B33928
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-317 <GUI>
 A:Cross-references: GB:M24194; NID:9187701; PIDN:AAA59626.1; PID:9307218
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:11-45/Domain: WD repeat homology <WD1>
 F:59-92/Domain: WD repeat homology <WD2>
 F:101-134/Domain: WD repeat homology <WD3>
 F:144-179/Domain: WD repeat homology <WD4>
 F:188-221/Domain: WD repeat homology <WD5>
 F:231-261/Domain: WD repeat homology <WD6>
 F:279-312/Domain: WD repeat homology <WD7>

Query Match 33.9%; Score 63; DB 2; Length 317;
 Best Local Similarity 64.7%; Pred. No. 0.48;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 18 DDOKIVSGLRDNTIKIM 34
 DB 116 DNRQIVSGSRDRTIKIM 132

RESULT 15

S45054
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-May-2000
 C/Accession: S45054
 R:Chou, Y.; Huang, J.; Liu, H.
 submitted to the EMBL Data Library, May 1994
 A:Description: cDNA of porcine G-beta like protein.
 A/Reference number: S45054
 A/Accession: S45054
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-317 <CHO>
 A:Cross-references: EMBL:Z33879; NID:9495143; PIDN:CAA83944.1; PID:9495144
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:11-45/Domain: WD repeat homology <WD1>
 F:59-92/Domain: WD repeat homology <WD2>
 F:101-134/Domain: WD repeat homology <WD3>
 F:144-179/Domain: WD repeat homology <WD4>
 F:188-221/Domain: WD repeat homology <WD5>
 F:231-261/Domain: WD repeat homology <WD6>
 F:279-312/Domain: WD repeat homology <WD7>

Query Match 33.9%; Score 63; DB 2; Length 317;
 Best Local Similarity 64.7%; Pred. No. 0.48;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 18 DDOKIVSGLRDNTIKIM 34
 DB 116 DNRQIVSGSRDRTIKIM 132

Search completed: April 10, 2003, 13:23:00
 Job time : 4.93423 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 2.44336 Seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_259_292

Perfect score: 186
Sequence: 1 RHCNSETSKGVYCLQYDDQKIVSGLRDNTIKIW 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	518	1	TRCB_XENLA
2	186	100.0	605	1	FW1A_HUMAN
3	165	88.7	542	1	FW1B_HUMAN
4	165	88.7	665	1	LI23_CAEEL
5	90	48.4	678	1	SCOB_EMENT
6	89	47.8	506	1	POFB_SCHPO
7	85	45.7	605	1	POFI_SCHPO
8	82	44.1	650	1	SC02_NEUCR
9	76	40.9	684	1	CC4_CANAL
10	73	39.2	640	1	MT30_YEAST
11	70	37.6	659	1	YK16_YEAST
12	69	37.1	317	1	GBLP_HYAT
13	66	35.5	379	1	SE10_CAEEL
14	64	34.4	314	1	GBLP_CAEEL
15	63	33.9	316	1	GBLP_BIOGL
16	63	33.9	316	1	GBLP_NEUCR
17	63	33.9	317	1	GBLP_BRARE
18	63	33.9	317	1	GBLP_HUMAN
19	63	33.9	317	1	GBLP_ORENI
20	63	33.9	318	1	GBLP_CHRE
21	63	33.9	318	1	GBLP_DROME
22	63	33.9	1356	1	HET1_PODAN
23	62	33.3	422	1	FBW2_HUMAN
24	62	33.3	422	1	FBW2_MOUSE
25	61	32.8	422	1	GBLP_DICDI
26	61	32.8	703	1	POP2_SCHPO
27	61	32.8	904	1	COPP_RAT
28	61	32.8	905	1	COPP_BOVIN
29	61	32.8	905	1	COPP_HUMAN
30	61	32.8	905	1	COPP_MOUSE
31	60	32.3	732	1	KHMB_DICDI
32	60	32.3	914	1	COPP_DROME
33	59.5	32.0	586	1	TU12_SCHPO

34	59	31.7	324	1	GBLP_CAEEL	Q21215 caenorhabdi
35	59	31.7	779	1	CC4_YEAST	P07834 saccharomyc
36	59	31.7	1000	1	COPP_CAEEL	Q20168 caenorhabdi
37	58	31.2	318	1	GBLP_TRYBB	Q94775 trypanosoma
38	58	31.2	531	1	SR02_XENLA	P13116 xenopus lae
39	58	31.2	682	1	TU01_KL0LA	P56094 kiuyveromyc
40	58	31.2	1146	1	KHMA_DICDI	P42527 dictyosteli
41	57	30.6	325	1	GBLP_MEDSA	Q24076 medicago sa
42	57	30.6	325	1	GBLP_SOYBN	Q39836 glycine max
43	57	30.6	327	1	GBLP_ARATH	Q24456 arabidopsis
44	57	30.6	327	1	GBLP_BRANA	Q39336 brassica na
45	57	30.6	334	1	GBLP_ORYSA	P49027 oryza sativ

ALIGNMENTS

RESULT 1
TRCB_XENLA STANDARD; PRT; 518 AA.
AC Q91854: P70037; P70038;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-TTCP (Beta-transducin repeat-containing protein).
GN FBXW1 OR BTCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330289; PubMed=8393141;
RA Spevak W., Keiper B.D., Stratawa C., Castanon M.J.;
RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
anaphase are rescued by Xenopus CNAs encoding N-ras or a protein
with beta-transducin repeats."
RL Mol. Cell. Biol. 13:4953-4966(1993).
RN [2]
RP SEQUENCE OF 302-518 FROM N.A.
RX MEDLINE=97109804; PubMed=8952061;
RA Hudson J.W., Alarcon V.B., Elinson R.P.;
RT "Identification of new localized RNAs in the Xenopus oocyte by
differential display PCR."
RL Dev. Genet. 19:190-198(1996).
CC - FUNCTION: Probably recognizes and binds to some phosphorylated
proteins and promotes their ubiquitination and degradation.
CC - SUBUNIT: PART OF A SCF (SKP1-CUL1N-F-BOX) PROTEIN LIGASE COMPLEX
(BY SIMILARITY).
CC - DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
TADPOLE EMBRYO.
CC - SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC - SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
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or send an email to license@sib-sib.ch).
CC EMBL, M98268; AA02810.1; -
DR EMBL, U63921; AAB49671.1; -
DR EMBL, U63922; AAB49672.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.

DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.
 FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
 FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
 SQ SEQUENCE 518 AA: 59507 MW: 2A52EC19028127F3 CRC64;

Query Match 100.0%; Score 186; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 1.5e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCYCLODQKIVSGLRDNTIKIM 34
 Db 224 RHCRSETSKGYCYCLODQKIVSGLRDNTIKIM 257

RESULT 2
 FW1A_HUMAN STANDARD; PRT; 605 AA.
 AC 09Y297; 09Y213;
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP)
 DE FBXW1A OR FBW1A OR BTCP OR BTCP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996;
 RA Varon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.,
 RT "Identification of the receptor component of the ikappaalpha-
 RT ubiquitin ligase";
 RL Nature 396:590-594(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940;
 RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.;
 RT "A novel human WD protein, h-beta TrCP, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif";
 RL Mol. Cell 1:565-574(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035;
 RA Genetelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RP CHARACTERIZATION
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,

RA Harper J.W.;
 RT "The SCF(beta-TrCP)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and
 RT beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro";
 RL Genes Dev. 13:270-283(1999).
 CC - FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA
 CC (FKBPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR
 CC UBIQUITINATION AND DEGRADATION.
 CC - SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC - SUBCELLULAR LOCATION: Cytoplasmic.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -
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DR EMBL: AF101784; AAD08702.1; -
 DR EMBL: Y14153; CA74572.1; -
 DR EMBL: AF129530; AAF04464.1; -
 DR GENB: HGNC:1144; BTCP.
 DR MIM: 603482; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF004400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 190 228 F-BOX.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 52 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 605 AA: 68866 MW: 4C67F3B7E400FD37 CRC64;

Query Match 100.0%; Score 186; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHCRSETSKGYCYCLODQKIVSGLRDNTIKIM 34
 Db 295 RHCRSETSKGYCYCLODQKIVSGLRDNTIKIM 328

RESULT 3
 FW1B_HUMAN STANDARD; PRT; 542 AA.
 AC 09YK81; 09Y4C6; 09P2S8; 09P2S9;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP2).
 DE FBXW1B OR FBW1B OR BTCP2 OR KIAA0696.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=200303050; PubMed=10531035;
 RA Cenciarrelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RT Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Fetal lung;
 RX MEDLINE=20160458; PubMed=10694485;
 RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katoh M.;
 RT "Molecular cloning and genomic structure of the betatropin gene on
 RT chromosome 5q35.1.";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A, B AND C (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: AF176022; AAF04528.1; -;
 DR EMBL: AB033279; BAA92329.1; -;
 DR EMBL: AB033280; BAA92330.1; -;
 DR EMBL: AB033281; BAA92331.1; -;
 DR EMBL: AB014596; BAA31671.1; ALT_INIT.
 DR Genew: HGNC:13607; FBXW1B.
 DR MIM: 605651; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 129 167 F-BOX.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VANSPLIC 16 49 MISSING (IN ISOFORM A).

FT VARSPLIC 16 48 CSVPSLW/GCANLIVSMCALSCQSMPSVACL -> NTSV
 FT SEQUENCE 542 AA: 62090 MW: 7CD40087EFAA55C8A CRC64;
 SQ MEDONEDSPKNTLM (IN ISOFORM B).
 Query Match 88.7%; Score 165; DB 1; Length 542;
 Best Local Similarity 85.3%; Pred. No. 1,4e-15;
 Matches 29; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 RICHRETSKGYVCLOYDDOKIVSGLRDTIKIM 34
 DB 232 RIQRENSKGYVCLOYDEKIIISGLRDSIKIM 265
 RESULT 4
 LIT3.CAEEL
 ID LIT3.CAEEL STANDARD; PRT; 665 AA.
 AC 009990; O96GN6; 36, Created)
 DT 15-JUL-1998 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein Lin-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION: DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RX MEDLINE=20515608; PubMed=11060233.
 RA Kipreos E.T., Gohei S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein Lin-23 functions
 RT to limit cell division during development.";
 RL Development 127:5071-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 CC cycle progression. Required to restrain cell proliferation in
 CC response to developmental cues. Probably recognizes and binds to
 CC some proteins and promotes their ubiquitination and degradation
 CC (By similarity).
 CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 CC levels in larvae. Maternal expression results in high zygotic
 CC levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
 CC -----
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 CC -----
 DR EMBL: AF275253; AAG28037.1; -;
 DR EMBL: U28730; AAA68258.2; -;
 DR WormPep: K10B2.1; CE28600.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.

DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PS50181; FBOX; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS500678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Developmental protein; Cell cycle; Cell division;
 KW ubi conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 81 127 F-BOX.
 FT REPEAT 220 257 WD 1.
 FT REPEAT 260 299 WD 2.
 FT REPEAT 301 337 WD 3.
 FT REPEAT 343 380 WD 4.
 FT REPEAT 383 420 WD 5.
 FT REPEAT 423 460 WD 6.
 FT REPEAT 472 509 WD 7.
 FT DOMAIN 525 582 ALA-RICH.
 FT MUTAGEN 441 441 G->R: IN LIN-32(RH293).
 SQ SEQUENCE 665 AA; 75916 MW; BF3E9AF51F12ECCC CRC64;
 Query Match 88.7%; Score 165; DB 1; Length 665;
 Best Local Similarity 88.2%; Pred. No. 1,7e-15;
 Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RHCRSETSKGVCLQYDDOKIVSGLRDNTIKIW 34
 DB 214 RINCSEKSKGVCLQYDDOKIVSGLRDNTIKIW 247
 RESULT 5
 SCOB_EMENT
 ID SCOB_EMENT STANDARD; PRT; 678 AA.
 AC 000659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sulfur metabolite repression control protein.
 GN SCONB OR MAPBI.
 OS Emeritella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emeritella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mactort R;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
 REPRESSION.
 CC -1- SIMILARITY: CONTAINS 8 WD_REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
 PROTEINS.
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 CC -----
 DR EMBL: U21220; AAC15905.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00440; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS500678; WD_REPEATS_1; 4.

DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transcription regulation; Repeat; WD repeat.
 FT DOMAIN 178 224 F-BOX.
 FT REPEAT 347 375 WD 1.
 FT REPEAT 387 415 WD 2.
 FT REPEAT 427 455 WD 3.
 FT REPEAT 466 496 WD 4.
 FT REPEAT 508 543 WD 5.
 FT REPEAT 553 595 WD 6.
 FT REPEAT 607 635 WD 7.
 FT REPEAT 647 675 WD 8.
 SQ SEQUENCE 678 AA; 76070 MW; D840DX52E3784C53 CRC64;
 Query Match 48.4%; Score 90; DB 1; Length 678;
 Best Local Similarity 58.3%; Pred. No. 5.6e-05;
 Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 11 GVCYCLQYDDOKIVSGLRDNTIKIW 34
 DB 391 GIRCLOFDDTKLISGSMRTIKIW 414
 RESULT 6
 POFR_SCHPO
 ID POFR_SCHPO STANDARD; PRT; 506 AA.
 AC 009855; O9P7V1;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein profilin.
 GN POFL1 OR SPAC29E6.01 OR SPAC30.05.
 GN Schizosaccharomyces pombe (fission yeast).
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harrison C.L., Toda T.;
 RT "Systematic genome-wide analysis of F-box protein-encoding genes in
 RT fission yeast."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliland R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris N., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton K., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Robben J., Gymnopoulos B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito G.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).

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CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
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CC -----
DR EMBL: AB061694; BAB5543.1; -
DR EMBL: AL136538; CAB66464.1; -
DR EMBL: Z66525; CA91423.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 3.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS.1; 3.
DR PROSITE: PS50082; WD_REPEATS.2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT DOMAIN 70 116 F-BOX.
FT REPEAT 219 256 WD 1.
FT REPEAT 259 298 WD 2.
FT REPEAT 301 338 WD 3.
FT REPEAT 345 386 WD 4.
FT REPEAT 388 426 WD 5.
FT REPEAT 427 464 WD 6.
FT REPEAT 468 505 WD 7.
SQ SEQUENCE 506 AA; 58257 MW; CEF34DAEFFBC2E10 CRC64;

Query Match 47.8%; Score 89; DB 1; Length 506;
Best Local Similarity 51.9%; Pred. No. 5.7e-05;
Matches 14; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 8 TSKGYCYCLQYDDOKIVSGLRDNTIKIW 34
1 |||:||||:||||:|:|:|
Db 220 TLDYVCYQYDDEIMVSGSKDRFVSVM 246

RESULT 7
POFI_SCHPO STANDARD; PRT: 605 AA.
ID POFI_SCHPO
AC P87053;
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DE F-box/WD-repeat protein pofi (Skp1-binding protein 1).
OS POPI OR SBP1 OR SPAC57A10.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-972;
RA Katayama S., Kitamura K., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RT fission yeast."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Najandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell J., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Moore P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Welfens I., Vanstreels E., Rieger M., Scheffer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym M., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Mamhuth R., Punnett B.,
RA Goffeau A., Giddey E., Dreano S., Gloux S., Ielaue V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.
RL Nature 415:871-880(2002).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB032410; BAA84528.1; -
DR EMBL: Z94864; CAB08168.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 5.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS.1; 2.
DR PROSITE: PS50082; WD_REPEATS.2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Ubl conjugation; Repeat; WD repeat.
FT DOMAIN 107 153 F-BOX.
FT REPEAT 271 299 WD 1.
FT REPEAT 311 339 WD 2.
FT REPEAT 350 379 WD 3.
FT REPEAT 390 420 WD 4.
FT REPEAT 432 460 WD 5.
FT REPEAT 472 500 WD 6.
FT REPEAT 510 538 WD 7.
SQ SEQUENCE 605 AA; 67110 MW; 7118C9379EC5C1F0 CRC64;

Query Match 45.7%; Score 85; DB 1; Length 605;
Best Local Similarity 57.7%; Pred. No. 0.00025;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 9 SKGYCYCLQYDDOKIVSGLRDNTIKIW 34
1 |||:||||:||||:|:|:|
Db 313 SSGVTCLQFDQCKLISGMDKTRIKIW 338

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AC      P53699;    01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
CD      Cell division control protein 4.
GN      CDC4.
OS      Candida albicans (Yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC      Saccharomycetales; mitosporic Saccharomycetales; Candida.
CX      NCBI_TaxId=5476;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SGY126;
RA      Shieh J.C., White A.M., Rosamond J.;
RL      Submitted (APR-1996) to the EMBL/GenBank/DDI databases.
CC      -! FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
CC      REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM THE
CC      POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
CC      DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
CC      VARIOUS ASPECTS OF SPOULATION. REQUIRED FOR HTA1-HTB1 LOCUS
CC      TRANSCRIPTION ACTIVATION (BY SIMILARITY).
CC      -! SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC      -! SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce,
CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; X96763; CAA65358.1; -.
DR      InterPro; IPR001810; F-box.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF004400; WD40; 7.
DR      Pfam; PF00646; F-box; 1.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      ProDom; PD000018; WD40; 1.
DR      SMART; SM00256; FBOX; 1.
DR      SMART; SM00320; WD40; 7.
DR      PROSITE; PS50181; FBOX; 1.
DR      PROSITE; PS00678; WD_REPEATS_1; 4.
DR      PROSITE; PS50082; WD_REPEATS_2; 4.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW      Cell division; Mitosis; Sporulation; Repeat; WD repeat.
FT      DOMAIN                212       258
FT      REPEAT                322       351             WD 1.
FT      REPEAT                363       391             WD 2.
FT      REPEAT                403       431             WD 3.
FT      REPEAT                442       468             WD 4 (POTENTIAL).
FT      REPEAT                478       506             WD 5.
FT      REPEAT                519       549             WD 6.
FT      REPEAT                561       589             WD 7.
SQ      SEQUENCE        684 AA; 76090 MW; 3DD65DB31293B107 CRC64;
Query Match          40.9%; Score 76; DB 1; Length 684;
Best Local Similarity 44.1%; Pred. NO. 0.0052;
Matches 15; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY      1 RHCHSETSKGYCYCLDYDOKIVSGLRDNITKIIM 34
Db      317 RISVSGHGKNKVYTCGLQHDEKVTGVVDKCKISLY 350

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OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydrozoa; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zurich;
RA Hassel M.E.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL; X97800; CAA66387.1; -
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 5.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 4.
DR PROSITE; PS00682; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 3 45 WD 1.
FT REPEAT 52 93 WD 2.
FT REPEAT 94 135 WD 3.
FT REPEAT 137 180 WD 4.
FT REPEAT 181 221 WD 5.
FT REPEAT 222 262 WD 6.
FT REPEAT 263 313 WD 7.
SQ SEQUENCE 317 AA; 35256 MW; 5D3087F3B50E8A4F CRC64;

Query Match 37.1%; Score 69; DB 1; Length 317;
Best Local Similarity 70.6%; Pred. No. 0.022;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 18 DDQKIVSGIRDNTIKIM 34
DB 116 DNRQIVSGSRDNTIKIM 132

RESULT 13
SE10.CAEEL STANDARD; PRT; 579 AA.
AC 093794;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sel-10 protein.
GN SEL-10 OR P55B12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sims M.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC [2]
CC REVISIONS.
CC Jones S.J.M.;
CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL; 279757; CAB02129.1; -
DR WormRep; P55B12.3; CE16120.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 5.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT DOMAIN 113 159 F-BOX.
FT REPEAT 245 274 WD 1.
FT REPEAT 286 316 WD 2.
FT REPEAT 328 356 WD 3.
FT REPEAT 368 396 WD 4.
FT REPEAT 408 438 WD 5.
FT REPEAT 453 481 WD 6.
FT REPEAT 493 522 WD 7.
SQ SEQUENCE 579 AA; 64275 MW; 0647245AF5964663 CRC64;

Query Match 35.5%; Score 66; DB 1; Length 579;
Best Local Similarity 43.5%; Pred. No. 0.11;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 12 VYCLQDDQKIVSGIRDNTIKIM 34
DB 251 ITCMQIHDDVLVTGSDNTIKIM 273

RESULT 14
GBLP_SCHPO STANDARD; PRT; 314 AA.
AC 010281; P78896;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Guanine nucleotide-binding protein beta subunit-like protein (Receptor
DE of activated protein kinase C).
GN RKP1 OR CPC2 OR SPAC6812.15.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED616;
RA Park S.-K., Yoo H.-S.;
RA Park S.-K., Yoo H.-S.;
RA Kim H.-B., Yoo H.-S.;
RA "Rkp1/Cpc2, a fission yeast RACK1 homolog, is involved in actin
cytoskeleton organization through protein kinase C, Pck2, signaling."
Biochem. Biophys. Res. Commun. 282:10-15(2001).
RN [3]

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RP SEQUENCE FROM N.A.
 RC STRAIN-972:
 RA MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor J., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckart G., Aert R., Robben J., Gymnopoulos B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Beger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sipakovski G.V., Ussery D., Barrell B.G., Nuse P.,
 RA "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 RN [4]
 RP SEQUENCE OF 5-314 FROM N.A.
 RC STRAIN-PR745:
 RX MEDLINE-9816722; PubMed-9501991;
 RA Yoshida S., Kato K., Nakai K., Okayama H., Nojima H.,
 RT "Identification of open reading frames in Schizosaccharomyces pombe
 RT cDNAs."
 RL DNA Res. 4:363-369(1997).
 CC -1- FUNCTION: MAY BE A RECEPTOR FOR PROTEIN KINASE C IN THE REGULATION
 CC OF ACTIN CYTOSKELETON ORGANIZATION DURING CELL WALL SYNTHESIS AND
 CC MORPHOGENESIS.
 CC -1- SUBUNIT: INTERACTS WITH PKC2.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH PARTICULATE FRACTIONS.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: L37885; AAA56865.2; -;
 DR EMBL: AF320333; AAK38633.1; -;
 DR EMBL: Z98531; CAB11079.1; -;
 DR EMBL: D89247; BAA13908.1; -;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 5.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 KM REPEAT 13 44 WD 1.
 FT REPEAT 13 44 WD 1.
 FT REPEAT 61 91 WD 2.
 FT REPEAT 103 133 WD 3.
 FT REPEAT 146 178 WD 4.
 FT REPEAT 190 220 WD 5.
 FT REPEAT 231 260 WD 6.
 FT REPEAT 281 311 WD 7.
 FT REPEAT 41 41 WD 7.
 FT CONFLICT 41 41 I -> L (IN REF. 1).

SQ SEQUENCE 314 AA: 34851 MW: 4E14707164E68ACD CRC64;
 Query Match 34.4%; Score 64; DB 1; Length 314;
 Best Local Similarity 64.7%; Pred. No. 0.11;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 18 DDQKIVSGLRDNTIKIM 34
 Db 116 DNRQVVGSRDRTIKIM 132
 ::::|||||
 RESULT 15
 GBLP_BIOGL
 ID GBLP_BIOGL STANDARD; PRT; 316 AA.
 AC 093134;
 DT 01-NOV-1997 (rel. 35. Created)
 DT 01-NOV-1997 (rel. 35. Last sequence update)
 DT 16-OCT-2001 (rel. 40. Last annotation update)
 DE Guanine nucleotide-binding protein beta subunit-like protein
 DE (Receptor of activated protein kinase C) (RACK).
 OS Biophalaris glabrata (Bloodfluke planorb).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Planorbidae; Biophalarina.
 OX NCBI_TaxID=6526;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lardans V.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: U49437; AAB07039.1; -;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 5.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 KM REPEAT 4 46 WD 1.
 FT REPEAT 52 93 WD 2.
 FT REPEAT 94 135 WD 3.
 FT REPEAT 137 180 WD 4.
 FT REPEAT 181 221 WD 5.
 FT REPEAT 222 263 WD 6.
 FT REPEAT 264 312 WD 7.
 SO SEQUENCE 316 AA: 35008 MW: B6668144BC7B81DB CRC64;
 QY 18 DDQKIVSGLRDNTIKIM 34
 Db 116 DNRQVVGSRDRTIKIM 132
 ::::|||||
 Search completed: April 10, 2003, 13:19:33
 Job time: 3.44336 secs

1. The first part of the paper is devoted to a discussion of the general principles of the theory of the structure of the atom. It is shown that the structure of the atom is determined by the laws of quantum mechanics, which are based on the principle of the uncertainty of the position and momentum of the particles.

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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 8.03411 Seconds

(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_259_292

Sequence: 1 RHCRSEKSGVCLQYDDQKIVSGLRDNFTIKW 34

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-ryinus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	569	11	Q9R1G7 mus musculus
2	186	100.0	569	11	Q9R1G7 mus musculus
3	186	100.0	569	11	Q9R1G7 mus musculus
4	171	91.9	47	13	Q8U0N5 mus musculus
5	167	89.8	510	5	Q44382 drosophila
6	167	89.8	510	5	Q9VDE3 drosophila
7	166	89.2	430	5	Q9HJ54 heterodera
8	163	87.6	563	11	Q9J3H0 mus musculus
9	87	46.8	252	11	Q9J2C7 mus musculus
10	75	40.3	1326	5	Q9VZF4 drosophila
11	72	38.7	122	13	Q8U0N3 mus musculus
12	72	38.7	553	4	Q9N0X6 homo sapien
13	72	38.7	561	4	Q96R12 homo sapien
14	72	38.7	589	4	Q96IE0 homo sapien
15	72	38.7	627	4	Q96A16 homo sapien
16	72	38.7	629	11	Q8VHP4 mus musculus

ALIGNMENTS

17	72	38.7	629	11	Q8VHP4	Q8VHP4 mus musculus
18	72	38.7	707	4	Q969H0	Q969H0 homo sapien
19	67	36.0	942	5	Q96611	Q96611 dictyosteli
20	66	35.5	585	5	Q95ZT0	Q95ZT0 caenorhabdi
21	66	35.5	587	5	Q44083	Q44083 caenorhabdi
22	64	34.4	781	5	Q8SVW7	Q8SVW7 encephalito
23	63.5	34.1	589	16	Q8YN14	Q8YN14 anabaena sp
24	63	33.9	280	11	Q9CS00	Q9CS00 mus musculus
25	63	33.9	296	11	Q9ERM6	Q9ERM6 mus musculus
26	63	33.9	313	5	Q9UAY2	Q9UAY2 euryyma sc
27	63	33.9	316	3	Q9HGV7	Q9HGV7 emericella
28	63	33.9	317	13	Q9W711	Q9W711 xenopus lae
29	63	33.9	319	5	Q9SPD5	Q9SPD5 heliothis v
30	63	33.9	349	16	Q8YJY6	Q8YJY6 anabaena sp
31	63	33.9	823	10	Q9F9Y6	Q9F9Y6 arabidopsis
32	63	33.9	914	4	Q9C0F5	Q9C0F5 homo sapien
33	63	33.9	1065	3	Q8X1P6	Q8X1P6 podospora a
34	63	33.9	1356	3	Q8X1P5	Q8X1P5 podospora a
35	63	33.9	1356	3	Q8X1P4	Q8X1P4 podospora a
36	63	33.9	1356	3	Q8X1P3	Q8X1P3 podospora a
37	62	33.3	245	11	Q9CP06	Q9CP06 mus musculus
38	62	33.3	245	11	Q99153	Q99153 mus musculus
39	62	33.3	454	4	Q8WV51	Q8WV51 homo sapien
40	62	33.3	454	4	Q9HA09	Q9HA09 homo sapien
41	62	33.3	454	11	Q9Q0H1	Q9Q0H1 mus musculus
42	62	33.3	1101	5	Q62471	Q62471 caenorhabdi
43	62	33.3	1573	11	Q90X12	Q90X12 mus musculus
44	61	32.8	329	5	Q8SP4	Q8SP4 dictyosteli
45	61	32.8	932	10	Q9FHL5	Q9FHL5 arabidopsis

RESULT 1

Q9R1G7: PRELIMINARY: PRT: 569 AA.

AC Q9R1G7: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Beta-transducin repeat-containing protein.

GN BTRC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Winston J., Elledge S.J., Harper J.W.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL: AF110396; AAD41025.1; -

DR MGD: MGI:1338871; BTRC.

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001680; WD40.

DR Pfam: PF00646; F-box; 1.

DR Pfam: PF00400; WD40; 7.

DR PRINTS: PR00320; GPROTEINBPT.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00236; FBOX; 1.

DR SMART: SM00320; WD40; 7.

DR PROSITE: PS00181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.

DR PROSITE: PS00882; WD_REPEATS_2; 7.

DR PROSITE: PS0294; WD_REPEATS_REGION; 1.

DR Repeat: WD repeat.

KW SEQUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;

Query Match 100.0%; Score 186; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 34
      |||||||
Db      259 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 292

RESULT 2
ID      092159      PRELIMINARY:      PRT:      569 AA.
AC      092159;
DT      01-MAY-1999 (TrEMBLrel. 10, Created)
DT      01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Beta-transducin repeat containing protein.
GN      BTRC.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_Taxid=10090;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99145465; PubMed=9990853;
RA      Spencer E., Jiang J., Chen Z.J.,
RT      "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
RL      Slim/Delta-Tricp."
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR      EMBL: AF112979; AAD04181.1;
DR      MGD: MGI:1338871; Btrc.
DR      InterPro: IPR001810; F-box.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00646; F-box; 1.
DR      PRINTS: PR00320; GPROTEINBPT.
DR      ProDom: PD000018; WD40; 4.
DR      SMART: SM00256; FBOX; 1.
DR      SMART: SM00320; WD40; 7.
DR      PROSITE: PS50181; FBOX; 1.
DR      PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
DR      PROSITE: PS50082; WD_REPEATS_2; 7.
DR      PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW      Repeat; WD repeat.
SQ      SEQUENCE 569 AA; 65047 MW; BC7C7444815BED96 CRC64;

Query Match      100.0%; Score 186; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 34
      |||||||
Db      259 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 292

RESULT 3
ID      090015      PRELIMINARY:      PRT:      569 AA.
AC      090015;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Ubiquitin ligase FMD1 (Beta-transducin repeat containing protein)
      (F-box-WD40 repeat protein 1).
GN      BTRC OR FBXW1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_Taxid=10090;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99199275; PubMed=10097128;
RA      Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
RA      Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
RA      Nakayama K.-I.;
RT      "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a

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RT      ubiquitin ligase Skp1/Cul 1/F-box protein FMD1."
RL      Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99075339; PubMed=9859996;
RA      Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA      Andersen J.S., Mann M., Mercutio F., Ben-Neriah Y.;
RT      "Identification of the receptor component of the IkappaBalpha-
RT      ubiquitin ligase."
RL      Nature 396:590-594(1998).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SV;
RX      MEDLINE=21601157; PubMed=11735228;
RA      Nakayama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA      Nakayama K.-I.;
RT      "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
RT      Caenorhabditis elegans SEL-10."
RL      Genomics 78:214-222(2001).
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR      EMBL: AF081887; AAD17755.1;
DR      EMBL: AF099932; AAD08701.1;
DR      EMBL: BC003989; AAH03989.1;
DR      EMBL: AF391190; AAL40929.1;
DR      EMBL: AF391178; AAL40929.1; JOINED.
DR      EMBL: AF391179; AAL40929.1; JOINED.
DR      EMBL: AF391180; AAL40929.1; JOINED.
DR      EMBL: AF391181; AAL40929.1; JOINED.
DR      EMBL: AF391182; AAL40929.1; JOINED.
DR      EMBL: AF391183; AAL40929.1; JOINED.
DR      EMBL: AF391184; AAL40929.1; JOINED.
DR      EMBL: AF391185; AAL40929.1; JOINED.
DR      EMBL: AF391187; AAL40929.1; JOINED.
DR      EMBL: AF391188; AAL40929.1; JOINED.
DR      EMBL: AF391189; AAL40929.1; JOINED.
DR      MGD: MGI:1338871; Btrc.
DR      InterPro: IPR001810; F-box.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00646; F-box; 1.
DR      Pfam: PF00400; WD40; 7.
DR      PRINTS: PR00320; GPROTEINBPT.
DR      ProDom: PD000018; WD40; 4.
DR      SMART: SM00256; FBOX; 1.
DR      SMART: SM00320; WD40; 7.
DR      PROSITE: PS50181; FBOX; 1.
DR      PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
DR      PROSITE: PS50082; WD_REPEATS_2; 7.
DR      PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW      Ligase; Repeat; WD repeat.
SQ      SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match      100.0%; Score 186; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 34
      |||||||
Db      259 RHCRSETSKGVCLQYDDQKIVSGLRDNTIKIM 292

RESULT 4
ID      0800N5      PRELIMINARY:      PRT:      47 AA.
AC      0800N5;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Beta-Trcp protein (Fragment).

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GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RL "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
RT Thesis (2001);
RL Department of Genetics and Molecular Biology "Charles Darwin",
RL University of Rome La Sapienza, Rome, Italy.
DR EMBL: AJ428936; CAD21933.1; -.
FT NON_TER 1 47
FT SEQUENCE 47 AA; 5499 MW; 1C18C15B13EE9F5F CRC64;
SQ
Query Match 91.9%; Score 171; DB 13; Length 47;
Best local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RHCSETSKGVYCLQYDDOKIVSGLRDNTIK 32
Db 15 RHCSETSKGVYCLQYDDOKIVSGLRDNTIK 46
|||||
RESULT 5
ID 044382 PRELIMINARY; PRT; 510 AA.
AC 044382;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SLIMB
GN SLIMB OR SLIMB OR CG3412.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98121115; PubMed=9461217;
RA Jiang J.; Struhl G.;
RL "Regulation of the Hedgehog and Wingless signalling pathways by the F-box/WD40-repeat protein Slimb.";
RT box/WD40-repeat protein Slimb.";
RL Nature 391:493-496(1998).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF032878; AAC38852.1; -.
DR FlyBase: FBgn0023423; slmb.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPOTEINBRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;
Query Match 89.8%; Score 167; DB 5; Length 510;
Best local Similarity 91.2%; Pred. No. 1.8e-15;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 RHCSETSKGVYCLQYDDOKIVSGLRDNTIK 34
Db 202 RHCSETSKGVYCLQYDDOKIVSGLRDNTIK 235
|||||
RESULT 6
ID 09VDE3 PRELIMINARY; PRT; 510 AA.
AC 09VDE3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SLIMB protein (SLIMB).
GN SLIMB OR CG3412.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers Y.-H.C.; Blaise R.G.; Champe M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA Abril J.F.; Agbayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;
RA Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolshakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brotlier P.;
RA Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablos J.M.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dudson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Foster C.; Gabrielian A.E.; Gary N.S.; Gelbart W.M.; Glasser K.;
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegyan C.;
RA Jaisli M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.B.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
RA Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Mishina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.;
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Paclet J.M.;
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.;
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.;
RA Svitskas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wasserman D.A.; Weinstein G.M.; Weissbach J.;
RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;
RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhu G.; Zhao Q.; Zheng L.;
RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.;
RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=OVARY, AND IMAGINAL DISC;
RX MEDLINE=20245299; PubMed=10781936;
RA Miletich I.; Limbourg-Bouchon B.;
RT "Drosophila null slimb clones transiently deregulate Hedgehog-
independent transcription of wingless in all limb discs and induce
RT decapentaplegic transcription linked to imaginal disc regeneration.";
RL Mech. Dev. 93:15-26(2000).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AE003733; AAF55853.1; -.

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DR EMBL; AF222924; AAF63214.1; -
 DR EMBL; AF222923; AAF63213.1; -
 DR FlyBase; FBgn0023423; slmb.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00320; FBOX; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PS00181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SO SEQUENCE 510 AA; 58952 MW; F4D5DF126F58A012 CRC64;

Query Match 89.8%; Score 167; DB 5; Length 510;
 Best Local Similarity 91.2%; Pred. No. 1.8e-15;
 Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RHCRSEKSGVYCLQYDDQKIVSGLRDNTIKIW 34
 Db 202 RINCSEKSGVYCLQYDDQKIVSGLRDNTIKIW 235

RESULT 7
 O9BJ54 PRELIMINARY; PRT; 430 AA.
 AC O9BJ54; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Beta-transducin repeat-containing protein (Fragment).
 OS Heterodera glycines (Soybean cyst nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera;
 OX NCBI_TaxID=51029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kovalova E.S., Yakovlev A.G., Masler E.P.;
 RT "Plant parasitic nematode b-TRCP";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL; AF339101; AAK26376.1; -
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER
 SO SEQUENCE 430 AA; 47916 MW; 4ABC3FF2DDE3A50B CRC64;

Query Match 89.2%; Score 166; DB 5; Length 430;
 Best Local Similarity 85.3%; Pred. No. 2.2e-15;
 Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RHCRSEKSGVYCLQYDDQKIVSGLRDNTIKIW 34
 Db 83 RINCSEKSGVYCLQYDDQKIVSGLRDNTIKIW 116

RESULT 8
 O923H0 PRELIMINARY; PRT; 563 AA.
 AC O923H0; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE F-box/WD40 repeat-containing protein HOS.
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Bhatia N., Heter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
 RT "Mouse homolog of HOS (MHOS) is overexpressed in skin tumors and
 RT implicated in constitutive activation of NF-kappaB";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL; AY038079; AAK72095.1; -
 DR MGI; MGI:2144023; Fbxw1b.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR ProDom; PD000018; WD40; 4.
 DR PROSITE; PS00181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SO SEQUENCE 563 AA; 64741 MW; 9AB562F3FE5E3496 CRC64;

Query Match 87.6%; Score 163; DB 11; Length 563;
 Best Local Similarity 85.3%; Pred. No. 7.6e-15;
 Matches 29; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RHCRSEKSGVYCLQYDDQKIVSGLRDNTIKIW 34
 Db 253 RINCSEKSGVYCLQYDDQKIVSGLRDNTIKIW 286

RESULT 9
 O922C7 PRELIMINARY; PRT; 252 AA.
 AC O922C7; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to f-box and WD-40 domain protein 1B (Fragment).
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL; BC008552; AAK08552.1; -
 DR MGI; MGI:2144023; Fbxw1b.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 6.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER
 SO SEQUENCE 252 AA; 28424 MW; F71737CBD7A9F75F CRC64;

Query Match 46.8%; Score 87; DB 11; Length 252;
 Best Local Similarity 56.0%; Pred. No. 0.00022;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 10 KGVYCYLDYDOKIVSGLRDNTIKIM 34
 DB 114 KGIACIQYDRDLVSGSSDNTIKIM 138

RESULT 10

OY9VZF4 PRELIMINARY: PRT: 1326 AA.

AC O9VZF4; 09VZF4; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG15010 protein (LD213322p) (LD30271p).
 GN AGO OR CG15010.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Plannkuch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glied A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jaitai M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Meklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL thesis 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
 RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RC SEQUENCE FROM N.A.
 RN STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AE003480; AAC2246.1; -
 DR EMBL: AY061300; AAL28848.1; -
 DR EMBL: AY075401; AAL68231.1; -
 DR FlyBase: FBgn0041171; ago.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR000320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 2.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS0082; WD_REPEATS_2; 7.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 1326 AA; 141360 MW; 3F42C873CFA3027F CRC64;

Query Match 40.3%; Score 75; DB 5; Length 1326;

Best Local Similarity 52.2%; Pred. No. 0.061; Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 12 VYCYLDYDOKIVSGLRDNTIKIM 34
 DB 998 ITCIQGSGNRIVSGSDNTIKIM 1020

RESULT 11

ID08UN3 PRELIMINARY: PRT: 122 AA.

AC 08UN3; 08UN3; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta-TrCP protein (Fragment).
 GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=6335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carnevali F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ballarín M.;
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis".
 RL thesis (2001).
 RL Department of Genetics and Molecular Biology "Charles Darwin",
 RL University of Rome La Sapienza, Rome, Italy.
 DR EMBL: AJ428938; CAD21935.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 3.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 2.
 DR SMART: SM00320; WD40; 3.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE: PS0082; WD_REPEATS_2; 3.
 DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
 FT NON_TER 1 1
 FT NON_TER 122 122

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SQ SEQUENCE 122 AA: 13682 MW: 36BB6B39AC8F5387 CRC64;
Query Match 38.7%; Score 72; DB 13; Length 122;
Best Local Similarity 59.1%; Pred. No. 0.015;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 KGYCLOYDDOKIVSGLRDNTKI 31
:|:|||||:|||||
DB 101 KGIACLOYRDLRVSSGSDNTKI 122

RESULT 12
O96R12 PRELIMINARY; PRT; 553 AA.
AC O96R12;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDNA FLJ11071 fis, clone PLACE1004937, moderately similar to SEL-10
DE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuno Y., Sasaki N.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AK001933; BAA91986.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 553 AA: 62280 MW: CA829C221986A3F2 CRC64;

Query Match 38.7%; Score 72; DB 4; Length 553;
Best Local Similarity 52.2%; Pred. No. 0.067;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCIQYDDOKIVSGLRDNTKI 34
:|:|||||:|||||
DB 230 ITCLQFCGNRIYSGSDNTLKW 252

RESULT 13
O96R12 PRELIMINARY; PRT; 561 AA.
AC O96R12;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F-box protein FBX30 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF383178; AAK60269.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRODOM: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 561 AA: 63165 MW: B81CC1E2205B0D88 CRC64;

Query Match 38.7%; Score 72; DB 4; Length 561;
Best Local Similarity 52.2%; Pred. No. 0.068;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCIQYDDOKIVSGLRDNTKI 34
:|:|||||:|||||
DB 238 ITCLQFCGNRIYSGSDNTLKW 260

RESULT 14
O96LE0 PRELIMINARY; PRT; 569 AA.
AC O96LE0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F-box protein SEL10.
GN SEL10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R.,
RA Buhl A.E., Gurney M.E.;
RT "SEL-10 interacts with Presenilin 1, facilitates its ubiquitination,
RT and Alters A-beta production."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY008274; AAC16640.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRODOM: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA: 66120 MW: 2AFB6E8A36E68DE CRC64;

Query Match 38.7%; Score 72; DB 4; Length 589;
Best Local Similarity 52.2%; Pred. No. 0.072;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 12 VYCIQYDDOKIVSGLRDNTKI 34
:|:|||||:|||||
DB 266 ITCLQFCGNRIYSGSDNTLKW 288

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RESULT 15

Q96A16 PRELIMINARY; PRT; 627 AA.

AC Q96A16; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Archipelago beta form (F-box protein FBW7).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21449047; PubMed=11565033;

RA Moberg K.H., Bell D.W., Wahner D.C., Haber D.A., Hartharan I.K.;

RT "Archipelago regulates Cyclin E levels in Drosophila and is mutated in human cancer cell lines.";

RL Nature 413:311-316(2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20003061; PubMed=10531037;

RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;

RT "A family of mammalian F-box proteins.";

RL Curr. Biol. 9:1180-1182(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL: AF411972; AAL06291.1; -;

DR EMBL: AY033553; AAK57547.1; -;

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001880; WD40.

DR Pfam: PF00646; F-box; 1.

DR Pfam: PF00400; WD40; 7.

DR ProDom: PD000018; WD40; 2.

DR PROSITE: PS50181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

KM Repeat; WD repeat.

SQ SEQUENCE 627 AA; 70324 MW; 3D4107C053381BED CRC64;

Query Match

38.7%; Score 72; DB 4; Length 627;

Best Local Similarity 52.2%; Pred. No. 0.076;

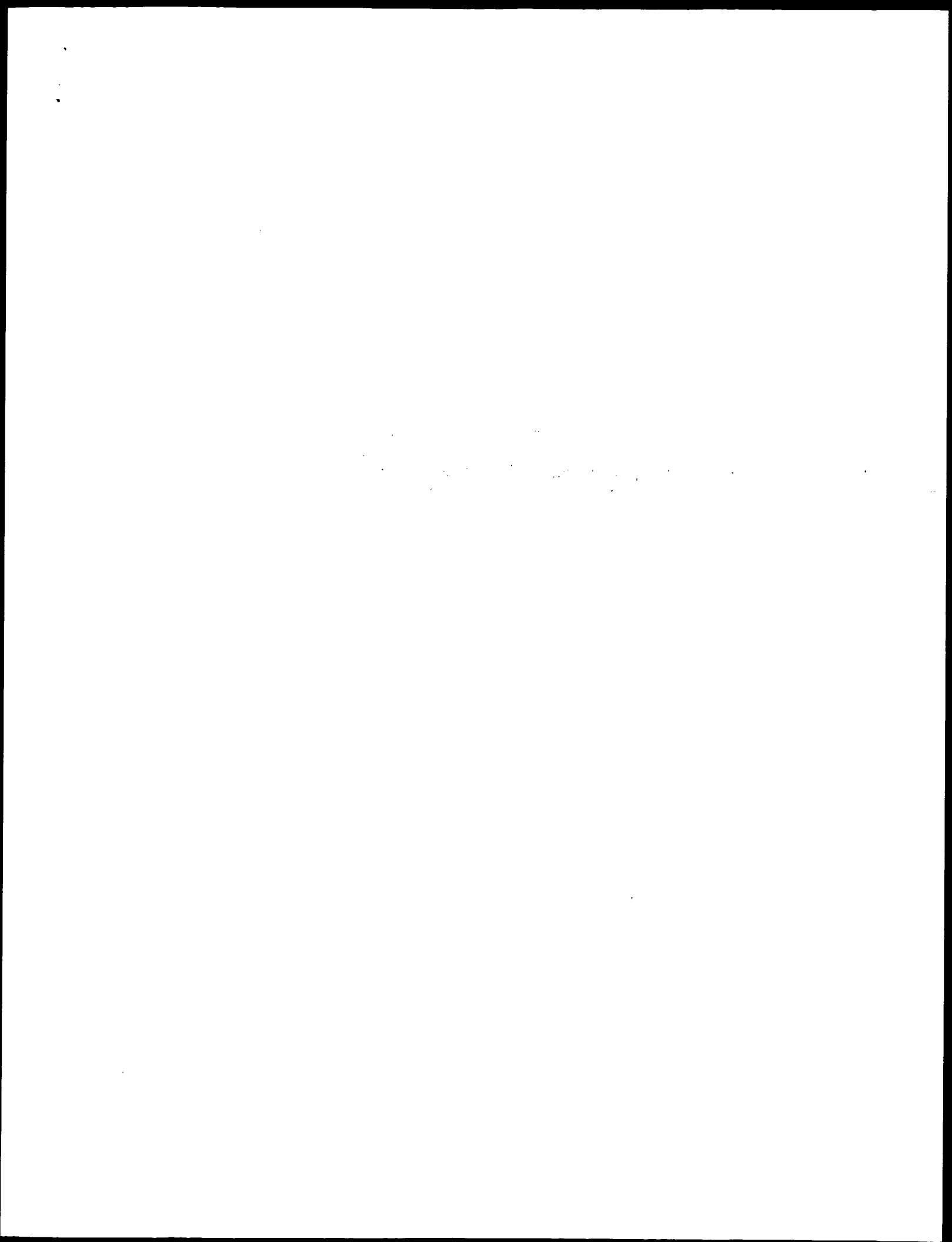
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 12 VYCIQYDDOKIVSGLRNTIKIW 34

DB 304 ITCIQFCGNRIVSGSDNDITLKW 326

Search completed: April 11, 2003, 11:51:32

Job time : 9.03411 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 : Search time 8.93666 Seconds

(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3:	/SID2/gcgdata/geneseq-emb1/AA1982.DAT.*
4:	/SID2/gcgdata/geneseq-emb1/AA1983.DAT.*
5:	/SID2/gcgdata/geneseq-emb1/AA1984.DAT.*
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7:	/SID2/gcgdata/geneseq-emb1/AA1986.DAT.*
8:	/SID2/gcgdata/geneseq-emb1/AA1987.DAT.*
9:	/SID2/gcgdata/geneseq-emb1/AA1988.DAT.*
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16:	/SID2/gcgdata/geneseq-emb1/AA1995.DAT.*
17:	/SID2/gcgdata/geneseq-emb1/AA1996.DAT.*
18:	/SID2/gcgdata/geneseq-emb1/AA1997.DAT.*
19:	/SID2/gcgdata/geneseq-emb1/AA1998.DAT.*
20:	/SID2/gcgdata/geneseq-emb1/AA1999.DAT.*
21:	/SID2/gcgdata/geneseq-emb1/AA2000.DAT.*
22:	/SID2/gcgdata/geneseq-emb1/AA2001.DAT.*
23:	/SID2/gcgdata/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	153	100.0	569	20	AAV24054
2	153	100.0	569	21	AA12812
3	153	100.0	569	21	AA12813
4	153	100.0	569	21	AAV96697
5	153	100.0	569	21	AAV83041
6	153	100.0	569	21	AAV83250
7	153	100.0	569	21	AAV83254
8	153	100.0	569	21	AAV44249
9	153	100.0	579	22	AAV78563
10	153	100.0	590	22	AAW00847

11	153	100.0	605	22	AAV78582	Human protein SEQ
12	153	100.0	608	22	AAW00960	Human bone marrow
13	153	100.0	632	22	AAV78584	Human protein SEQ
14	153	100.0	654	22	AAV79566	Human protein SEQ
15	153	100.0	654	22	AAV79567	Human protein SEQ
16	153	100.0	654	22	AAV79568	Human protein SEQ
17	152	99.3	542	21	AAV96696	Human E3 ubiquitin
18	152	99.3	542	21	AAV9127	Human protein SEQ
19	152	99.3	542	22	AAW40208	Human polypeptide
20	152	99.3	550	22	AAW41994	Human polypeptide
21	146	95.4	569	22	AAW48298	Human F21 protein
22	138	90.2	510	22	AAW59857	Drosophila melanog
23	133.5	87.3	28	16	AAW4936	Peptide r11 from a
24	133.5	87.3	517	16	AAW85852	WD-40 domain-contg
25	97	63.4	29	16	AAW4939	Peptide rv from a
26	86	56.2	640	21	AAV83252	F-box protein Met3
27	84	54.9	540	20	AAV22465	Human hippocampal
28	84	54.9	540	20	AAV22466	Human mammary sel-
29	84	54.9	540	22	AAW59197	Human mammary sel-
30	84	54.9	540	22	AAW59200	Human mammary sel-
31	84	54.9	545	20	AAV22464	Human hippocampal
32	84	54.9	545	22	AAW59196	Human hippocampal
33	84	54.9	553	20	AAV22463	Human hippocampal
34	84	54.9	553	22	AAW93475	Human protein sequ
35	84	54.9	553	22	AAW59195	Human mammary sel-
36	84	54.9	559	22	AAV22467	Human mammary sel-
37	84	54.9	559	22	AAW59199	Human mammary sel-
38	84	54.9	589	20	AAV22466	Human mammary sel-
39	84	54.9	589	21	AAW01204	Human GTPase assoc
40	84	54.9	589	22	AAW59198	Human mammary sel-
41	84	54.9	592	20	AAV22462	Human hippocampal
42	84	54.9	592	22	AAW59194	Human hippocampal
43	84	54.9	626	20	AAV22469	Human myc-N-sel-1
44	84	54.9	626	22	AAW59201	Protein encoded by
45	84	54.9	627	20	AAV22461	Human hippocampal

ALIGNMENTS

RESULT 1			
ID	AAV24054	standard: Protein: 569 AA.	
XX	AAV24054;		
XX	30-SEP-1999	(first entry)	
DE	A human beta-transducin repeat containing protein.		
XX			
KW	Beta-transducin repeat containing protein; beta-Trcp; Sklp;		
KW	proteosome degradation pathway; Vpu protein; beta-catenin;		
KW	human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;		
KW	ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's		
KW	antiviral; antitumour; cell cycle regulation; protein degradation;		
KW	and anti-inflammatory; osteo-articular inflammation; acute inflammation;		
KW	tumour necrosis factor.		
XX			
OS	Homo sapiens.		
XX			
EH	Key	Location/Qualifiers	
FT	Region	147..191	
FT	Region	/note="F box sequence"	
FT	Region	259..292	
FT	Region	/note="WD motif"	
FT	Region	304..332	
FT	Region	/note="WD motif"	
FT	Region	343..372	
FT	Region	/note="WD motif"	
FT	Region	387..415	
FT	Region	/note="WD motif"	
FT	Region	427..455	
FT	Region	/note="WD motif"	

```

FT Region 467..492
FT /note="WD motif"
FT Region 516..544
FT /note="WD motif"
XX
XX WO9938969-A1.
XX
XX 05-AUG-1999.
XX
XX 29-JAN-1999; 99WO-FR00196.
XX
XX 09-DEC-1998; 98FR-0015545.
XX 30-JAN-1998; 98FR-0001100.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (INSP ) INST PASTEUR.
XX
XX Arenzana Seisdedos F, Benarous R, Concordet J, Durand H;
XX Kroll M, Margottin F;
XX WPI; 1999-469329/39.
XX N-PSDB; AAX86501.
XX
XX New human beta-transducin repeat containing protein and its
XX fragments useful as, or to screen for, antiviral, antitumour,
XX anti-inflammatory and anti-Alzheimer's agents
XX
XX Claim 1; Page 60-61; 71pp; French.
XX
XX The present sequence represents a human beta-transducin repeat containing
XX protein (beta-trcp). The protein directs proteins to the proteosome
XX degradation pathways. The protein is able to interact with the Ypu
XX protein of human immune deficiency virus-1 (HIV-1), cellular proteins
XX IkappaB or beta-catenin (bc) and/or protein Skp1. The protein controls
XX ubiquitinylation of phosphorylated proteins and thus their targeting to
XX proteosomes for degradation. Depending on whether the process is
XX inhibited or promoted, the result may be delayed breakdown of CD4 (in
XX cases of HIV-1 infection); increased activity of Ikb (and thus reduced
XX activity of NFkappaB); increased degradation of mutant bc; in tumour
XX cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
XX patients. The beta-trcp protein, and its active peptide fragments, or its
XX nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
XX antitumour agents that disrupt cell cycle regulation or protein
XX degradation in human tumour cells, and anti-inflammatory agents that
XX disrupt activation by NFkappaB. Fragments of the protein are also
XX useful for treating osteo-articular inflammation or acute inflammation
XX associated with release of tumour necrosis factor.
XX
XX Sequence 569 AA:
SQ
Query Match 100.0%; Score 153; DB 20; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGHGTGVLQYDERVITIGSSDSTVRW 29
DB 304 TGHGTGVLQYDERVITIGSSDSTVRW 332

```

```

XX
XX Mus musculus.
XX
XX JP2000166542-A.
XX
XX 20-JUN-2000.
XX
XX 02-DEC-1998; 98JP-0343437.
XX
XX 02-DEC-1998; 98JP-0343437.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX WPI; 2000-485550/43.
XX N-PSDB; AAA73131.
XX
XX F-box protein of ubiquitin ligase SCF complex which promotes the
XX ubiquitinylation of IkappaB or beta-catenin
XX
XX Claim 2; Page 9-10; 19pp; Japanese.
XX
XX The present invention describes an F-box motif protein of ubiquitin
XX ligase SCF complex which promotes the ubiquitinylation of IkappaB or
XX beta-catenin and is constituted by Skp1 protein, Cull protein and a
XX complex (SCF complex) of F-box protein containing F-box motif and WD40
XX repeat motif and has the amino acid sequence of 45 residues (AAB12811)
XX or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
XX ligase FMD1 protein) and (AAB12813, which is human beta-transducin
XX repeat containing protein (beta-trcp)). The F-box protein can be used for
XX the gene therapy of colon cancer by being recombined to a virus vector.
XX
XX Sequence 569 AA:
SQ
Query Match 100.0%; Score 153; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGHGTGVLQYDERVITIGSSDSTVRW 29
DB 304 TGHGTGVLQYDERVITIGSSDSTVRW 332

```

```

RESULT 3
AAB12813
ID AAB12813 standard; protein: 569 AA.
XX
XX AAB12813;
XX
XX 27-NOV-2000 (first entry)
XX
XX Human beta-transducin repeat containing protein (beta-Trcp) SEQ ID NO:3.
XX
XX Ubiquitin ligase SCF complex; F-box protein: ubiquitinylation; IkappaB;
XX beta-catenin; Skp1; Cull; F-box motif; WD40 repeat motif; FMD1;
XX gene therapy; colon cancer; beta-transducin repeat containing protein;
XX beta-Trcp.
XX
XX Homo sapiens.
XX
XX JP2000166542-A.
XX
XX 20-JUN-2000.
XX
XX 02-DEC-1998; 98JP-0343437.
XX
XX 02-DEC-1998; 98JP-0343437.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2000-485550/43.
XX N-PSDB; AAA73132.
XX
XX F-box protein of ubiquitin ligase SCF complex which promotes the

```

ubiquitination of IkappaB or beta-catenin -

XX Claim 3; Page 10-12; 19pp; Japanese.

XX The present invention describes an F-box motif protein of ubiquitin

CC ligase SCF complex which promotes the ubiquitination of IkappaB or

CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a

CC complex (SCF complex) of F-box protein containing F-box motif and WD40

CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)

CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin

CC ligase FWD1 protein) and (AAB12813, which is human beta-transducin

CC repeat containing protein (beta-TrCP)). The F-box protein can be used for

CC the gene therapy of colon cancer by being recombined to a virus vector.

XX

SO Sequence 569 AA:

Query Match 100.0%; Score 153; DB 21; Length 569;

Best Local Similarity 100.0%; Pred. No. 1.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGHTGSLVLCLOYDERVITIGSSDSTVRW 29

DB 304 TGHTGSLVLCLOYDERVITIGSSDSTVRW 332

RESULT 4

AA96697

ID AAY96697 standard; Protein; 569 AA.

XX

AC AAY96697;

XX

DT 26-SEP-2000 (first entry)

XX

DE Human beta-TrCP.

XX

KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;

KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;

KW anti-inflammatory; immunosuppressive; cytostatic.

XX

OS Homo sapiens.

XX

PN WO200034447-A2.

XX

PD 15-JUN-2000.

XX

PF 10-DEC-1999; 99WO-US29371.

XX

PR 10-DEC-1998; 98US-0210060.

XX

PA (SIGN-) SIGNAL PHARM INC.

PA (YISS) YISSUM RES & DEV CO.

XX

PI Manning AM, Mercutio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;

PI Lavon I, Yaron A;

XX

DR WPI: 2000-431294/37.

DR N-PSDB: AAA51229.

XX

PT Polypeptide enhancing phosphorylated IkappaB ubiquitination useful for

PT treating disorder associated with NF-kappaB activation e.g. cancer,

PT comprising amino acid sequence of human E3 ubiquitin ligase or its

PT variant

XX

PS Claim 21; Page 72-74; 77pp; English.

XX

CC Human beta-TrCP, an F-box/WD protein family member, has been shown to

CC have homology to human E3 ubiquitin ligase (E3). E3 enhances

CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of

CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B

CC degradation via the ubiquitin pathway is useful for identifying

CC modulators of this process for use in treating diseases associated with

CC activation of NF-kappa-B. In vitro analysis suggests that deletion of

CC the F-box results in a protein that functions as a dominant negative

CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a

CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha

CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated

CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B

CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat

CC inflammatory diseases, autoimmune diseases, cancer and viral infections.

XX

SO Sequence 569 AA:

Query Match 100.0%; Score 153; DB 21; Length 569;

Best Local Similarity 100.0%; Pred. No. 1.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGHTGSLVLCLOYDERVITIGSSDSTVRW 29

DB 304 TGHTGSLVLCLOYDERVITIGSSDSTVRW 332

RESULT 5

AA93041

ID AAY83041 standard; Protein; 569 AA.

XX

AC AAY83041;

XX

DT 16-AUG-2000 (first entry)

XX

DE F-box protein FBP-1.

XX

KW F-box protein; FBP; diagnosis; treatment; screening; agonist;

KW antagonist; proliferative disorder; differentiative disorder;

KW breast cancer; prostate cancer; ovarian cancer; cancer;

KW small cell lung carcinoma; immune disorder; cardiovascular disorder;

KW inflammatory disorder; human.

XX

OS Homo sapiens.

XX

PN WO200012679-A1.

XX

PD 09-MAR-2000.

XX

PF 27-AUG-1999; 99WO-US19560.

XX

PR 28-AUG-1998; 98US-0098355.

PR 03-FEB-1999; 99US-0118568.

PR 15-MAR-1999; 99US-0124449.

XX

PA (UYNV) UNIV NEW YORK STATE.

XX

PI Chiaur DS, Pagano M, Latres E;

XX

DR WPI: 2000-256635/22.

DR N-PSDB: AA293350.

XX

PT Novel nucleic acid for screening compounds useful for treating

PT proliferative and differentiative disorders such as cancer and immune

PT disorders comprises sequences encoding ubiquitin ligases

XX

PS Disclosure; Figure 3a; 245pp; English.

XX

CC Nucleic acids encoding substrate-targeting subunits of ubiquitin

CC ligases with F-box motifs (F-box proteins) are useful for diagnosis

CC of proliferative and differentiated related disorders by measuring

CC FBP gene expression. Cells expressing such proteins or

CC their fragments are useful for screening compounds. The compounds

CC are agonists or antagonists, which are useful for treating a

CC proliferative or differentiative disorder in a mammal such as

CC breast, ovarian and prostate cancer and small cell lung carcinoma

CC and also major opportunistic infections, immune disorders,

CC cardiovascular diseases and inflammatory disorders. FBP protein,

CC analogs, derivatives and their subsequences, anti-FBP antibodies

CC are also useful in diagnosis of the disorders.

XX

SO Sequence 569 AA:

Query Match 100.0%; Score 153; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1.7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLOYDERVITITGSSDSTVRW 29
 |||||
 DB 304 TGHGTVLCLOYDERVITITGSSDSTVRW 332

RESULT 6

AAV83250
 ID AAV83250 standard; Protein; 569 AA.

AC AAV83250;

DT 16-AUG-2000 (first entry)

DE F-box protein hbeta1CP.

XX Ubiquitin ligase; SCF; F-box protein; targeted degradation;

KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;

KM oncoprotein; Huntington's disease; gene knockout; delivery systems;

human.

XX Homo sapiens.

PN W0200022110-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23705.

XX 09-OCT-1998; 98US-0103787.

XX (HARD) HARVARD COLLEGE.

XX Zhou P, Howley P;

XX WPI: 2000-317970/27.

XX DR N-PSDB; AA293710.

XX Targeting degradation of polypeptide useful for treating cancer and

PT other proliferative disorders, involves conjugating polypeptide with

PT ubiquitin protein ligase or inhibiting ubiquitination using organic

PT compound

XX Claim 9; Page 171; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

XX Sequence 569 AA;

Query Match 100.0%; Score 153; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1.7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLOYDERVITITGSSDSTVRW 29
 |||||
 DB 304 TGHGTVLCLOYDERVITITGSSDSTVRW 332

RESULT 7

AAV83254
 ID AAV83254 standard; Protein; 569 AA.

AC AAV83254;

DT 16-AUG-2000 (first entry)

DE F-box protein FWD1P.

XX Ubiquitin ligase; SCF; F-box protein; targeted degradation;

KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;

KM oncoprotein; Huntington's disease; gene knockout; delivery systems;

mouse; ss.

XX Mus musculus.

PN W0200022110-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23705.

XX 09-OCT-1998; 98US-0103787.

XX (HARD) HARVARD COLLEGE.

XX Zhou P, Howley P;

XX WPI: 2000-317970/27.

XX DR N-PSDB; AA293714.

XX Targeting degradation of polypeptide useful for treating cancer and

PT other proliferative disorders, involves conjugating polypeptide with

PT ubiquitin protein ligase or inhibiting ubiquitination using organic

PT compound

XX Claim 9; Page 184-185; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

XX Sequence 569 AA;

Query Match 100.0%; Score 153; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 1.7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLOYDERVITITGSSDSTVRW 29
 |||||
 DB 304 TGHGTVLCLOYDERVITITGSSDSTVRW 332

PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51716.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3504-3505; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53425) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 SQ Sequence 579 AA;
 QY 1 TGHGTGVLQYDERVITITGSSDSTVRVW 29
 DB 314 TGHGTGVLQYDERVITITGSSDSTVRVW 342
 RESULT 10
 AAM00847
 ID AAM00847 standard; Protein; 590 AA.
 XX
 AC AAM00847;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human bone marrow protein, SEQ ID NO: 210.
 XX
 KW Human; bone marrow; antiinflammatory; cytosolic; neuroprotective;
 KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 KW immunosuppressive; gene therapy; cytokine cell proliferation;
 KW cell differentiation modulator; immune disorder; infection; cancer;
 KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153453-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 23-DEC-2000; 2000WO-US34960.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0633450.
 PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.
 PR 30-NOV-2000; 2000US-0250583.
 XX
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
 PI Ren F, Wang J, Wejhrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Drmanac RT;
 XX
 DR WPI; 2001-488707/53.
 DR N-PSDB; AAH89966.
 XX
 PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
 PT for treating e.g. cancer and immune deficiency disorders -
 XX
 PS Claim 10; Page 354-355; 648pp; English.
 XX
 CC The present sequence is one of 251 novel human polypeptides encoded
 CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
 CC polypeptide encoded by it are useful in the treatment of various
 CC immune deficiencies and disorders. The deficiencies and disorders may
 CC be genetic, or may be caused by a viral (e.g. HIV), bacterial or fungal
 CC infection, or may result from an autoimmune disorder, a coagulation
 CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
 CC suppression of an inflammatory response or treatment of a nervous
 CC system disorder such as Alzheimer's disease. Detection of the presence
 CC or increased expression of the polynucleotide or the protein it
 CC encodes is useful for the diagnosis and/or prognosis of one
 CC or more types of cancer. The polynucleotide and polypeptide can be
 CC used as nutritional sources or supplements and in the screening of
 CC chemical compounds as potential drugs.
 XX
 SQ Sequence 590 AA;
 QY 1 TGHGTGVLQYDERVITITGSSDSTVRVW 29
 DB 325 TGHGTGVLQYDERVITITGSSDSTVRVW 353
 RESULT 11
 AAM78582
 ID AAM78582 standard; Protein; 605 AA.
 XX
 AC AAM78582;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1244.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.


```

PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dirmnac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX N-PSDB: AAK51715.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3503-3504; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAW80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX SQ
XX
XX Sequence 605 AA:
XX
XX Query Match 100.0%; Score 153; DB 22; Length 605;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-15;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGHGTGVLCTGYDERVITITGSSDSTVRW 29
XX |||||||||||||||||||
XX Db 340 TGHGTGVLCTGYDERVITITGSSDSTVRW 368
XX
XX RESULT 12
XX AAW00960
XX ID AAW00960 standard; Protein: 608 AA.
XX
XX AC AAW00960;
XX
XX DT 01-OCT-2001 (first entry)
XX
XX DE Human bone marrow protein, SEQ ID NO: 436.
XX
XX KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
XX antifungal; antibacterial; antifungal; anti-HIV; haemostatic;
XX immunosuppressive; gene therapy; cytokine cell proliferation;
XX cell differentiation modulator; immune disorder; infection; cancer;
XX human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
XX
XX OS Homo sapiens.
XX
XX PN WO200153453-A2.
XX
XX PD 26-JUL-2001.
XX
XX PE 23-DEC-2000; 2000WO-US34960.
XX
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.

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PR 30-NOV-2000; 2000US-0250583.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
XX Ren F, Wang J, Wejhrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Dirmnac RT;
XX
XX WPI: 2001-488707/53.
XX N-PSDB: AAH90079.
XX
XX Novel bone-marrow-expressed polynucleotides and polypeptides, useful
XX for treating e.g. cancer and immune deficiency disorders -
XX
XX Claim 10; Page 523-524; 648pp; English.
XX
XX The present sequence is one of 251 novel human polypeptides encoded
XX by a bone marrow-expressed polynucleotide. The polynucleotide and the
XX polypeptide encoded by it are useful in the treatment of various
XX immune deficiencies and disorders. The deficiencies and disorders may
XX be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
XX infection, or may result from an autoimmune disorder, a coagulation
XX disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
XX suppression of an inflammatory response or treatment of a nervous
XX system disorder such as Alzheimer's disease. Detection of the presence
XX or increased expression of the polynucleotide or the protein it
XX encodes is useful for the diagnosis and/or prognosis of one
XX or more types of cancer. The polynucleotide and polypeptide can be
XX used as nutritional sources or supplements and in the screening of
XX chemical compounds as potential drugs.
XX
XX SQ
XX
XX Sequence 608 AA:
XX
XX Query Match 100.0%; Score 153; DB 22; Length 608;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-15;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGHGTGVLCTGYDERVITITGSSDSTVRW 29
XX |||||||||||||||||||
XX Db 343 TGHGTGVLCTGYDERVITITGSSDSTVRW 371
XX
XX RESULT 13
XX AAW78584
XX ID AAW78584 standard; Protein: 632 AA.
XX
XX AC AAW78584;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human protein SEQ ID NO 1246.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX OS Homo sapiens.
XX
XX PN WO200157190-A2.
XX
XX PD 09-AUG-2001.
XX
XX PE 05-FEB-2001; 2001WO-US04098.
XX
XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.

```

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XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejrtman T, Goodrich R;
XX WPI: 2001-476283/51.
XX N-PSDB; AAK51717.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy.
XX
XX Claim 20: Page 3505-3507; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAK80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 632 AA:
SQ

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Query Match 100.0%; Score 153; DB 22; Length 632;
 Best local similarity 100.0%; Pred. No. 1.9e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGHGTVLCLQYDERVITGSSDSTVRW 29
 |||||||
 DB 367 TGHGTVLCLQYDERVITGSSDSTVRW 395

RESULT 14
 AAM79566
 ID AAM79566 standard; Protein: 654 AA.
 XX
 AC AAM79566;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3212.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX

```

PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejrtman T, Goodrich R;
XX WPI: 2001-476283/51.
XX N-PSDB; AAK52699.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy.
XX
XX Claim 20: Page 285-286; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAK80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 654 AA:
SQ

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Query Match 100.0%; Score 153; DB 22; Length 654;
 Best local similarity 100.0%; Pred. No. 2e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGHGTVLCLQYDERVITGSSDSTVRW 29
 |||||||
 DB 389 TGHGTVLCLQYDERVITGSSDSTVRW 417

RESULT 15
 AAM79567
 ID AAM79567 standard; Protein: 654 AA.
 XX
 AC AAM79567;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3213.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX

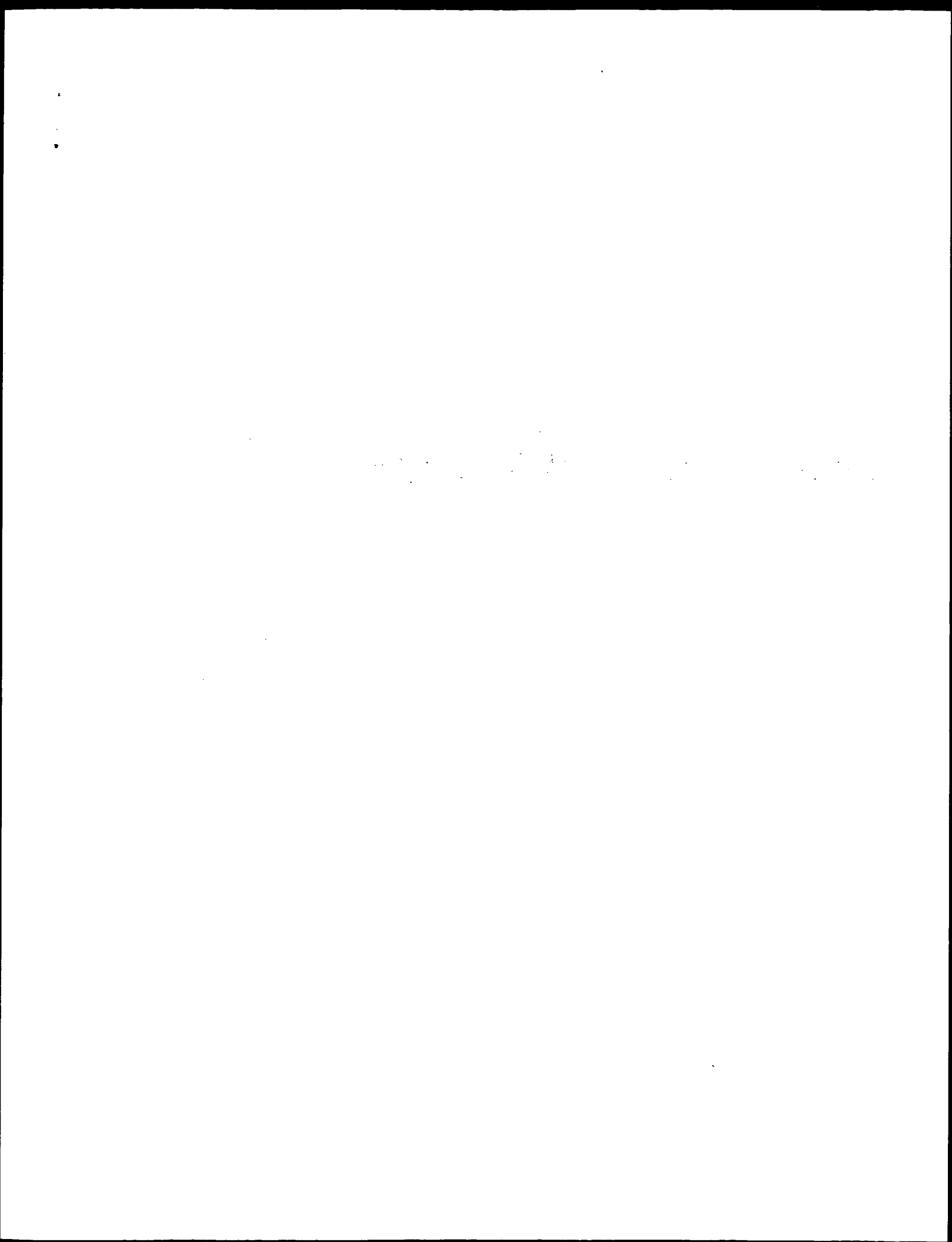
(HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK52700.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 286; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 SO Sequence 654 AA;

Query Match 100.0%; Score 153; DB 22; Length 654;
 Best Local Similarity 100.0%; Pred. No. 2e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHTGSVLCIYDERVITIGSSDSTVRW 29
 |||||||||||||||||||||||||||||
 DB 389 TGHTGSVLCIYDERVITIGSSDSTVRW 417

Search completed: April 11, 2003, 11:48:14
 Job time : 9.93666 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.00244 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332

Perfect score: 153
Sequence: 1 TGHGTVLCLOYDERVITGSSDSTVRW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133.5	87.3	28	1	US-08-190-802A-84
2	133.5	87.3	28	4	US-08-477-346-84
3	133.5	87.3	28	4	US-08-473-089-84
4	133.5	87.3	28	4	US-08-487-072A-84
5	133.5	87.3	517	1	US-08-190-802A-30
6	133.5	87.3	517	4	US-08-477-346-30
7	133.5	87.3	517	4	US-08-473-089-30
8	133.5	87.3	517	4	US-08-487-072A-30
9	97	63.4	29	1	US-08-190-802A-87
10	97	63.4	29	4	US-08-477-346-87
11	97	63.4	29	4	US-08-473-089-87
12	97	63.4	29	4	US-08-487-072A-87
13	86	56.2	640	4	US-09-177-165A-30
14	82	53.6	209	3	US-08-899-578-6
15	81	52.9	3	3	US-08-899-578-2
16	78	51.0	325	2	US-08-828-922-3
17	77	50.3	34	4	US-08-190-802A-83
18	77	50.3	34	4	US-08-477-346-83
19	77	50.3	34	4	US-08-473-089-83
20	77	50.3	34	4	US-08-487-072A-83
21	75	49.0	31	1	US-08-190-802A-249
22	75	49.0	31	4	US-08-477-346-249
23	75	49.0	31	4	US-08-473-089-249
24	75	49.0	31	4	US-08-487-072A-249
25	75	49.0	514	1	US-08-190-802A-66
26	75	49.0	514	4	US-08-477-346-66
27	75	49.0	514	4	US-08-473-089-66

28	75	49.0	514	4	US-08-487-072A-66	Sequence 66, App1
29	73.5	48.0	41	4	US-08-988-856B-23	Sequence 23, App1
30	73.5	48.0	779	1	US-08-190-802A-32	Sequence 32, App1
31	73.5	48.0	779	4	US-08-477-346-32	Sequence 32, App1
32	73.5	48.0	779	4	US-08-473-089-32	Sequence 32, App1
33	73.5	48.0	779	4	US-08-487-072A-32	Sequence 32, App1
34	73.5	48.0	779	4	US-09-177-165A-29	Sequence 29, App1
35	73	47.7	31	1	US-08-190-802A-93	Sequence 93, App1
36	73	47.7	31	1	US-08-477-346-93	Sequence 93, App1
37	73	47.7	31	4	US-08-477-346-196	Sequence 196, App
38	73	47.7	31	4	US-08-473-089-93	Sequence 93, App1
39	73	47.7	31	4	US-08-473-089-196	Sequence 196, App
40	73	47.7	31	4	US-08-487-072A-93	Sequence 93, App1
41	73	47.7	31	4	US-08-487-072A-196	Sequence 196, App
42	73	47.7	422	1	US-08-190-802A-52	Sequence 52, App1
43	73	47.7	422	4	US-08-477-346-52	Sequence 52, App1
44	73	47.7	422	4	US-08-473-089-52	Sequence 52, App1
45	73	47.7	422	4	US-08-473-089-52	Sequence 52, App1

ALIGNMENTS

RESULT 1

US-08-190-802A-84

Sequence 84, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: WD-40 - Derived peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESS: Dehlinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190, 802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP I1, Fig. 13

US-08-190-802A-84

Query Match 87.3%; Score 133.5; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29

Db 1 GHTGSVLCQYDERVITIG-SDSTVRW 27

RESULT 2

US-08-477-346-84
; Sequence 84, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP rII, Fig. 13
US-08-477-346-84
Query Match 87.3%; Score 133.5; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 1 GHTGSVLCQYDERVITIG-SDSTVRW 27

RESULT 3

US-08-473-089-84
; Sequence 84, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rII, Fig. 13
US-08-473-089-84

Query Match 87.3%; Score 133.5; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 1 GHTGSVLCQYDERVITIG-SDSTVRW 27

RESULT 4

US-08-487-072A-84
; Sequence 84, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP r11, Fig. 13
 US-08-487-072A-84

Query Match 87.3%; Score 133.5; DB 4; Length 28;
 Best Local Similarity 96.4%; Pred. No. 2,7e-13;
 Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHTGSVLCLOYDERVITIGSSDSSTVRW 29
 DB 1 GHTGSVLCLOYDERVITIG-SDSTVRW 27

RESULT 5
 US-08-190-802A-30
 Sequence 30, Application US/08190802A
 Patent No. 3519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dellinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190, 802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 517 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 US-08-190-802A-30

Query Match 87.3%; Score 133.5; DB 1; Length 517;
 Best Local Similarity 96.4%; Pred. No. 7.5e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHTGSVLCLOYDERVITIGSSDSSTVRW 29

DB 270 GHTGSVLCLOYDERVITIG-SDSTVRW 296

RESULT 6
 US-08-477-346-30
 Sequence 30, Application US/08477346
 Patent No. 6262023
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,346
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,072
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 517 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 US-08-477-346-30

Query Match 87.3%; Score 133.5; DB 4; Length 517;
 Best Local Similarity 96.4%; Pred. No. 7.5e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHTGSVLCLOYDERVITIGSSDSSTVRW 29
 DB 270 GHTGSVLCLOYDERVITIG-SDSTVRW 296

RESULT 7
 US-08-473-089-30
 Sequence 30, Application US/08473089
 Patent No. 6342368
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match
Best Local Similarity 87.3%; Score 133.5; DB 4; Length 517;
Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHGGSVLCLOYDERVITIGSSDSIVRW 29
Db 270 GHGGSVLCLOYDERVITIG-SDSTVRW 296

RESULT 8
US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match
Best Local Similarity 87.3%; Score 133.5; DB 4; Length 517;
Matches 27; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GHGGSVLCLOYDERVITIGSSDSIVRW 29
Db 270 GHGGSVLCLOYDERVITIG-SDSTVRW 296

RESULT 9
US-08-190-802A-87
Sequence 87, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-190-802A-87

Query Match
Best Local Similarity 63.4%; Score 97; DB 1; Length 29;
Matches 14; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHGGSVLCLOYDERVITIGSSDSIVRW 29

Db 1 GHKRGICLQYRDRLVVGSSDNTIRLW 28

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      11 : |||| :|:::||||:|:|:|
      1 GHKRGICLQYRDRLVVGSSDNTIRLW 28

RESULT 10
US-08-477-346-87
; Sequence 87, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
; US-08-477-346-87

Query Match 63.4%; Score 97; DB 4; Length 29;
Best Local Similarity 50.0%; Pred. No. 7e-08;
Matches 14; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHGSVLCLODYDERVITIGSSDSTVRVW 29
Db 1 GHKRGICLQYRDRLVVGSSDNTIRLW 28

RESULT 11
US-08-473-089-87
; Sequence 87, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
; US-08-473-089-87

Query Match 63.4%; Score 97; DB 4; Length 29;
Best Local Similarity 50.0%; Pred. No. 7e-08;
Matches 14; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHGSVLCLODYDERVITIGSSDSTVRVW 29
Db 1 GHKRGICLQYRDRLVVGSSDNTIRLW 28

RESULT 12
US-08-487-072A-87
; Sequence 87, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
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      STREET: 2000 Pennsylvania Avenue, NW
      CITY: Washington
      STATE: DC
      COUNTRY: USA
      ZIP: 20006-1812
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      OPERATING SYSTEM: IBM PC compatible
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/473,089
      FILING DATE: 07-JUN-1995
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION:
      NAME: MURASHIGE, KATE H.
      REGISTRATION NUMBER: 29,959
      REFERENCE/DOCKET NUMBER: 2550-0025.22
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (202) 887-1500
      TELEFAX: (202) 887-0763
      INFORMATION FOR SEQ ID NO: 87:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 29 amino acids
      TYPE: amino acid
      TOPOLOGY: unknown
      MOLECULE TYPE: peptide
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      ORIGINAL SOURCE:
      INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
      US-08-473-089-87

Query Match 63.4%; Score 97; DB 4; Length 29;
Best Local Similarity 50.0%; Pred. No. 7e-08;
Matches 14; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHGSVLCLODYDERVITIGSSDSTVRVW 29
Db 1 GHKRGICLQYRDRLVVGSSDNTIRLW 28

RESULT 12
US-08-487-072A-87
; Sequence 87, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/899,578
? FILING DATE: 24-JUL-1997
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 278-0525
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 209 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-899-578-6

Query Match 53.6%; Score 82; DB 3; Length 209;
Best Local Similarity 44.8%; Pred. No. 0.00011;
Matches 13; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGTGSGVLCLOYDERVITITGSSDSITVRW 29
:||||:|: ::||| |:-|||
Db 61 SGHTSVRCMAMGSLITGSRPTLRW 89

RESULT 15
US-08-899-578-2
? Sequence 2, Application US/08899578
? Patent No. 6087153
? GENERAL INFORMATION:
? APPLICANT: Greenwald, Iva
? APPLICANT: Hubbard, E. Jane
? TITLE OF INVENTION: SEL-10 AND USES THEREOF
? NUMBER OF SEQUENCES: 7
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham LLP
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/899,578
? FILING DATE: 24-JUL-1997
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 278-0525
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 587 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-899-578-2

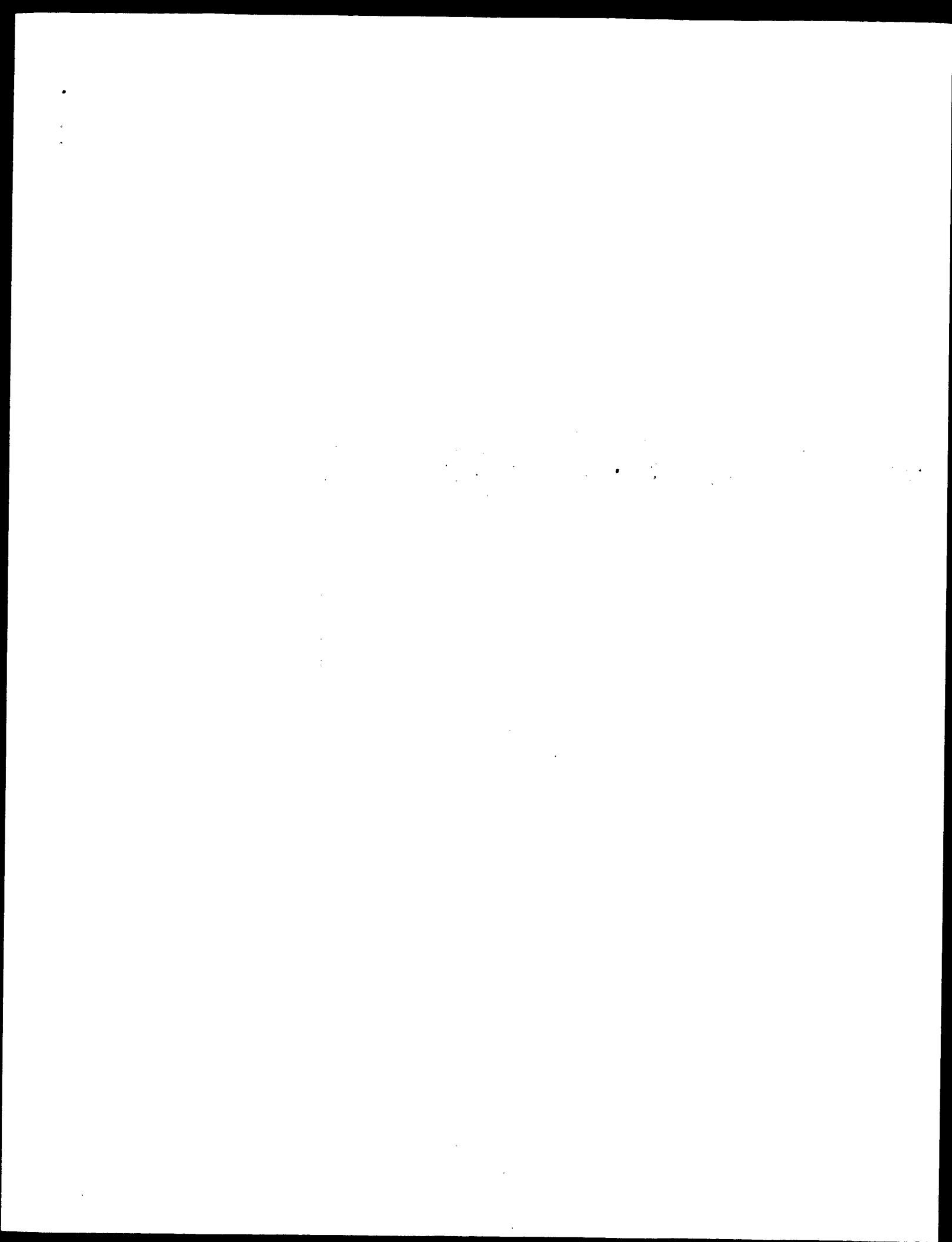
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Fri Apr 11 13:31:09 2003

us-09-601-168b-2_copy_304_332.ra

Page 7

Query Match 52.9%; Score 81; DB 3; Length 587;
Best Local Similarity 46.4%; Pred. NO. 0.00049;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Caps 0;
QY 2 GHTGSVLCLOYDERVITITGSSDSTVRW 29
||| : | : : : ||| | : |||
Db 336 GHTSTVRNCMAMAGSILVTGSRDTTLRW 363
Search completed: April 10, 2003, 12:51:18
Job time : 4.00244 secs



GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 2.96711 Seconds
(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332

Perfect score: 153
Sequence: 1 TGHGTVLCIQDYDERVITGSSDSIVRW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
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- 5: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	153	100.0	569	9 US-10-038-010-8	Sequence 8, Appli
2	153	100.0	569	12 US-10-042-417-2	Sequence 2, Appli
3	98	64.1	678	10 US-09-801-368-314	Sequence 30, Appl
4	86	56.2	640	9 US-10-060-019-30	Sequence 3, Appli
5	84	54.9	540	9 US-09-213-888-7	Sequence 7, Appli
6	84	54.9	540	9 US-09-213-888-10	Sequence 10, Appl
7	84	54.9	540	9 US-09-328-877A-7	Sequence 7, Appli
8	84	54.9	540	9 US-09-328-877A-10	Sequence 10, Appl
9	84	54.9	545	9 US-09-213-888-6	Sequence 6, Appli
10	84	54.9	545	9 US-09-328-877A-6	Sequence 6, Appli
11	84	54.9	553	9 US-09-213-888-5	Sequence 5, Appli
12	84	54.9	553	9 US-09-328-877A-5	Sequence 5, Appli
13	84	54.9	559	9 US-09-213-888-9	Sequence 9, Appli
14	84	54.9	559	9 US-09-328-877A-9	Sequence 9, Appli
15	84	54.9	589	9 US-09-213-888-8	Sequence 8, Appli
16	84	54.9	589	9 US-09-328-877A-8	Sequence 8, Appli
17	84	54.9	592	9 US-09-213-888-4	Sequence 4, Appli
18	84	54.9	592	9 US-09-328-877A-4	Sequence 4, Appli
19	84	54.9	626	9 US-09-213-888-21	Sequence 21, Appl

20	84	54.9	626	9 US-09-328-877A-21	Sequence 21, Appl
21	84	54.9	627	9 US-09-213-888-3	Sequence 3, Appli
22	84	54.9	627	9 US-09-328-877A-3	Sequence 3, Appli
23	84	54.9	666	9 US-09-213-888-27	Sequence 27, Appl
24	84	54.9	666	9 US-09-328-877A-27	Sequence 27, Appl
25	84	54.9	669	9 US-09-213-888-25	Sequence 25, Appl
26	84	54.9	669	9 US-09-328-877A-25	Sequence 25, Appl
27	79	51.6	422	12 US-10-042-417-4	Sequence 4, Appli
28	73.5	48.0	41	10 US-09-843-845-23	Sequence 23, Appl
29	73.5	48.0	9	9 US-10-083-357-897	Sequence 897, App
30	73.5	48.0	9	9 US-10-060-019-29	Sequence 29, Appl
31	73	47.7	744	10 US-09-925-300-1347	Sequence 1347, Ap
32	72.5	47.4	64	10 US-09-843-845-20	Sequence 20, Appl
33	72	47.1	261	9 US-10-132-744A-4	Sequence 4, Appli
34	72	47.1	484	9 US-10-132-744A-2	Sequence 2, Appli
35	72	47.1	485	9 US-10-132-744A-6	Sequence 6, Appli
36	72	47.1	1146	9 US-09-832-292-10	Sequence 10, Appl
37	72	47.1	1146	10 US-09-994-465-6	Sequence 6, Appli
38	70.5	46.1	425	9 US-09-893-519A-25	Sequence 25, Appl
39	70.5	46.1	466	10 US-09-925-301-997	Sequence 997, App
40	70	45.8	67	10 US-09-864-761-46849	Sequence 46849, A
41	70	45.8	114	9 US-09-796-692-1445	Sequence 1445, Ap
42	70	45.8	114	9 US-09-796-692-1541	Sequence 1541, Ap
43	70	45.8	114	9 US-09-796-692-1895	Sequence 1895, Ap
44	70	45.8	316	10 US-09-828-310-12	Sequence 12, Appl
45	70	45.8	317	9 US-09-998-042-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-038-010-8 Application US/10038010
Sequence 8, Appli
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: PIERRE, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta-Trcp1
LOCATION: (1)..(569)
OTHER INFORMATION:
US-10-038-010-8

Query Match 100.0%; Score 153; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCIQDYDERVITGSSDSIVRW 29
Db 304 TGHGTVLCIQDYDERVITGSSDSIVRW 332

RESULT 2
US-10-042-417-2
Sequence 2, Appli Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 153; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHTGSVLCLODYDERVITIGSSDSYRVW 29
DB 304 TGHTGSVLCLODYDERVITIGSSDSYRVW 332

RESULT 3
US-09-801-368-314
Sequence 314, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 314
LENGTH: 678
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-801-368-314

Query Match 64.1%; Score 98; DB 10; Length 678;
Best Local Similarity 46.4%; Pred. No. 4.8e-07;
Matches 13; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHTGSVLCLODYDERVITIGSSDSYRVW 29
DB 347 GHTGSVLCLODYDERVITIGSSDSYRVW 374

RESULT 4
US-10-060-019-30
Sequence 30, Application US/10060019
Publication No. US2003003564A1
GENERAL INFORMATION:
APPLICANT: Tyers, Mike
APPLICANT: Williams, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN

TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.100S01
CURRENT APPLICATION NUMBER: US/10/060,019
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/177,165
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-060-019-30

Query Match 56.2%; Score 86; DB 9; Length 640;
Best Local Similarity 51.7%; Pred. No. 3.3e-05;
Matches 15; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGHTGSVLCLODYDERVITIGSSDSYRVW 29
DB 339 SGHSDGVKTLVFDKRLITGSLDKTIRW 367

RESULT 5
US-09-213-888-7
Sequence 7, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 54.9%; Score 84; DB 9; Length 540;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLODYDERVITIGSSDSYRVW 29
DB 292 GHTSTVRCHLHKRVVSGSRDATLRW 319

RESULT 6
US-09-213-888-10
Sequence 10, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-10

Query Match 54.9%; Score 84; DB 9; Length 540;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOYDERVITIGSSDSTVRW 29
Db 292 GHTSTVRCHMLHEKRVSGSRDATLRW 319

RESULT 7
US-09-328-877A-7
; Sequence 7, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-7

Query Match 54.9%; Score 84; DB 9; Length 540;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOYDERVITIGSSDSTVRW 29
Db 292 GHTSTVRCHMLHEKRVSGSRDATLRW 319

RESULT 8
US-09-328-877A-10
; Sequence 10, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-10

Query Match 54.9%; Score 84; DB 9; Length 540;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOYDERVITIGSSDSTVRW 29
Db 292 GHTSTVRCHMLHEKRVSGSRDATLRW 319

RESULT 9
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6

Query Match 54.9%; Score 84; DB 9; Length 545;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOYDERVITIGSSDSTVRW 29
Db 297 GHTSTVRCHMLHEKRVSGSRDATLRW 324

RESULT 10
US-09-328-877A-6
; Sequence 6, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-6

Query Match 54.9%; Score 84; DB 9; Length 545;
Best Local Similarity 46.4%; Pred. No. 5.6e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOYDERVITIGSSDSTVRW 29
Db 297 GHTSTVRCHMLHEKRVSGSRDATLRW 324

RESULT 11
US-09-213-888-5
; Sequence 5, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-5

Query Match 54.9%; Score 84; DB 9; Length 553;
Best Local Similarity 46.4%; Pred. No. 5.7e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29
DB 305 GHTSTVRCMHLEKRVVSGSRDATTLRW 332

RESULT 12
US-09-328-877A-5
Sequence 5, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Pharmacla & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match 54.9%; Score 84; DB 9; Length 553;
Best Local Similarity 46.4%; Pred. No. 5.7e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29
DB 305 GHTSTVRCMHLEKRVVSGSRDATTLRW 332

RESULT 13
US-09-213-888-9
Sequence 9, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacla & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 9

LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-9

Query Match 54.9%; Score 84; DB 9; Length 559;
Best Local Similarity 46.4%; Pred. No. 5.8e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29
DB 311 GHTSTVRCMHLEKRVVSGSRDATTLRW 338

RESULT 14
US-09-328-877A-9
Sequence 9, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Pharmacla & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-9

Query Match 54.9%; Score 84; DB 9; Length 559;
Best Local Similarity 46.4%; Pred. No. 5.8e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29
DB 311 GHTSTVRCMHLEKRVVSGSRDATTLRW 338

RESULT 15
US-09-213-888-8
Sequence 8, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacla & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 8
LENGTH: 589
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-8

Query Match 54.9%; Score 84; DB 9; Length 589;
Best Local Similarity 46.4%; Pred. No. 6.2e-05;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITGSSDSTVRW 29
DB 311 GHTSTVRCMHLEKRVVSGSRDATTLRW 338

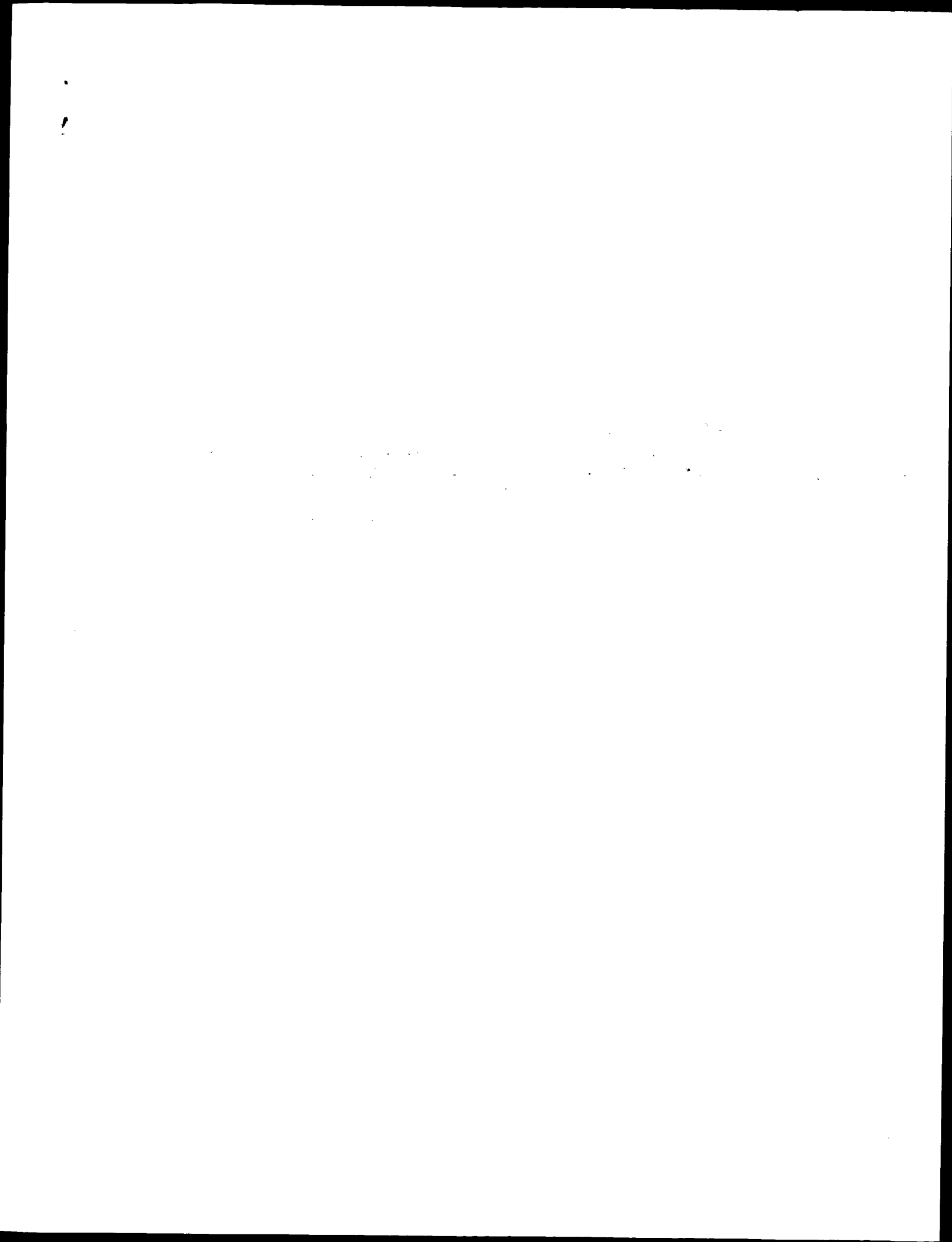
Fri Apr 11 13:31:09 2003

us-09-601-168b-2_copy_304_332.rapb

Page 5

Db 341 GHTSTVCMHLEKRVVSGSRDATLRW 368

Search completed: April 10, 2003, 13:16:44
Job time : 3.96711 secs



GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.35566 Seconds
(without alignments)
830,804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332
Perfect score: 153
Sequence: 1 TGTGTVLCLODYDERVITGSSDSTVRW 29

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pIR1:
2: pIR2:
3: pIR3:
4: pIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	148	96.7	518	2 B48088	beta-transducin re
2	137	89.5	701	2 T16607	hypothetical prote
3	96	62.7	605	2 T38932	probable sulfur me
4	90	58.8	267	2 S62507	hypothetical trp-a
5	90	58.8	506	2 T50211	WD-repeat protein
6	89	58.2	650	2 T46660	sulfur controller-
7	86	56.2	640	2 S49932	MEF30 protein - ye
8	83.5	54.6	1446	2 T13018	hypothetical prote
9	83	54.2	714	2 S56893	hypothetical prote
10	81	52.9	579	2 T22703	hypothetical prote
11	81	52.9	659	2 S38108	hypothetical prote
12	78	51.0	325	2 S60335	hypothetical prote
13	77.5	50.7	473	2 T33805	TGF-beta receptor
14	76	49.7	715	2 S38051	hypothetical prote
15	76	49.7	1189	2 A12493	DOAI protein - yea
16	76	49.7	1258	2 A12155	WD-repeat protein
17	75.5	49.3	519	2 A49367	transducin homolog
18	75	49.0	515	2 S19487	hypothetical prote
19	75	49.0	558	2 AE2415	WD-repeat protein
20	75	49.0	651	2 T50289	probable coatomer
21	75	49.0	926	2 G96563	probable WD-repeat
22	74	48.4	333	2 G85034	hypothetical prote
23	74	48.4	438	2 T45823	probable pleiotrop
24	74	48.4	504	2 T50983	hypothetical prote
25	74	48.4	559	2 AB2202	trp-asp repeat pro
26	73.5	48.0	404	2 T40553	cell division cont
27	73.5	48.0	779	2 S56245	CDC4 repeat unit-c
28	73	47.7	422	2 A56640	Golg1-associated p
29	73	47.7	906	2 S35342	

30	73	47.7	906	2 S35312	coatomer complex b
31	73	47.7	1224	1 ERH04H	coatomer complex a
32	72.5	47.4	593	2 E96526	hypothetical prote
33	72	47.1	316	2 S57839	CPC2 protein - Neu
34	72	47.1	356	2 T22478	hypothetical prote
35	72	47.1	437	2 S05357	hypothetical prote
36	72	47.1	502	2 T41148	trp-asp repeat con
37	72	47.1	704	2 S33263	transcription init
38	72	47.1	755	2 T00066	hypothetical prote
39	72	47.1	1019	2 JC7538	neuronal different
40	72	47.1	1151	2 A55532	myosin-heavy-chain
41	72	47.1	1146	2 T33777	hypothetical prote
42	71.5	46.7	495	2 T47172	hypothetical prote
43	71	46.4	317	2 T46032	WD-40 repeat regul
44	71	46.4	328	2 A84901	hypothetical prote
45	71	46.4	589	2 AG2400	WD-repeat protein

ALIGNMENTS

RESULT 1

B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-trcp
C:Species: Xenopus laevis (African clawed frog)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; MUID:93330289; PMID:8393141
A:Accession: B48088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SPE>
A:Cross-references: GB:M98268; NID:q295542; PIDN:AAA02810.1; PID:q295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <WD1>

Query Match 96.7%; Score 148; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHTGTVLCLODYDERVITGSSDSTVRW 29
DB 270 GHTGTVLCLODYDERVITGSSDSTVRW 297

RESULT 2

T16607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16607
R:Miller, N.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: Z18545
A:Accession: T16607
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-701 <ML>
A:Cross-references: EMBL:U28730; NID:q860694; PID:q860695; PIDN:AAA68258.1; CESP:K10B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.1
A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
Query Match 89.5%; Score 137; DB 2; Length 701;
Best Local Similarity 86.2%; Pred. No. 9.8e-13;
Matches 25; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 543 GHTDGIITSLKFDSEKIVTGSMDNSVRIM 570

RESULT 12

S60335
TGF-beta receptor interacting protein 1 - human
N:Alternate names: WD domain-containing protein TRIP-1
C:Species: Homo sapiens (man)
C>Date: 14-Sep-1996 #sequence_revision 27-Feb-1997 #text_change 28-May-1999
C:Accession: S60335
R:Chen, R.H.; Miettinen, P.J.; Maruoka, E.M.; Choy, L.; Derynck, R.
Nature 377, 548-552, 1995
A:Title: A WD-domain protein that is associated with and phosphorylated by the type II T
A:Reference number: S60256, MUID:96013749, PMID:7566156
A:Accession: S60335
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-325 <CHE>
A:Cross-references: GB:U36764; NID:q1036804; PIDN:AAC50224.1; PID:q1036805
C:Superfamily: TGF-beta receptor interacting protein, WD repeat homology
F:184-217/Domain: WD repeat homology <MD1>

Query Match

Best Local Similarity 51.0%; Score 78; DB 2; Length 325;
Matches 13; Conservative 10; Mismatches 5; Indels 2; Gaps 1;

QY 2 GHTGSVLCI--QYDERVITGSSDSTVRW 29

Db 50 GHTGAVWCVDADMDTKHVLTGSDNCRIM 79

RESULT 13

T33805
hypothetical protein W07E6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 26-May-2000
C:Accession: T33805
R:Latreille, P.; Wamsley, P.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid W07E6.
A:Reference number: 221414
A:Accession: T33805
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <LAT>
A:Cross-references: EMBL:AF106576; PIDN:AAC78176.1; GSPDB:GN00020; CESP:W07E6.2
A:Experimental source: strain Bristol N2; clone W07E6
C:Genetics:
A:Gene: CESP:W07E6.2
A:Map position: 2
A:Insertions: 46/2; 77/3; 103/1; 195/2; 256/3; 311/3; 399/2
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match

Best Local Similarity 50.7%; Score 77.5; DB 2; Length 473;
Matches 15; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 TGHGTVLCI--QYDERVITGSSDSTVRW 29

Db 234 SGHTASVTLRWGEGLYSGSDRTVKWM 263

RESULT 14

S38051
DOAI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein F715; protein YKL213c
C:Species: Saccharomyces cerevisiae
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-May-2000
C:Accession: S38051; S38056; S44325; S46544; S61942; S71950
R:Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S7897
A:Accession: S38051

A:Molecule type: DNA

A:Residues: 1-715 <POH>

A:Cross-references: EMBL:Z28213; NID:9486380; PIDN:CAA82058.1; PID:9486381; MIPS:YKL2

A:Experimental source: strain S288C

R:Alexandraki, D.; Tzermita, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: S38054

A:Accession: S38056

A:Molecule type: DNA

A:Residues: 1-715 <ALE>

A:Cross-references: EMBL:Z28213; NID:9486380; PIDN:CAA82058.1; PID:9486381; MIPS:YKL2

A:Experimental source: strain S288C

R:Tzermita, M.; Horaitis, O.; Alexandraki, D.
Yeast 10, 663-679, 1994

A:Title: The complete sequencing of a 24.6 kb segment of yeast chromosome XI identify
e dehydratases, membrane transporters, hydantoinases and the phospholipase A(2)-activ

A:Reference number: S44319; MUID:95028164; PMID:7941750

A:Accession: S44325

A:Molecule type: DNA

A:Residues: 1-345 <TZE>

A:Cross-references: EMBL:X75951

R:Alexandraki, D.
submitted to the EMBL Data Library, December 1993

A:Reference number: S43546

A:Accession: S46544

A:Molecule type: DNA

A:Residues: 1-715 <ALM>

A:Cross-references: EMBL:X75951; NID:9473130; PIDN:CAA53560.1; PID:9473137

R:Hochstrasser, M.; Gang, G.
submitted to the EMBL Data Library, November 1995

A:Reference number: S61941

A:Accession: S61942

A:Molecule type: DNA

A:Residues: 1-715 <HOC>

A:Cross-references: EMBL:U39947; NID:q1086568; PIDN:AAA82258.1; PID:q1086570

R:Ghislin, M.; Dohmen, R.J.; Levy, F.; Varshavsky, A.
EMBO J. 15, 4884-4899, 1996

A:Title: Cdc48p interacts with Ufd3p, a WD repeat protein required for ubiquitin-mediated

A:Reference number: S71950; MUID:97045097; PMID:8690162

A:Accession: S71950

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-715 <GHI>

A:Genetics:
A:Gene: SGD:DOAI; UFD3

A:Cross-references: SGD:S0001696; MIPS:YKL213c

C:Function:
A:Description: required for ubiquitin-dependent proteolysis

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

F:95-126/Domain: WD repeat homology <MD1>

F:133-167/Domain: WD repeat homology <MD2>

Query Match

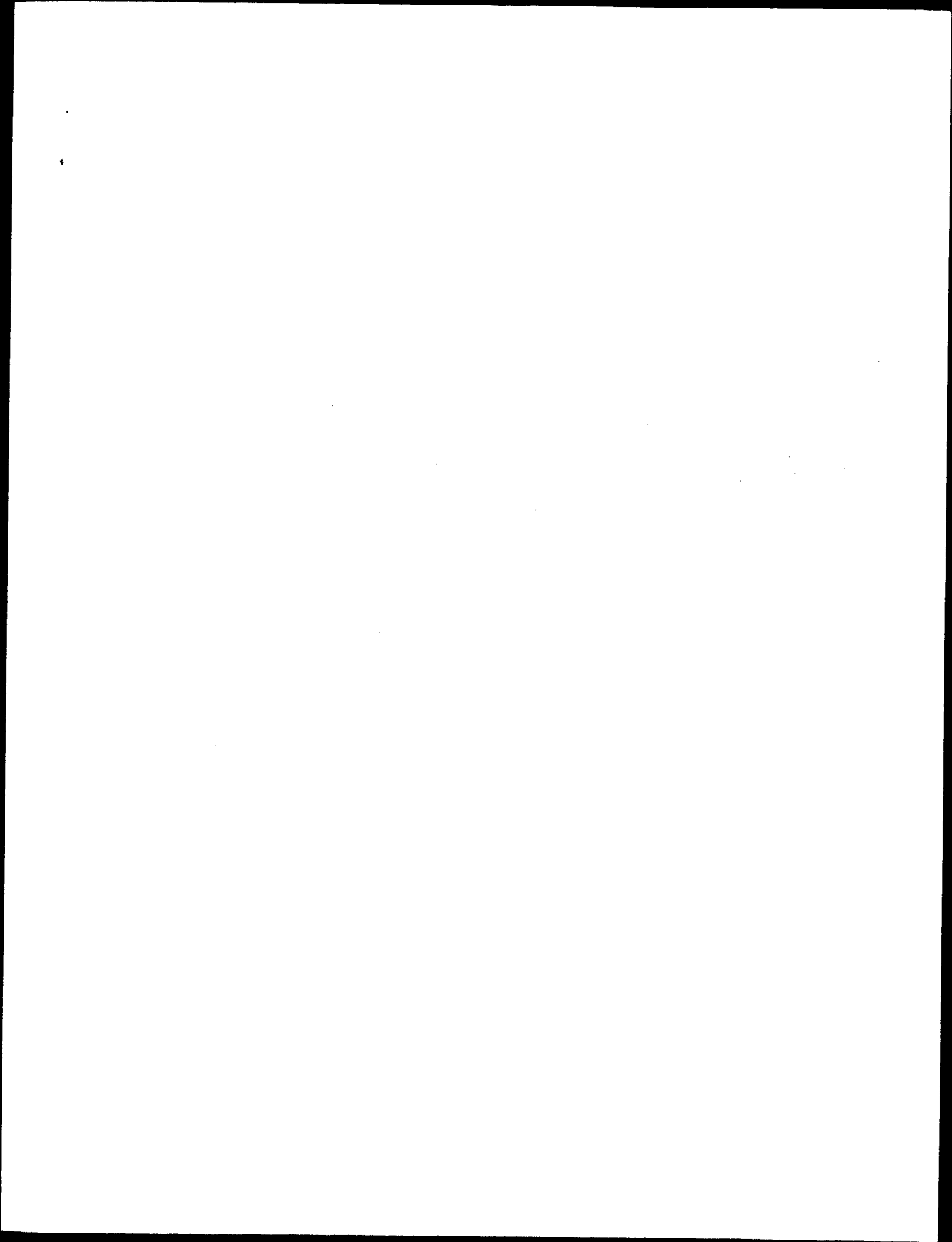
Best Local Similarity 49.7%; Score 76; DB 2; Length 715;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 GHTGSVLCI--QYDERVITGSSDSTVRW 29

Db 97 GHGNCVCSLTFQDGVVISGSMKTKAKVM 124

RESULT 15

A12493
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120alpha
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: A12493
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium



GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 2.08404 Seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332
Perfect score: 153
Sequence: 1 TGHGTVLCLOYDERVITITGSSDSTVRVW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	153	100.0	605 1 FW1A_HUMAN	Q9Y297 homo sapien
2	152	99.3	542 1 FW1B_HUMAN	Q9UKB1 homo sapien
3	148	96.7	518 1 TRCB_XENLA	Q91854 xenopus lae
4	137	89.5	665 1 LIT3_CAEEL	Q09990 caenorhabd
5	98	64.1	678 1 SCOB_EMRNT	Q00659 caenorhabd
6	96	62.7	603 1 POF1_SCHPO	P87053 schizosacch
7	90	58.8	506 1 POFB_SCHPO	Q09655 schizosacch
8	89	58.2	650 1 SC02_NEUCR	Q01277 neurospora
9	86	56.2	640 1 MT30_YEAST	P39014 saccharomyc
10	85	55.6	684 1 CC4_CANAL	P53699 candida alb
11	83	54.2	714 1 YJ12_YEAST	P47025 saccharomyc
12	81	52.9	579 1 SE10_CAEEL	Q93794 caenorhabd
13	81	52.9	659 1 YK16_YEAST	P36130 saccharomyc
14	79	51.6	422 1 FBW2_HUMAN	Q9UK18 homo sapien
15	78	51.0	325 1 IF32_HUMAN	Q13347 homo sapien
16	78	51.0	325 1 IF32_MOUSE	Q9QZ09 mus musculu
17	76	49.7	326 1 IP32_DROME	Q02195 drosophila
18	76	49.7	715 1 IP32_MOUSE	P16037 saccharomyc
19	76	49.7	1258 1 YS00_ANASP	O8YTC2 anabaena sp
20	75.5	49.3	519 1 TBL3_HUMAN	Q12788 homo sapien
21	75	49.0	515 1 YCM2_YEAST	P25382 saccharomyc
22	75	49.0	651 1 YX11_SCHPO	Q9P713 schizosacch
23	74	48.4	1224 1 COPA_BOVIN	P07954 bos taurus
24	73.5	48.0	779 1 CC4_YEAST	P27834 saccharomyc
25	73	47.7	332 1 GBLP_DICDI	P68800 dictyostell
26	73	47.7	422 1 FBW2_MOUSE	P05654 mus musculu
27	73	47.7	905 1 COPP_BOVIN	P35606 homo sapien
28	73	47.7	905 1 COPP_HUMAN	O55029 mus musculu
29	73	47.7	905 1 COPP_MOUSE	P53621 homo sapien
30	72	47.1	1224 1 GBLP_HUMAN	Q01369 neurospora
31	72	47.1	356 1 GBB2_CAEEL	Q20636 caenorhabd
32	72	47.1	437 1 AAC3_DICDI	P14197 dictyostell
33	72	47.1	437 1	

34	72	47.1	704 1 T2D4_DROME	P49846 drosophila
35	72	47.1	904 1 COPP_RAT	O3142 ratius norv
36	72	47.1	1146 1 KMHA_DICDI	P42527 dictyostell
37	71.5	46.7	474 1 CO1C_HUMAN	Q9UNM4 homo sapien
38	71.5	46.7	474 1 CO1C_MOUSE	Q9UNM4 mus musculu
39	71	46.4	317 1 GBLP_HYDAT	Q25189 hydra atten
40	71	46.4	775 1 POP1_SCHPO	P87060 schizosacch
41	71	46.4	1261 1 APAF_BRARE	Q91918 drachydanio
42	70.5	46.1	425 1 RBB4_HUMAN	Q09028 h chromatin
43	70.5	46.1	425 1 RBB7_HUMAN	Q16576 homo sapien
44	70.5	46.1	425 1 RBB7_MOUSE	Q60973 mus musculu
45	70.5	46.1	430 1 CAP1_DROME	Q24572 drosophila

ALIGNMENTS

RESULT 1	FW1A_HUMAN	STANDARD:	PRT:	605 AA.
ID	FW1A_HUMAN			
AC	Q9Y297: Q9Y213:			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP)			
DE	(E3RS1kappab) (pikappaBalpha-E3 receptor subunit).			
GN	FAFWIA OR FW1A OR BTCP OR BTCP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=99075339; PubMed=9859996;			
RA	Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,			
RA	Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;			
RT	"Identification of the receptor component of the IkappaBalpha-			
RT	ubiquitin ligase."			
RL	Nature 396:590-594(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	TISUE=lymphoid;			
RX	MEDLINE=96325370; PubMed=9660940;			
RA	Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,			
RA	Thomas D., Strebel K., Benarous R.;			
RT	"A novel human WD protein, h-beta TrCP, that interacts with HIV-1 Vpu			
RT	connects CD4 to the ER degradation pathway through an F-box motif."			
RL	Mol. Cell 1:565-574(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=20003060; PubMed=10531035;			
RA	Cenciarelli C., Chlaud D.S., Guardavaccaro D., Parks W., Vidal M.,			
RA	Pagan M.;			
RT	"Identification of a family of human F-box proteins."			
RL	Curr. Biol. 9:1177-1179(1999).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=99145464; PubMed=9990852;			
RA	Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,			
RA	Harper J.W.;			
RT	"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically			
RT	with phosphorylated destruction motifs in I-kappa-B-alpha and			
RT	beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."			
RL	Genes Dev. 13:270-283(1999).			
CC	- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA			
CC	(PIKAPPALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR			
CC	UBIQUITINATION AND DEGRADATION.			
CC	- SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX.			
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING.			
CC	- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.			
CC	- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			

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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF101784; AAD08702.1;
DR EMBL: Y14153; CAZ74572.1;
DR EMBL: AF129530; AAF04464.1;
DR Genew; HGNC:1144; BTRC.
DR MIM: 603482;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE: PSS0181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
KW DOMAIN
FT REPEAT 190 228 F-BOX.
FT REPEAT 301 338 WD 1.
FT REPEAT 341 378 WD 2.
FT REPEAT 381 418 WD 3.
FT REPEAT 424 461 WD 4.
FT REPEAT 464 503 WD 5.
FT REPEAT 505 541 WD 6.
FT REPEAT 553 590 WD 7.
FT VARSPLIC 17 52 MISSING (IN ISOFORM 2).
SQ SEQUENCE 605 AA; 68866 MW; 4C673B7E400FD37 CRC64;

Query Match 100.0%; Score 153; DB 1; Length 605;
Best Local Similarity 100.0%; Pred. No. 1; 7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLOYDERVITIGSSDSSTVRW 29
DB 340 TGHGTVLCLOYDERVITIGSSDSSTVRW 368

RESULT 2
FWIB_HUMAN STANDARD; PRT; 542 AA.
ID FWIB_HUMAN
AC Q90KB1; Q9Y4C6; Q9P2S8; Q9P2S9;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein 1b (F-box and WD-repeats protein beta-Trop2).
GN FBXW1B OR FBW1B OR BTBRCP2 OR KIAA0696.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=20003060; PubMed=10531035;
RA Cenciarelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RL "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=fetal lung;
RA MEDLINE=20106458; PubMed=10694485;
RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
RA Katoh M.;

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RT "Molecular Cloning and genomic structure of the betaTRCP2 gene on
RT chromosome 5q35.1.";
RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A, B AND C (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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CC -----
DR EMBL: AF176022; AAF04528.1;
DR EMBL: AB033279; BAA92329.1;
DR EMBL: AB033280; BAA92330.1;
DR EMBL: AB033281; BAA92331.1;
DR EMBL: AB014596; BAA31671.1; ALT_INTT.
DR Genew; HGNC:13607; FBXW1B.
DR MIM: 605651;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE: PSS0181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
KW DOMAIN
FT REPEAT 129 167 F-BOX.
FT REPEAT 238 275 WD 1.
FT REPEAT 278 315 WD 2.
FT REPEAT 318 355 WD 3.
FT REPEAT 361 398 WD 4.
FT REPEAT 401 440 WD 5.
FT REPEAT 442 478 WD 6.
FT REPEAT 490 527 WD 7.
FT VARSPLIC 16 49 MISSING (IN ISOFORM A).
FT VARSPLIC 16 49 CSVPRLIMIGCANLWESKALSCLOSMPVSRL -> NTSV
SQ SEQUENCE 542 AA; 62090 MW; 7CD40087EFAA5C8A CRC64;

Query Match 99.3%; Score 152; DB 1; Length 542;
Best Local Similarity 96.6%; Pred. No. 2; 2e-15;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLOYDERVITIGSSDSSTVRW 29
DB 277 TGHGTVLCLOYDERVITIGSSDSSTVRW 305

RESULT 3

```

TRCB_XENLA STANDARD: PRT: 518 AA.
 ID TRCB_XENLA 091854; P70037; P70038;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-1rcp (beta-transducin repeat-containing protein).
 GN FBXW1 OR BTXCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_Taxid=6355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9330289; PubMed=8393141;
 RA Shevak W., Keiper B.D., Stralowa C., Castanon M.J.;
 RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
 anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein
 with beta-transducin repeats";
 RL Mol. Cell. Biol. 13:4953-4966(1993).
 RN [2]
 RP SEQUENCE OF 302-518 FROM N.A.
 RX MEDLINE=97109804; PubMed=8952061;
 RA Hudson J.W., Alarcon V.B., Elinson R.P.;
 RT "Identification of new localized RNAs in the Xenopus oocyte by
 differential display PCR";
 RL Dev. Genet. 19:190-198(1996).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
 (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
 MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
 GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
 NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
 TADPOLE EMBRYO.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG. TO C.ELEGANS K10B2.1.
 CC -----
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 CC -----
 DR EMBL: M98268; AAA02810.1; -;
 DR EMBL: U63921; AAB49671.1; -;
 DR EMBL: U63922; AAB49672.1; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001810; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00400; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS50678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ub1 conjugation pathway. Repeat: WD repeat.
 FT DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.

FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
 FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
 FT SEQUENCE 518 AA: 59507 MW: 2A52EC19028127F3 CRC64:
 Query Match 96.7%; Score 148; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.3e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GHTGSVLCQYDERVITIGSSDSSTVRW 29
 DB 270 GHTGSVLCQYDERVITIGSSDSSTVRW 297
 RESULT 4
 ID LI23_CAEEL STANDARD: PRT: 665 AA.
 AC 009990; 096GN6;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein Lin-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodidae; Caenorhabditis.
 NC NCBL_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.; FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RX MEDLINE=20515608; PubMed=11060233;
 RA Kipreos E.T., Gohel S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein Lin-23 functions
 to limit cell division during development";
 RL Development 127:5071-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 cycle progression. Required to restrain cell proliferation in
 response to developmental cues. Probably recognizes and binds to
 some proteins and promotes their ubiquitination and degradation
 (BY SIMILARITY).
 CC -1- SUBUNIT: Part of a SCF (SKP1-CULLIN-F-BOX) protein ligase complex
 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 levels in larvae. Maternal expression results in high zygotic
 levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG. TO X.LAEVIS FBXW1.
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 CC -----
 DR EMBL: AF275253; AAG28037.1; -;
 DR EMBL: U28730; AAG6258.2; -;
 DR WormBase: K10B2.1; CE28600.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001810; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00400; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.


```

RL Nature 415:871-880(2002).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY)
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
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CC -----
DR EMBL: AB032410; BAA84528.1; -
DR EMBL: Z94864; CAB08168.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF004400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 5.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Ub1 conjugation; Repeat; WD repeat.
FT DOMAIN 107 153 F-BOX.
FT REPEAT 271 299 WD 1.
FT REPEAT 311 339 WD 2.
FT REPEAT 350 379 WD 3.
FT REPEAT 390 420 WD 4.
FT REPEAT 432 460 WD 5.
FT REPEAT 472 500 WD 6.
FT REPEAT 510 538 WD 7.
SQ SEQUENCE 605 AA; 67110 MW; 7118C9379EC5C1F0 CRC64;

Query Match 62.7%; Score 96; DB 1; Length 605;
Best Local Similarity 53.6%; Pred. No. 8e-07;
Matches 15; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVITGSSDSTVRW 29
DB 351 GHTDSVLCITFDSTLVSQSDACTVKLM 378

RESULT 7
POPB_SCHPO STANDARD; PRT; 506 AA.
AC 009855; 0987V1;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein foll.
GN POP11 OR SPAC29E6.01 OR SPAC30.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison C.L., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RT fission yeast."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=9712;

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RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymopre B.,
RA Wellens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Pitz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Mambrot R., Purnelle B.,
RA Goffeau A., Cadieu E., Diano S., Gloux S., Lelaue V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: AB061694; BAB55543.1; -
DR EMBL: AL136538; CAB66464.1; -
DR EMBL: Z66525; CAA91423.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF004400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 3.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 3.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT DOMAIN 70 116 F-BOX.
FT REPEAT 219 256 WD 1.
FT REPEAT 259 298 WD 2.
FT REPEAT 301 338 WD 3.
FT REPEAT 345 386 WD 4.
FT REPEAT 368 426 WD 5.
FT REPEAT 427 464 WD 6.
FT REPEAT 468 505 WD 7.
SQ SEQUENCE 506 AA; 58257 MW; CEF34DAEFFBC2E10 CRC64;

Query Match 58.8%; Score 90; DB 1; Length 506;
Best Local Similarity 53.3%; Pred. No. 5.3e-06;
Matches 16; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 2 GHTGSVLCQYDERVITGSSDSTVRW 29
DB 259 GHTGSVLCQYDERVITGSSDSTVRW 288

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RESULT 8
SC02_NEUCR          STANDARD:          PRT:          650 AA.
ID SC02_NEUCR
AC 001277:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfur controller-2 (SCON2).
GN SCON-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=95241499; PubMed=7724564;
RA Kumar A., Paietta J.V.;
RT "The sulfur controller-2 negative regulatory gene of Neurospora
RL crassa encodes a protein with beta-transducin repeats."
RC Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
CC -1- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
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CC -----
DR EMBL: 017251; AAA68968.1; -
DR InterPro: IPR001810; F-box.
DR Pfam: PF00400; WD40; 7
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00320; WD40; 7.
DR SMART: SM00326; FBOX; 1.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Transcription regulation; Repeat; WD repeat.
KM DOMAIN 124 170
FT REPEAT 292 320 WD 1.
FT REPEAT 332 360 WD 2.
FT REPEAT 372 400 WD 3.
FT REPEAT 411 441 WD 4.
FT REPEAT 453 488 WD 5.
FT REPEAT 528 564 WD 6.
FT REPEAT 576 604 WD 7.
FT REPEAT 616 644 WD 8.
SQ SEQUENCE 650 AA; 72189 MW; 7473859C9F91B028 CRC64;

Query Match 58.28; Score 89; DB 1; Length 650;
Best Local Similarity 46.48; Pred. No. 1e-05;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 GHTGSVLQYDERVITIGSSDSTVRW 29
Db 292 CHENGVTCLQDNLATGSDITIKITW 319

RESULT 9
MT30_YEAST          STANDARD:          PRT:          640 AA.
ID MT30_YEAST

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AC p39014;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MET30 protein.
GN MET30 OR YIL046W.
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X2180-1A;
RX MEDLINE=96069360; PubMed=8524217;
RA Thomas D., Kuras L., Barbey R., Charest H., Blaiseau P.L.,
RA Surlin-Kerjan Y.;
RT "Met30p, a yeast transcriptional inhibitor that responds to S-
RL Mol. Cell. Biol. 15:6526-6534(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Bartell B.G., Badcock R., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jags K., Jones M.,
RA Louis E., Lye G., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RT Submitted (Dec-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR AMINO BIOSYNTHESIS
CC GENES EXPRESSION.
CC -1- SUBUNIT: SEEMS TO INTERACT WITH MET4.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
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CC -----
DR EMBL: Z46861; CA86905.1; -
DR EMBL: L26505; AAA96717.1; -
DR SCD: S0001308; MET30.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 6.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Transcription regulation; Methionine biosynthesis;
KW Cysteine biosynthesis; Repeat; WD repeat.
KM DOMAIN 181 227
FT REPEAT 300 328 WD 1.
FT REPEAT 340 368 WD 2.
FT REPEAT 380 408 WD 3.
FT REPEAT 419 449 WD 4.
FT REPEAT 461 499 WD 5.
FT REPEAT 509 538 WD 6.
FT REPEAT 550 578 WD 7.
FT REPEAT 607 635 WD 8 (POTENTIAL).
FT CONFLICT 61 61 M -> I (IN REF. 1).
SQ SEQUENCE 640 AA; 72835 MW; 5135DABCA2EB97 CRC64;

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Query Match 56.2%; Score 86; DB 1; Length 640;
 Best Local Similarity 51.7%; Pred. No. 2.8e-05;
 Matches 15; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGHTGSVLCLOYDERVITITGSSDSTVRW 29
 DB 339 SGHSDGVKTLVFDRLKLTIGSLDKTIRW 367

RESULT 10
 CC4_CANAL STANDARD; PRT; 684 AA.

AC P53699;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cell division control protein 4.

GN CC4.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=5476;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=SGY126;
 RA Shieh J.C., White A.M., Rosamond J.;
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
 REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM THE
 POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
 DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
 VARIOUS ASPECTS OF SPOULATON. REQUIRED FOR HVAL-HTB1 LOCUS
 TRANSCRIPTION ACTIVATION (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.

CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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CC
 DR EMBL: X96763; CA65538.1;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 1.
 DR SMART: SM00320; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 4.
 DR PROSITE: PS00294; WD_REPEATS_REGION; 1.
 KW Cell division; Mitosis; Sporulation; Repeat; WD repeat.
 KM
 FT DOMAIN 212 258 F-BOX.
 FT REPEAT 322 351 WD 1.
 FT REPEAT 363 391 WD 2.
 FT REPEAT 403 431 WD 3.
 FT REPEAT 442 468 WD 4 (POTENTIAL).
 FT REPEAT 478 506 WD 5.
 FT REPEAT 519 549 WD 6.
 FT REPEAT 561 589 WD 7.
 SQ SEQUENCE 684 AA; 76090 MW; 3DD65DB31293B107 CRC64;

Query Match 55.6%; Score 85; DB 1; Length 684;
 Best Local Similarity 53.6%; Pred. No. 4.4e-05;
 Matches 15; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 GHTGSVLCLOYDERVITITGSSDSTVRW 29
 DB 363 GHEGVWALKYTGNTLVGSDTRVRW 390

RESULT 11
 YJL2_YEAST STANDARD; PRT; 714 AA.

AC P47025;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 80.0 kDa Trp-Asp repeats containing protein in ASF1-CT7
 DE intergenic region.

GN YJL112W OR J0802.
 OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=S288C / FY1679;
 RX MEDLINE=97103775; PubMed=8948101;

RA Cziepluch C., Kordes E., Pujoil A., Jauniaux J.-C.;
 RT "Sequencing analysis of a 40.2 kb fragment of yeast chromosome X
 reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2,
 RT SPT10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes,
 RT three remnant delta elements and a Ty4 transposon."
 RL Yeast 12:1471-1474(1996).

RN [2]
 RP SEQUENCE OF 596-714 FROM N.A.

RC STRAIN=S288C / FY1679;
 RX MEDLINE=96090136; PubMed=7483851;

RA Rasmussen S.W.;

RT "A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1
 and GCD3 genes, a TCP-1-related gene, an open reading frame similar
 to the DAL80 gene, and a tRNA(Arg).";

RL Yeast 11:873-883(1993).

CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).

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CC
 DR EMBL: Z49387; CA89407.1;
 DR SGD: S0003648; YJL112W.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 2.
 DR SMART: SM00320; WD40; 5.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 6.
 DR PROSITE: PS00294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 KM
 FT REPEAT 396 427 WD 1.
 FT REPEAT 439 469 WD 2.
 FT REPEAT 500 528 WD 3.
 FT REPEAT 564 592 WD 4.
 FT REPEAT 604 632 WD 5.
 FT REPEAT 643 672 WD 6.
 SQ SEQUENCE 714 AA; 80032 MW; CA8A23DBB06193A6 CRC64;

Query Match 54.2%; Score 83; DB 1; Length 714;
 Best Local Similarity 46.4%; Pred. No. 9.3e-05;
 Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```

Db 604 GHTDAITSLKFPDSACTVGTGSDTVRIM 631

RESULT 12
SEIO_CAEEL
ID SEIO_CAEEL STANDARD; PRT; 579 AA.
AC 093794;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sel-10 protein
GN Sel-10 OR F55B12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN=BRISTOL N2;
RA Sims M.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Jones S.J.M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: 279757; CAB02129.1; -
DR WormBep: F55B12.3; CE16120.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 5.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
KM DOMAIN
FT REPEAT 113 159 F-BOX.
FT REPEAT 245 274 WD 1.
FT REPEAT 286 316 WD 2.
FT REPEAT 328 356 WD 3.
FT REPEAT 368 396 WD 4.
FT REPEAT 408 438 WD 5.
FT REPEAT 453 481 WD 6.
FT REPEAT 493 522 WD 7.
SO SEQUENCE 579 AA; 64275 MW; 0647245AF5964663 CRC64;

Query Match 52.98; Score 81; DB 1; Length 579;
Best Local Similarity 46.48; Pred. No. 0.00015;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHTGSVLCLOQDERVITGSSDSTVRVW 29
Db 328 GHTSTVRCMAMAGSIIVTGSRTTLKRW 355

RESULT 13
YK16_YEAST
ID YK16_YEAST STANDARD; PRT; 659 AA.

Db 604 GHTDAITSLKFPDSACTVGTGSDTVRIM 631

P36130;
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 74.7 kDa Trp-Asp repeats containing protein in DAL80-GAP1
DE intergenic region.
GN YKR036C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Drestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD_REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: 228261; CAAB2110.1; -
DR PIR: S36108; S36108.
DR TRANSFAC: T04326; -
DR SGD: S0001744; YKR036C.
DR InterPro: IPR001744; YKR036C.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 1.
DR SMART: SM00320; WD40; 5.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS50082; WD_REPEATS_2; 5.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 333 364 WD 1.
FT REPEAT 376 407 WD 2.
FT REPEAT 438 466 WD 3.
FT REPEAT 503 531 WD 4.
FT REPEAT 543 571 WD 5.
FT REPEAT 582 610 WD 6.
SO SEQUENCE 659 AA; 74709 MW; 139593554C56DD37 CRC64;

Query Match 52.98; Score 81; DB 1; Length 659;
Best Local Similarity 42.98; Pred. No. 0.00017;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

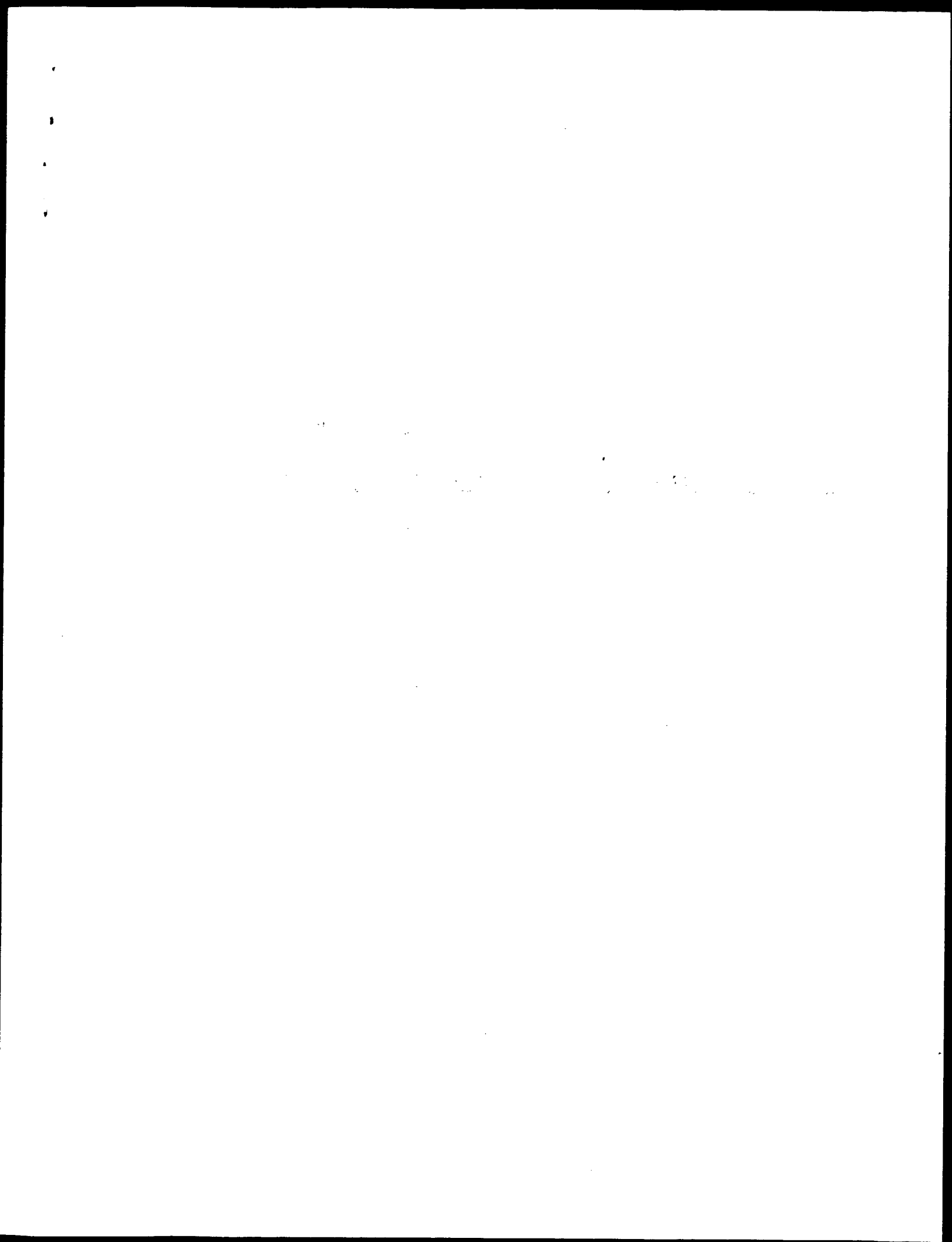
OY 2 GHTGSVLCLOQDERVITGSSDSTVRVW 29
Db 543 GHTDITSLKFPDSKLVGTGSMDSVRIM 570

RESULT 14
FBW2_HUMAN
ID FBW2_HUMAN STANDARD; PRT; 422 AA.
AC 09UKT8; Q9UKA3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein 2.
GN FBXW2 OR FBW2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20003060; PubMed=10531035;
RA Cenciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;

```


RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2003061; PubMed=10531037;
 RA Winston J.T., Koepf D.M., Zhu C., Ellledge S.J., Harper J.W.;
 RT "A family of mammalian F-box proteins.";
 RL Curr. Biol. 9:1180-1182(1999).
 CC -1- FUNCTION: PROBABLY RECOGNIZE AND BINDS TO SOME PHOSPHORYLATED
 CC PROTEINS AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-COLLIN-F-BOX) PROTEIN LIGASE COMPLEX
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: AF129531; AAF04465.1; -;
 DR EMBL: AF176698; AAF13226.1; -;
 DR Genew: HGNC:13608; FBXW2.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00440; WD40; 4.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 1.
 DR SMART: SM00320; FBOX; 1.
 DR SMART: SM00320; WD40; 4.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 1.
 DR PROSITE: PS50082; WD_REPEATS_2; 2.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat: WD repeat.
 KW DOMAIN 54 101 F-BOX.
 FT REPEAT 146 183 WD 1.
 FT REPEAT 185 221 WD 2.
 FT REPEAT 224 265 WD 3.
 FT REPEAT 276 314 WD 4.
 FT CONFLICT 408 408 E -> K (IN REF. 2).
 FT SEQUENCE 422 AA; 47966 MW; 2874BARF233D83E CRC64;
 SQ
 Query Match 51.6%; Score 79; DB 1; Length 422;
 Best Local Similarity 43.3%; Pred. No. 0.00021;
 Matches 13; Conservative 10; Mismatches 5; Indels 2; Gaps 1;
 Oy 2 GHTGSVLCLOYDER--VITGSSDSTVRVW 29
 Db 224 GHTGAVSVVDYNDLIDLVGSADFTYKVV 253
 RESULT 15
 IF32_HUMAN
 ID IF32_HUMAN STANDARD: PRT: 325 AA.
 AC Q13347;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta)
 DE (eIF3 p36) (TGF-beta receptor interacting protein 1) (TRIP-1).
 GN EIF3S2 OR TRIP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=97150873; PubMed=8995409;
 RA Asano K., Kinzy T.G., Merrick W.C., Hershey J.W.B.;
 RT "Conservation and diversity of eukaryotic translation initiation
 RT factor eIF3.";
 RL J. Biol. Chem. 272:1101-1109(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96013749; PubMed=7566156;
 RA Chen R.H., Miettinen P.J., Maruka E.M., Choy L., Derynck R.;
 RT "A WD-domain protein that is associated with and phosphorylated by
 RT the type II TGF-beta receptor.";
 RL Nature 377:548-552(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Muscle;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
 CC METHIONYL-TRNAI AND MRNA.
 CC -1- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
 CC -1- PTM: PHOSPHORYLATED BY TYPE II TGF-BETA RECEPTOR.
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: U39067; AAC97144.1; -;
 DR EMBL: U36764; AAC50224.1; -;
 DR EMBL: BC000413; AAH00413.1; -;
 DR EMBL: BC003140; AAH03140.1; -;
 DR PHCI-2DPAGE; Q13347; -;
 DR Genew: HGNC:3272; EIF3S2.
 DR MIM: 603911; -;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 5.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 2.
 DR SMART: SM00320; WD40; 5.
 DR PROSITE: PS00678; WD_REPEATS_1; 1.
 DR PROSITE: PS50082; WD_REPEATS_2; 4.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
 DR Initiation factor; protein biosynthesis; Repeat: WD repeat;
 KW Phosphorylation.
 FT REPEAT 8 38 WD 1.
 FT REPEAT 50 80 WD 2.
 FT REPEAT 144 174 WD 3.
 FT REPEAT 186 216 WD 4.
 FT REPEAT 283 313 WD 5.
 FT SEQUENCE 325 AA; 36502 MW; 02797BB72A752A96 CRC64;
 SQ
 Query Match 51.0%; Score 78; DB 1; Length 325;
 Best Local Similarity 43.3%; Pred. No. 0.00021;
 Matches 13; Conservative 10; Mismatches 5; Indels 2; Gaps 1;
 Oy 2 GHTGSVLC--QYDERVITGSSDSTVRVW 29
 Db 50 GHTGAVWCVDADWTKHVLTVGSADNSCRLW 79
 Search completed: April 10, 2003, 13:19:34
 Job time : 3.08404 secs



GenCore version 5.1.4-P5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 6.85262 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_304_332

Sequence: 1 TGHGSGVICLDYDERVITITGSSDSTVRW 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertbrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriaph:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	569	11	Q9RI67 mus musculus
2	153	100.0	569	11	Q9QU15 mus musculus
3	152	99.3	563	11	Q923H0 mus musculus
4	146	95.4	569	11	Q92159 mus musculus
5	138	90.2	510	5	Q44382 drosophila
6	138	90.2	510	5	Q9VDE3 drosophila
7	124	81.0	38	13	Q8UUN4 xenopus lae
8	124	81.0	430	5	Q9BU54 heterodera
9	97	63.4	252	11	Q922C7 mus musculus
10	89	58.2	280	5	Q8ST59 encephalito
11	87.5	57.2	414	5	Q8SW59 homo sapien
12	84	54.9	553	4	Q9NUX6 homo sapien
13	84	54.9	561	4	Q96RI2 homo sapien
14	84	54.9	589	4	Q96LE0 homo sapien
15	84	54.9	627	4	Q96A16 homo sapien
16	84	54.9	629	11	Q8VHP4 mus musculus

17	84	54.9	629	11	Q8VBV4	Q8VBV4 mus musculus
18	84	54.9	707	4	Q969H0	Q969H0 homo sapien
19	83.5	54.6	1446	10	Q9SUT4	Q9SUT4 arabidopsis
20	83	54.2	388	10	Q9FC99	Q9FC99 arabidopsis
21	82	53.6	1228	5	Q9U4H2	Q9U4H2 drosophila
22	82	53.6	1240	5	Q9V815	Q9V815 drosophila
23	81	52.9	585	5	Q952T0	Q952T0 caenorhabd
24	81	52.9	587	5	Q44083	Q44083 caenorhabd
25	81	52.9	1326	5	Q9VZF4	Q9VZF4 drosophila
26	80	52.3	122	13	Q8UUN3	Q8UUN3 xenopus lae
27	79	51.6	454	4	Q8WV51	Q8WV51 homo sapien
28	79	51.6	454	4	Q9H403	Q9H403 homo sapien
29	79	51.6	562	10	Q9SC73	Q9SC73 oryza sativ
30	79	51.6	922	5	Q9VE98	Q9VE98 drosophila
31	79	51.6	1204	10	Q8S0C3	Q8S0C3 oryza sativ
32	78	51.0	1241	2	Q9XBD8	Q9XBD8 amycolatops
33	77.5	50.7	447	10	Q9AV17	Q9AV17 oryza sativ
34	77.5	50.7	473	5	Q9TVV3	Q9TVV3 caenorhabd
35	77	50.3	914	4	Q9C0E5	Q9C0E5 homo sapien
36	77	50.3	1573	11	Q9QXL2	Q9QXL2 mus musculus
37	76.5	50.0	613	5	Q960M2	Q960M2 drosophila
38	76.5	50.0	621	5	Q9VAT2	Q9VAT2 drosophila
39	76	49.7	307	11	Q8R315	Q8R315 mus musculus
40	76	49.7	367	4	Q9H8N5	Q9H8N5 homo sapien
41	76	49.7	415	4	Q9P2B3	Q9P2B3 h kiara135
42	76	49.7	992	16	Q98GJ0	Q98GJ0 rhizobium
43	76	49.7	1189	16	Q8Y109	Q8Y109 anabaena sp
44	75.5	49.3	808	4	Q96A78	Q96A78 homo sapien
45	75	49.0	304	11	Q9DAT2	Q9DAT2 mus musculus

ALIGNMENTS

RESULT 1

Q9RI67 PRELIMINARY: PRT: 569 AA.

AC Q9RI67; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Beta-transducin repeat-containing protein.

CN BTRC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Winston J., Elledge S.J., Harper J.W.;

Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRF-ASP DOMAINS).

DR EMBL: AF110396; A041025.1; -.

DR MGD: MGI:1338871; Btrc.

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001680; WD40.

DR Pfam: PF00645; F-box; 1.

DR Pfam: PF00400; WD40; 7.

DR PRINTS: PR00320; GPROTEINRPT.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00256; FBOX; 1.

DR SMART: SM00320; WD40; 7.

DR PROSITE: PS00181; PROX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.

DR PROSITE: PS00082; WD_REPEATS_2; 7.

DR PROSITE: PS0294; WD_REPEATS_REGION; 1.

KW Repeat; WD repeat.

SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;

Query Match 100.0%; Score 153; DB 11; Length 569;

Best local Similarity 100.0%; Pred. No. 3.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGHGTVLCLQYDERVITITGSSDSTVRW 29
 ID 09015 PRELIMINARY; PRT; 569 AA.
 AC 09015;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE Ubiquitin ligase FWD1 (beta-transducin repeat containing protein)
 DE (F-box-WD40 repeat protein 1).
 GN BTRC OR FBXW1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99199275; PubMed-10097128;
 RA Hakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
 RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
 RA Nakayama K.-I.;
 RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a
 RT ubiquitin ligase Skp1/Cul1/F-box protein FWD1";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99075339; PubMed-9859996;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase";
 RL Nature 396:590-594(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV;
 RX MEDLINE-21601157; PubMed-11735228;
 RA Matuyama S., Hakeyama S., Nakayama K., Ishida N., Kawakami K.,
 RA Nakayama K.-I.;
 RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
 RT Caenorhabditis elegans SEL-10.";
 RL Genomics 78:214-222(2001).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF081887; AAD17755.1;
 DR EMBL: AF099932; AAD08701.1;
 DR EMBL: BC003989; AAH03989.1;
 DR EMBL: AF391190; AAL40929.1;
 DR EMBL: AF391178; AAL40929.1; JOINED.
 DR EMBL: AF391179; AAL40929.1; JOINED.
 DR EMBL: AF391180; AAL40929.1; JOINED.
 DR EMBL: AF391181; AAL40929.1; JOINED.
 DR EMBL: AF391182; AAL40929.1; JOINED.
 DR EMBL: AF391183; AAL40929.1; JOINED.
 DR EMBL: AF391184; AAL40929.1; JOINED.
 DR EMBL: AF391185; AAL40929.1; JOINED.
 DR EMBL: AF391186; AAL40929.1; JOINED.
 DR EMBL: AF391187; AAL40929.1; JOINED.
 DR EMBL: AF391188; AAL40929.1; JOINED.
 DR EMBL: AF391189; AAL40929.1; JOINED.
 DR MGD; MGI:1338871; Btrc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.

DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Ligase; Repeat; WD repeat.
 SO SEQUENCE 569 AA; 65105 MW; BC7D6544815B296 CRC64;
 Query Match 100.0%; Score 153; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3; 7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGHGTVLCLQYDERVITITGSSDSTVRW 29
 ID 0923H0 PRELIMINARY; PRT; 563 AA.
 AC 0923H0;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE F-box-WD40 repeat-containing protein HOS.
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Bhatia N., Heter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
 RT "Mouse homolog of HOS (rhOS) is overexpressed in skin tumors and
 RT implicated in constitutive activation of NF-kappaB.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: A1038079; AAK72095.1;
 DR MGD; MGI:2144023; Fbxw1b.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRODOM: PD000018; WD40; 4.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS50078; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SO SEQUENCE 563 AA; 64741 MW; 9AB562F3FF5E3496 CRC64;
 Query Match 99.3%; Score 152; DB 11; Length 563;
 Best Local Similarity 96.6%; Pred. No. 5; 2e-15;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGHGTVLCLQYDERVITITGSSDSTVRW 29
 ID 092159 PRELIMINARY; PRT; 569 AA.
 AC 092159;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DE Beta-transducin repeat containing protein.
 GN BTRC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99145465; PubMed=9990853;
 RA Spencer E., Jiang J., Chen Z.J.,
 RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
 SLIMB/beta-TRCP.";
 RT Genes Dev. 13:284-294(1999).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF112979, AAD04181.1, -.
 DR MGD: MGI:1338871; Btfc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 569 AA; 65047 MW; BC7CA44815BED96 CRC64;

Query Match 95.4%; Score 146; DB 11; Length 569;
 Best Local Similarity 96.6%; Pred. No. 4,5e-14;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGHTGSLCQYDERVITSSSDSTVRW 29
 |||||||
 DB 304 TGHTGSLCQYDERVITSSSDSTVRW 332

RESULT 5

OC 044382 PRELIMINARY; PRT; 510 AA.
 ID 044382;
 AC 044382;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE SLIMB
 GN SLIMB OR SLIMB OR CG3412.. (fruit fly)
 OS Drosophila melanogaster (fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96121115; PubMed=9461217;
 RA Jiang J., Struhl G.,
 RT "Regulation of the Hedgehog and Wingless signalling pathways by the F-
 box/WD40-repeat protein Slmb.";
 RT Nature 391:493-496(1998).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF032878, AAC3885.1, -.
 DR Flybase: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;

Query Match 90.2%; Score 138; DB 5; Length 510;
 Best Local Similarity 89.3%; Pred. No. 6,9e-13;
 Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 GHTGSLCQYDERVITSSSDSTVRW 29
 |||||||
 DB 248 GHTGSLCQYDERVITSSSDSTVRW 275

RESULT 6

OC 09VDE3 PRELIMINARY; PRT; 510 AA.
 ID 09VDE3;
 AC 09VDE3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE SLIMB protein (SLIMB).
 GN SLIMB OR CG3412.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Aghayani A., An H.-J., Andrews-Plankh C., Ballow D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brostlein P., Brothier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jastali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,
 RA Reihart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY, AND IMAGINAL DISC;
 RX MEDLINE=20245299; PubMed=10781936;
 RA Mlecnik I., Limbourg-Bouchon B.;
 RT "Drosophila null slimb clones transiently deregulate Hedgehog-
 independent transcription of all limb discs, and induce

RT decapentaplegic transcription linked to imaginal disc regeneration."
RL Mech Dev. 93:15-26(2000).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF003733; AAF55853.1; -
DR EMBL; AF222923; AAF63214.1; -
DR EMBL; AF222923; AAF63213.1; -
DR FlyBase; FBgn0023423; slmb.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; FAD5DF126F58A012 CRC64;

Query Match
Best Local Similarity 90.2%; Score 138; DB 5; Length 510;
Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 GHTGSVLCLOYDERVLIITGSSDSTVRW 29
DB 248 GHTGSVLCLOYDDKVIITSSSDSTVRW 275

RESULT 7
ID 080UN4 PRELIMINARY; PRT; 38 AA.
AC 080UN4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis".
RT Thesis (2001),
RL Department of Genetics and Molecular Biology "Charles Darwin",
RL University of Rome, Rome, Italy.
DR EMBL; A428937; CAD21934.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 1.
DR ProDom; PD000018; WD40; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4270 MW; F825C0B481D54F03 CRC64;

Query Match
Best Local Similarity 81.0%; Score 124; DB 13; Length 38;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GHTGSVLCLOYDERVLIITGSSDST 25
DB 15 GHTGSVLCLOYDERVLIITGSSDST 38

RESULT 8
ID 09B5J4 PRELIMINARY; PRT; 430 AA.
AC 09B5J4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta transducin repeat-containing protein (Fragment).
OS Heterodera glycyces (Soybean cyst nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=51029;
RN [1]
RP SEQUENCE FROM N.A.
RA Kovaleva E.S.; Yakovlev A.G.; Masler E.P.;
RT "Plant parasitic nematode b-TRCP."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF339101; AAK26376.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
FT NON_TER 430
SQ SEQUENCE 430 AA; 47916 MW; 4ABC3F2DFE3A50B CRC64;

Query Match
Best Local Similarity 81.0%; Score 124; DB 5; Length 430;
Matches 21; Conservative 72.4%; Pred. No. 8.6e-11;
QY 1 TGHGTVLCLOYDERVLIITGSSDSTVRW 29
DB 128 SGHTGSVLCLOYDNMTAIGSSDSTVRW 156

RESULT 9
ID 0922C7 PRELIMINARY; PRT; 252 AA.
AC 0922C7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to f-box and WD-40 domain protein 1B (Fragment).
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC008552; AAH08552.1; -
DR MGD; MGI:2144023; Fbxw1b.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
FT NON_TER 252
SQ SEQUENCE 252 AA; 28424 MW; F71737CB7A9F75F CRC64;

Query Match
Best Local Similarity 50.0%; Score 97; DB 11; Length 252;
Pred. No. 7.3e-07;
Matches 11; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVITIGSSDSTVRW 29
DB 111 GHKRGIACTGYRDLRVVSGSSDNTIRLW 138

RESULT 10
Q8ST25 PRELIMINARY; PRT; 280 AA.

AC Q8ST25; 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
GN Hypothetical protein EC011_1970.

OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;

RA Sequence from N.A.

RC STRAIN=GB-M1;

RA Genoscope;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RA MEDLINE-21576510; PubMed-11719806;

RA Kacinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,

Prensler G., Barbe V., Peyretailade E., Brotlier P., Wincker P.,

Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,

Weissenbach J., Vivares C.P.;

"Genome sequence and gene compaction of the eukaryote parasite

RT Encephalitozoon cuniculi.";

RL Nature 414:450-453(2001).

DR EMBL; AL590450; CAD26107.1; -

KW Hypothetical protein.

SO SEQUENCE 280 AA; 31339 MW; 50176DF5970F538 CRC64;

Query Match
Best Local Similarity 58.2%; Score 89; DB 5; Length 280;
Pred. No. 1.4e-05;
Matches 17; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVITIGSSDSTVRW 29
DB 94 GHMSSVLCQYDERVITIGSSDSTVRW 121

RESULT 11

Q8SW59 PRELIMINARY; PRT; 414 AA.

AC Q8SW59;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE WD repeats-containing protein.

GN EC003_0430.

OS Encephalitozoon cuniculi.

OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.

NCBI_TaxID=6035;

RA Sequence from N.A.

RC STRAIN=GB-M1;

RA Genoscope;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RA MEDLINE-21576510; PubMed-11719806;

RA Kacinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,

Prensler G., Barbe V., Peyretailade E., Brotlier P., Wincker P.,

RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;

"Genome sequence and gene compaction of the eukaryote parasite

RT Encephalitozoon cuniculi.";

RL Nature 414:450-453(2001).

DR EMBL; AL590443; CAD26189.1; -

SO SEQUENCE 414 AA; 46065 MW; EBBCA38393981871 CRC64;

Query Match
Best Local Similarity 57.2%; Score 87.5; DB 5; Length 414;
Pred. No. 3.9e-05;
Matches 17; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 TGHGTVLCQYDERVITIGSSDSTVRW 29
DB 111 SGHEGTVLCVRYG-GVITVGGDSTVRW 138

RESULT 12
Q9NOX6 PRELIMINARY; PRT; 553 AA.

AC Q9NOX6;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE CDNA FLJ11071 f1s, clone PLACE1004937, moderately similar to SEL-10

DE protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RA Sequence from N.A.

RC TISSUE=PLACENTA;

RA Tsogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Matsunawa H., Ishii S., Sugano S., Aotsuka S., Yoshikawa Y.,

RA Nakamura Y., Nagai K., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

"MDO human cDNA sequencing project.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -3- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL; AK001933; BA09186.1; -

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001680; WD40.

DR Pfam: PF00646; F-box; 1.

DR Pfam: PF00400; WD40; 7.

DR PRINTS: PR00320; GPROTEINBRPT.

DR PRODOM: PD000018; WD40; 2.

DR SMART: SM00256; FBOX; 1.

DR SMART: SM00320; WD40; 7.

DR PROSITE: PS50181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

KW Repeat: WD repeat.

SO SEQUENCE 553 AA; 62280 MW; CA829C221986A3F2 CRC64;

Query Match
Best Local Similarity 54.9%; Score 84; DB 4; Length 553;
Pred. No. 0.00019;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVITIGSSDSTVRW 29
DB 305 GHTSVRCMHLEKRVVSGSRDATTIRW 332

RESULT 13

Q96RT2 PRELIMINARY; PRT; 561 AA.

AC Q96RT2;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE F-box protein FBX30 (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF383178; AAK60269.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS500678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER
SQ SEQUENCE 561 AA; 63165 MW; B81CCE2206B0D88 CRC64;

Query Match 54.9%; Score 84; DB 4; Length 561;
Best Local Similarity 46.4%; Pred. No. 0.00019;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVIITGSSDSTVRW 29
| | | : | | : | : | | | | | | |
Db 313 GHTSVRCMHLHKRVVSGSRDALTLRW 340

RESULT 14
QY 096LE0 PRELIMINARY; PRT; 589 AA.
AC 096LE0;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE F-box protein SEL10.
GN SEL10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R.,
RA Buhl A.E., Gurney M.E.;
RT "SEL-10 interacts with Presenilin 1, facilitates its ubiquitination,
RT and Alters A-beta production."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY008274; AAG1640.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS500678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 589 AA; 66120 MW; ZAFB6E8A36E6E8DE CRC64;

Query Match 54.9%; Score 84; DB 4; Length 589;

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Best Local Similarity 46.4%; Pred. No. 0.0002;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVIITGSSDSTVRW 29
| | | : | | : | : | | | | | | |
Db 341 GHTSVRCMHLHKRVVSGSRDALTLRW 368

RESULT 15
QY 096A16 PRELIMINARY; PRT; 627 AA.
AC 096A16;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Archipelago beta form (F-box protein FBW7).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21449047; PubMed=11565033;
RA Moberg K.H., Bell D.W., Wahner D.C., Haber D.A., Hariharan I.K.;
RT "Archipelago regulates Cyclin E levels in Drosophila and is mutated in
RT human cancer cell lines."
RL Nature 413:311-316(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper W., Elledge S.J.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF411972; AAL06291.1; -.
DR EMBL: AY033553; AAK57547.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS500678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 627 AA; 70324 MW; 3D4107C05381BED CRC64;

Query Match 54.9%; Score 84; DB 4; Length 627;
Best Local Similarity 46.4%; Pred. No. 0.00022;
Matches 13; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHTGSVLCQYDERVIITGSSDSTVRW 29
| | | : | | : | : | | | | | | |
Db 379 GHTSVRCMHLHKRVVSGSRDALTLRW 406

Search completed: April 11, 2003, 11:51:34
Job time : 8.85262 secs

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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 ; Search time 9.55298 Seconds
(without alignments)
432.406 Million cell updates/sec

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	510	22	ABBS9857
2	172	100.0	517	16	ABBS9857
3	172	100.0	569	20	AAV24054
4	172	100.0	569	21	AAI12812
5	172	100.0	569	21	AAI12813
6	172	100.0	569	21	AAV96697
7	172	100.0	569	21	AAV83041
8	172	100.0	569	21	AAV83250
9	172	100.0	569	21	AAV83254
10	172	100.0	569	21	AAV44249

ALIGNMENTS

RESULT 1	ID	ABBS9857	standard: Protein: 510 AA.	Human 2F1 protein		
11	172	100.0	569	22	AAV8298	Human 2F1 protein
12	172	100.0	579	22	AAV78583	Human protein SEQ
13	172	100.0	590	22	AAV00847	Human bone marrow
14	172	100.0	605	22	AAV78582	Human protein SEQ
15	172	100.0	608	22	AAV00960	Human bone marrow
16	172	100.0	632	22	AAV78584	Human protein SEQ
17	172	100.0	654	22	AAV79566	Human protein SEQ
18	172	100.0	654	22	AAV79567	Human protein SEQ
19	172	100.0	654	22	AAV79568	Human protein SEQ
20	172	100.0	654	22	AAV79569	Human protein SEQ
21	172	100.0	654	22	AAV79570	Human protein SEQ
22	172	100.0	654	22	AAV79571	Human protein SEQ
23	172	100.0	654	22	AAV79572	Human protein SEQ
24	172	100.0	654	22	AAV79573	Human protein SEQ
25	172	100.0	654	22	AAV79574	Human protein SEQ
26	172	100.0	654	22	AAV79575	Human protein SEQ
27	172	100.0	654	22	AAV79576	Human protein SEQ
28	172	100.0	654	22	AAV79577	Human protein SEQ
29	172	100.0	654	22	AAV79578	Human protein SEQ
30	172	100.0	654	22	AAV79579	Human protein SEQ
31	172	100.0	654	22	AAV79580	Human protein SEQ
32	172	100.0	654	22	AAV79581	Human protein SEQ
33	172	100.0	654	22	AAV79582	Human protein SEQ
34	172	100.0	654	22	AAV79583	Human protein SEQ
35	172	100.0	654	22	AAV79584	Human protein SEQ
36	172	100.0	654	22	AAV79585	Human protein SEQ
37	172	100.0	654	22	AAV79586	Human protein SEQ
38	172	100.0	654	22	AAV79587	Human protein SEQ
39	172	100.0	654	22	AAV79588	Human protein SEQ
40	172	100.0	654	22	AAV79589	Human protein SEQ
41	172	100.0	654	22	AAV79590	Human protein SEQ
42	172	100.0	654	22	AAV79591	Human protein SEQ
43	172	100.0	654	22	AAV79592	Human protein SEQ
44	172	100.0	654	22	AAV79593	Human protein SEQ
45	172	100.0	654	22	AAV79594	Human protein SEQ

CC	contng WD-40 motifs, as modulators of enzyme esp. isozyme, activity of CC proteins involved in protein-protein interaction and to screen for drugs that will affect protein-protein interaction involving WD-40 domains.
CC	
CC	
XX	Sequence 517 AA;
SQ	
Oy	1 LIHCEAVLHLRFNNGMVTCSKDRSLAWMD 31 Db 307 LIHCEAVLHLRFNNGMVTCSKDRSLAWMD 337
RESULT 3	
AAY24054	
ID	AMZ24054 standard; Protein: 569 AA.
AC	AAY24054;
XX	
DT	30-SEP-1999 (first entry)
XX	
DE	A human beta-transducin repeat containing protein.
XX	
KW	Beta-transducin repeat containing protein; beta-Trep; Skrip;
KW	proteosome degradation pathway; Vpu protein; beta-catenin;
KW	human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;
KW	ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
KW	antiviral; antitumour; cell cycle regulation; protein degradation;
KW	and anti-inflammatory; osteo articular inflammation; acute inflammation;
KW	tumour necrosis factor.
OS	Homo sapiens.
XX	
FH	Key
FT	Region Location/Qualifiers
FT	/note= "P box sequence"
FT	Region 259..292
FT	/note= "WD motif"
FT	Region 304..332
FT	/note= "WD motif"
FT	Region 343..372
FT	/note= "WD motif"
FT	Region 387..415
FT	/note= "WD motif"
FT	Region 427..455
FT	/note= "WD motif"
FT	Region 467..492
FT	/note= "WD motif"
FT	Region 516..544
FT	/note= "WD motif"
PN	WO9938969-A1.
PD	05-AUG-1999.
PF	
XX	
PR	29-JAN-1999; 99WO-FR00196.
PR	09-DEC-1998; 98FR-0015545.
PR	30-JAN-1998; 98FR-0001100.
PA	(INRM) INSEPM INST NAT SANTE & RECH MEDICALE.
PA	(INSP) INST PASTEUR.
XX	
PI	Arenzana Seisdedos F; Benarous R; Concordet J; Durand H;
PI	Kroll M, Margottin F;
XX	
DR	WP1: 1999-469329/39.
DR	N-PDB: AAX86501.
PT	New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumour,
PT	

PT anti-inflammatory and anti-Alzheimer's agents
XX
PS Claim 1: Page 60-61; 71pp; French.
XX
CC The present sequence represents a human beta-transducin repeat containing
CC protein (beta-TrCP). The protein directs proteins to the proteasome
CC degradation pathways. The protein is able to interact with the Vpu
CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
CC IkappaB or beta-catenin (bc) and/or protein Skp1. The protein controls
CC ubiquitinylation of phosphorylated proteins and thus their targeting to
CC proteasomes for degradation. Depending on whether the process is
CC inhibited or promoted, the result may be delayed breakdown of CD4 (in
CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
CC activity of NFkappaB) and increased degradation of mutant bc in tumour
CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
CC patients. The beta-TrCP protein, and its active peptide fragments, or its
CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
CC antitumour agents that disrupt cell cycle regulation or protein
CC degradation in human tumour cells, and anti-inflammatory agents that
CC disrupt activation by NFkappaB. Fragments of the protein are also
CC useful for treating osteo-articular inflammation or acute inflammation
CC associated with release of tumour necrosis factor.
XX
SQ Sequence 569 AA:
Query Match 100.0%; Score 172; DB 20; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.4e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 31
|||||
DB 343 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 373
RESULT 4
AAB12812
ID AAB12812 standard; protein: 569 AA.
XX
AC AAB12812;
XX
DT 27-NOV-2000 (first entry)
XX
DE Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.
XX
XX Ubiquitin ligase SCF complex; F-box protein: ubiquitination; IkappaB;
XX beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
XX gene therapy; colon cancer; beta-transducin repeat containing protein;
XX beta-TrCP.
XX
OS Mus musculus.
XX
PN JP200016542-A.
XX
PD 20-JUN-2000.
XX
PF 02-DEC-1998; 98JP-0343437.
XX
PR 02-DEC-1998; 98JP-0343437.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI: 2000-485550/43.
XX
DR N-PSDB; AAA73131.
XX
PT F-box protein of ubiquitin ligase SCF complex which promotes the
XX ubiquitination of IkappaB or beta-catenin
XX
PS Claim 2: Page 9-10; 19pp; Japanese.
XX
CC The present invention describes an F-box motif protein of ubiquitin
XX ligase SCF complex which promotes the ubiquitination of IkappaB or
XX beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
XX complex (SCF complex) of F-box protein containing F-box motif and WD40

CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
CC ligase FWD1 protein) and (AAB12813, which is human beta-transducin
CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
CC the gene therapy of colon cancer by being recombined to a virus vector.
XX
SQ Sequence 569 AA:
Query Match 100.0%; Score 172; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.4e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 31
|||||
DB 343 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 373
RESULT 5
AAB12813
ID AAB12813 standard; protein: 569 AA.
XX
AC AAB12813;
XX
DT 27-NOV-2000 (first entry)
XX
DE Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
XX
XX Ubiquitin ligase SCF complex; F-box protein: ubiquitination; IkappaB;
XX beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
XX gene therapy; colon cancer; beta-transducin repeat containing protein;
XX beta-TrCP.
XX
OS Homo sapiens.
XX
PN JP200016542-A.
XX
PD 20-JUN-2000.
XX
PF 02-DEC-1998; 98JP-0343437.
XX
PR 02-DEC-1998; 98JP-0343437.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI: 2000-485550/43.
XX
DR N-PSDB; AAA73132.
XX
PT F-box protein of ubiquitin ligase SCF complex which promotes the
XX ubiquitination of IkappaB or beta-catenin
XX
PS Claim 3: Page 10-12; 19pp; Japanese.
XX
XX The present invention describes an F-box motif protein of ubiquitin
XX ligase SCF complex which promotes the ubiquitination of IkappaB or
XX beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
XX complex (SCF complex) of F-box protein containing F-box motif and WD40
XX repeat motif and has the amino acid sequence of 45 residues (AAB12811)
XX or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
XX ligase FWD1 protein) and (AAB12813, which is human beta-transducin
XX repeat containing protein (beta-TrCP)). The F-box protein can be used for
XX the gene therapy of colon cancer by being recombined to a virus vector.
XX
SQ Sequence 569 AA:
Query Match 100.0%; Score 172; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.4e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 31
|||||
DB 343 LIHHC EAVLHLRFNNGMVTCSKDRSIAVWD 373

```

RESULT 6
ID AAY96697
XX AAY96697 standard; Protein; 569 AA.
AC AAY96697;
XX
DT 26-SEP-2000 (first entry)
DE Human beta-TrCP.
XX
KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytosolic.
XX
OS Homo sapiens.
XX
PN WO200034447-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US29371.
XX
PR 10-DEC-1998; 98US-0210060.
XX
PA (SIGN-) SIGNAL PHARM INC.
PA (YISS ) YISSUM RES & DEV CO.
XX
PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
PI Lavon I, Yaron A;
DR MPI: 2000-431294/37.
DR N-PSDB; AAY51229.
XX
PT Polypeptide enhancing phosphorylated Ikkappa ubiquitination useful for
PT treating disorder associated with NF-kappaB activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant
XX
PS Claim 21; Page 72-74; 77pp; English.
XX
CC Human beta-TrCP, an F-box/WD protein family member, has been shown to
CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
CC degradation via the ubiquitin pathway is useful for identifying
CC modulators of this process for use in treating diseases associated with
CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
CC the F-box results in a protein that functions as a dominant negative
CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a
CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
XX
SQ Sequence 569 AA;

```

Query Match 100.0%; Score 172; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LIHCEAVLHIRENNGMWTCSKDRSTAVWD 31
Db 343 LIHCEAVLHIRENNGMWTCSKDRSTAVWD 373

```

RESULT 7
 ID AAY83041
 XX AAY83041 standard; Protein; 569 AA.
 AC AAY83041;
 XX
 DT 16-AUG-2000 (first entry)

```

XX
DE F-box protein FBP-1.
XX
KW F-box protein; FBP; diagnosis; treatment; screening; agonist;
KW antagonist; proliferative disorder; differentiative disorder;
KW breast cancer; prostate cancer; ovarian cancer; cancer;
KW small cell lung carcinoma; immune disorder; cardiovascular disorder;
KW inflammatory disorder; human.
XX
OS Homo sapiens.
XX
PN WO200012679-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US19560.
XX
PR 28-AUG-1998; 98US-0098355.
PR 03-FEB-1999; 99US-0118568.
PR 15-MAR-1999; 99US-0124449.
XX
PA (UYNV ) UNIV NEW YORK STATE.
XX
PI Chiaur DS, Pagano M, Latres E;
XX
DR MPI: 2000-256635/22.
DR N-PSDB; AA293350.
XX
PT Novel nucleic acid for screening compounds useful for treating
PT proliferative and differentiative disorders such as cancer and immune
PT disorders comprises sequences encoding ubiquitin ligases
XX
PS Disclosure; Figure 3a; 245pp; English.
XX
CC Nucleic acids encoding substrate-targeting subunits of ubiquitin
CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
CC of proliferative and differentiative related disorders by measuring
CC FBP gene expression. Cells expressing such proteins or
CC their fragments are useful for screening compounds. The compounds
CC are agonists or antagonists, which are useful for treating a
CC proliferative or differentiative disorder in a mammal such as
CC breast, ovarian and prostate cancer and small cell lung carcinoma
CC and also major opportunistic infections, immune disorders,
CC cardiovascular diseases and inflammatory disorders. FBP protein,
CC analogs, derivatives and their subsequences, anti-FBP antibodies
CC are also useful in diagnosis of the disorders.
XX
SQ Sequence 569 AA;

```

Query Match 100.0%; Score 172; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LIHCEAVLHIRENNGMWTCSKDRSTAVWD 31
Db 343 LIHCEAVLHIRENNGMWTCSKDRSTAVWD 373

```

RESULT 8
 ID AAY83250
 XX AAY83250 standard; Protein; 569 AA.
 AC AAY83250;
 XX
 DT 16-AUG-2000 (first entry)
 DE F-box protein hbetaTrCP.
 XX
 KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human.

OS Homo sapiens.
 XX WO200022110-A2.
 PN 20-APR-2000.
 XX 08-OCT-1999; 99WO-0523705.
 PD 09-OCT-1998; 98US-0103787.
 XX (HARD) HARVARD COLLEGE.
 PA Zhou P, Howley P;
 PI WPI: 2000-317970/27.
 XX N-PSDB; AA293710.
 DR
 XX Targeting degradation of polypeptide useful for treating cancer and
 PT other proliferative disorders, involves conjugating polypeptide with
 PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 PT compound
 XX
 PS Claim 9; Page 171; 185pp; English.
 XX
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.
 CC
 XX
 SQ Sequence 569 AA;
 Query Match 100.0%; Score 172; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIHHC EAVLH LRFNNGMWTCSKDRSIAVWD 31
 Db 343 LIHHC EAVLH LRFNNGMWTCSKDRSIAVWD 373
 RESULT 9
 ID AAY83254 standard; Protein; 569 AA.
 XX
 AC AAY83254;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE F-box protein FWD1p.
 XX
 KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW mouse; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200022110-A2.
 XX
 PD 20-APR-2000.

XX
 PF 08-OCT-1999; 99WO-0523705.
 XX
 PR 09-OCT-1998; 98US-0103787.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Zhou P, Howley P;
 XX
 DR WPI: 2000-317970/27.
 XX N-PSDB; AA293714.
 PS
 XX Claim 9; Page 184-185; 185pp; English.
 XX
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.
 CC
 XX
 SQ Sequence 569 AA;
 Query Match 100.0%; Score 172; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIHHC EAVLH LRFNNGMWTCSKDRSIAVWD 31
 Db 343 LIHHC EAVLH LRFNNGMWTCSKDRSIAVWD 373
 RESULT 10
 ID AAY44249 standard; Protein; 569 AA.
 XX
 AC AAY44249;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Human cell signalling protein-12.
 XX
 KW Cell signalling protein-12; CSIGP-12; cell proliferation;
 KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
 KW arteriosclerosis; Addison's disease; multiple sclerosis.
 KW
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 19 /note= "Potential phosphorylation site"
 FT Modified-site 39 /note= "Potential phosphorylation site"
 FT Modified-site 91 /note= "Potential phosphorylation site"
 FT Modified-site 109 /note= "Potential phosphorylation site"
 FT Modified-site /note= "Potential phosphorylation site"

Db 343 LIHCEAVLHLRFNNGMWTGSKDRSIAYWD 373

RESULT 12

AA078583 standard; Protein; 579 AA.

AA078583:

06-NOV-2001 (first entry)

Human protein SEQ ID NO 1245.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.

Homo sapiens.

MO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001MO-US04098.

03-FEB-2000; 2000US-0496914.

27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0663325.

30-NOV-2000; 2000US-0728422.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
Zhou Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;

WPI: 2001-476283/51.

N-PSDB; AAK51716.

Nucleic acids encoding polypeptides with cytokine-like activities,
useful in diagnosis and gene therapy -

Claim 20; Page 3504-3505; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the
encoded polypeptides (AA078323-AA080302) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
(AA080020) are omitted as the relevant pages from the sequence listing
were missing at the time of publication.

Sequence 579 AA;

Query Match 100.0%; Score 172; DB 22; Length 579;

Best local Similarity 100.0%; Pred. No. 5.6e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LIHCEAVLHLRFNNGMWTGSKDRSIAYWD 31

|||||

Db 353 LIHCEAVLHLRFNNGMWTGSKDRSIAYWD 383

RESULT 13

AA00847 standard; Protein; 590 AA.

AA00847:

01-OCT-2001 (first entry)

Human bone marrow protein, SEQ ID NO: 210.

Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; cancer;
human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

Homo sapiens.

MO200153453-A2.

26-JUL-2001.

23-DEC-2000; 2000MO-US34960.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

30-NOV-2000; 2000US-0250583.

(HYSE-) HYSEQ INC.

Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao Q, Zhou P, Drmanac RT;

WPI: 2001-488707/53.

N-PSDB; AAH89966.

Novel bone-marrow-expressed polynucleotides and polypeptides, useful
for treating e.g. cancer and immune deficiency disorders -

Claim 10; Page 354-355; 648pp; English.

The present sequence is one of 251 novel human polypeptides encoded
by a bone marrow-expressed polynucleotide. The polynucleotide and the
polypeptide encoded by it are useful in the treatment of various
immune deficiencies and disorders. The deficiencies and disorders may
be genetic, or may result from an autoimmune disorder, a coagulation
infection, or may result from an autoimmune disorder, a coagulation
disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
suppression of an inflammatory response or treatment of a nervous
system disorder such as Alzheimer's disease. Detection of the presence
or increased expression of the polynucleotide or the protein it
encodes is useful for the diagnosis and/or prognosis of one
or more types of cancer. The polynucleotide and polypeptide can be
used as nutritional sources or supplements and in the screening of
chemical compounds as potential drugs.

Sequence 590 AA;

Query Match 100.0%; Score 172; DB 22; Length 590;

Best local Similarity 100.0%; Pred. No. 5.7e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LIHCEAVLHLRFNNGMWTGSKDRSIAYWD 31

|||||

Db 364 LIHCEAVLHLRFNNGMVTCSKDRSTAVMD 394

RESULT 14

AAM78582
ID AAM78582 standard; Protein; 605 AA.

XX AAM78582;

DI 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1244.

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

OS W0200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
PI N-PSDB; AAK51715.

PS Claim 20; Page 3503-3504; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

XX SQ Sequence 605 AA;

Query Match 100.0%; Score 172; DB 22; Length 605;
Best Local Similarity 100.0%; Pred. No. 5.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLRFNNGMVTCSKDRSTAVMD 31
Db 379 LIHCEAVLHLRFNNGMVTCSKDRSTAVMD 409

RESULT 15

AAM00960
ID AAM00960 standard; Protein; 608 AA.

XX AAM00960;

DI 01-OCT-2001 (first entry)

DE Human bone marrow protein, SEQ ID NO: 436.

XX Human: bone marrow; antiinflammatory; cytosolic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

XX Homo sapiens.

OS W0200153453-A2.

PD 26-JUL-2001.

PF 23-DEC-2000; 2000WO-US34960.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 30-NOV-2000; 2000US-0250583.

XX (HYSE-) HYSEQ INC.

PI Ford JE, Boyle BJ, Tang YF, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Drmanac RT;
PI N-PSDB; AAK90079.

PS Claim 10; Page 523-524; 648pp; English.

XX The present sequence is one of 251 novel human polypeptides encoded
CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one
CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.

XX SQ Sequence 608 AA;

Query Match 100.0%; Score 172; DB 22; Length 608;
Best Local Similarity 100.0%; Pred. No. 5.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

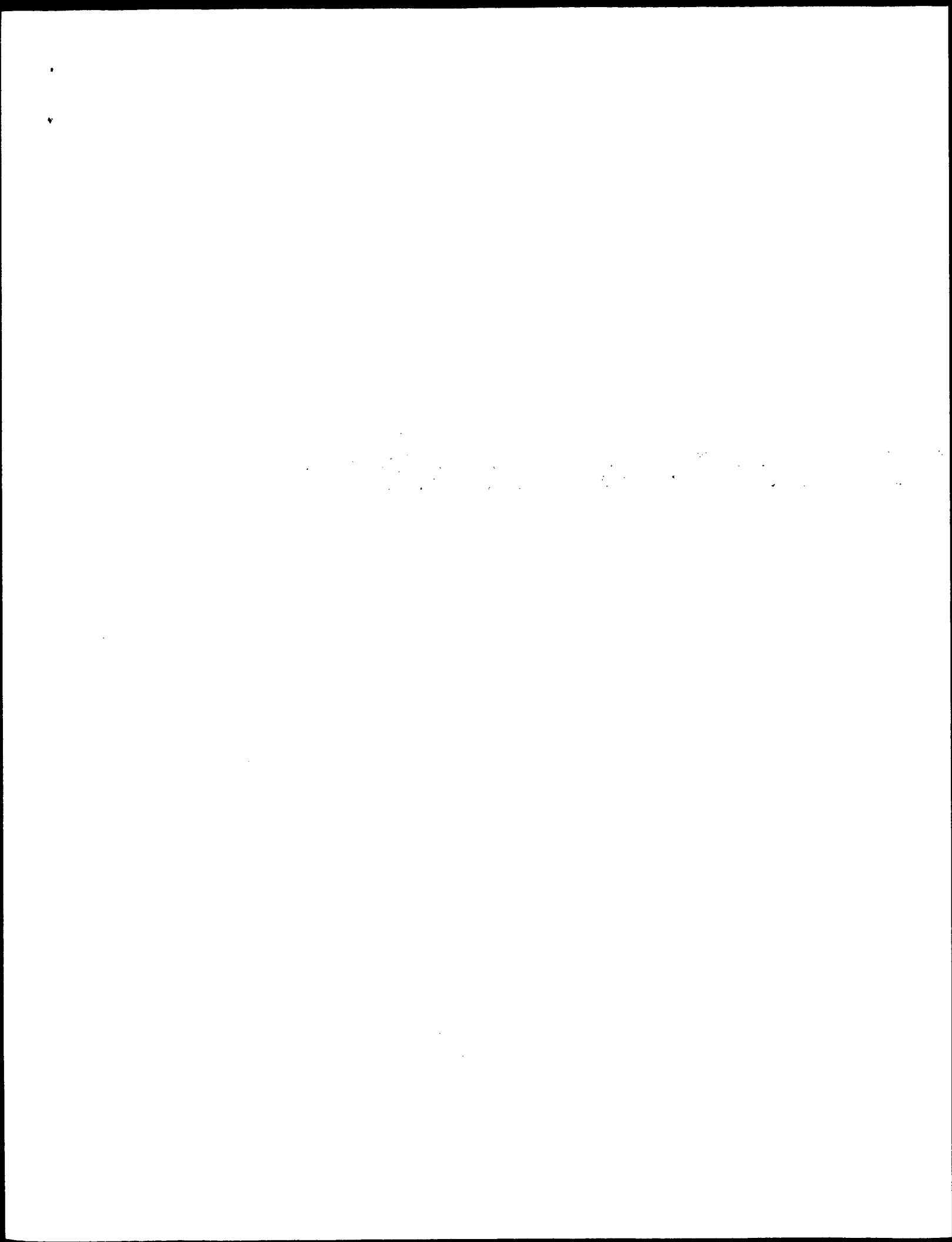
OY 1 LIHCEAVLHLRFNNGMVTCSKDRSTAVMD 31
Db 382 LIHCEAVLHLRFNNGMVTCSKDRSTAVMD 412

Fri Apr 11 13:31:09 2003

us-09-601-168b-2_copy_343_373.rag

Page 9

Search completed: April 11, 2003, 11:48:15
Job time : 10.553 secs



GenCore version 5.1.4-P5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.2095 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168b-2_COPY_343_373

Perfect score: 172
Sequence: 1 LHHCEAVLHLRFNNGMMVTCCKDRSLAVMD 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	517	1	US-08-190-802A-30
2	172	100.0	517	4	US-08-477-346-30
3	172	100.0	517	4	US-08-473-089-30
4	172	100.0	517	4	US-08-487-072A-30
5	168	97.7	30	1	US-08-190-802A-85
6	168	97.7	30	4	US-08-477-346-85
7	168	97.7	30	4	US-08-473-089-85
8	168	97.7	30	4	US-08-487-072A-85
9	65	37.8	640	4	US-09-177-165A-30
10	64	37.2	375	4	US-09-063-743-1
11	64	37.2	375	4	US-09-590-540-1
12	60	34.9	2629	2	US-08-751-189-4
13	60	34.9	2629	2	US-09-060-836-4
14	60	34.9	2629	4	US-09-184-445-4
15	58.5	34.0	421	4	US-09-302-769-14
16	57.5	33.4	37	1	US-08-190-802A-206
17	57.5	33.4	37	4	US-08-477-346-206
18	57.5	33.4	37	4	US-08-473-089-206
19	57.5	33.4	37	4	US-08-487-072A-206
20	57.5	33.4	576	1	US-08-190-802A-56
21	57.5	33.4	576	4	US-08-477-346-56
22	57.5	33.4	576	4	US-08-473-089-56
23	57.5	33.4	576	4	US-08-487-072A-56
24	57	33.1	431	1	US-08-190-802A-37
25	57	33.1	431	4	US-08-477-346-37
26	57	33.1	431	4	US-08-473-089-37
27	57	33.1	431	4	US-08-487-072A-37

28	57	33.1	1194	4	US-09-092-508-2	Sequence 2, Appl1
29	57	33.1	1194	4	US-09-435-115-2	Sequence 2, Appl1
30	57	33.1	1194	4	US-09-069-023-26	Sequence 26, Appl1
31	57	33.1	1194	4	US-09-098-310-2	Sequence 2, Appl1
32	57	33.1	1205	4	US-09-092-508-16	Sequence 16, Appl1
33	57	33.1	1205	4	US-09-435-115-16	Sequence 16, Appl1
34	56	32.6	31	1	US-08-190-802A-254	Sequence 254, App
35	56	32.6	31	4	US-08-477-346-254	Sequence 254, App
36	56	32.6	31	4	US-08-473-089-254	Sequence 254, App
37	56	32.6	31	4	US-08-487-072A-254	Sequence 52, Appl
38	56	32.6	422	1	US-08-477-346-52	Sequence 52, Appl
39	56	32.6	422	4	US-08-473-089-52	Sequence 52, Appl
40	56	32.6	422	4	US-08-487-072A-52	Sequence 52, Appl
41	56	32.6	422	4	US-08-190-802A-66	Sequence 66, Appl
42	56	32.6	514	1	US-08-477-346-66	Sequence 66, Appl
43	56	32.6	514	4	US-08-473-089-66	Sequence 66, Appl
44	56	32.6	514	4	US-08-487-072A-66	Sequence 66, Appl
45	56	32.6	514	4	US-08-487-072A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R. 33,875
REGISTRATION NUMBER: 8600-0139
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, F19, 13
US-08-190-802A-30

Query Match 100.0%; Score 172; DB 1; Length 517;
Best Local Similarity 100.0%; Pred. No. 43e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LHHCEAVLHLRFNNGMMVTCCKDRSLAVMD 31

Db 307 LIHCEAVLHLRFNNGMWTCKSDRSIAVWD 337

RESULT 2

US-08-477-346-30
Sequence 30, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match 100.0%; Score 172; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHCEAVLHLRFNNGMWTCKSDRSIAVWD 31
Db 307 LIHCEAVLHLRFNNGMWTCKSDRSIAVWD 337

RESULT 3
US-08-473-089-30
Sequence 30, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match

Best Local Similarity 100.0%; Score 172; DB 4; Length 517;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHCEAVLHLRFNNGMWTCKSDRSIAVWD 31

Db 307 LIHCEAVLHLRFNNGMWTCKSDRSIAVWD 337

RESULT 4

US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 100.0%; Score 172; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 31
Db 307 LIHCEAVLHLRFNNGMVTCSKDRSIAVMD 337

RESULT 5
US-08-190-802A-85
Sequence 85, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rIII, Fig. 13
US-08-190-802A-85

Query Match 97.7%; Score 168; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 31

Db 1 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 30

RESULT 6
US-08-477-346-85
Sequence 85, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rIII, Fig. 13
US-08-477-346-85

Query Match 97.7%; Score 168; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 31
Db 1 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 30

RESULT 7
US-08-473-089-85
Sequence 85, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rIII, Fig. 13
US-08-473-089-85

Query Match 97.7%; Score 168; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 31
Db 1 IHHCEAVLHLRFNNGMVTCSKDRSIAVMD 30

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STREET: 2000 Pennsylvania Avenue, NW
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE//DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP III, Fig. 13
US-08-473-089-85

Query Match          97.7%: Score 168; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IHCEAVLHLRFNNGMYTCSKDRSIAYWD 31
        |||||||
Db       1 IHC EAVLHLRFNNGMYTCSKDRSIAYWD 30

RESULT 8
US-08-487-072A-85
Sequence 85, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE//DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

```

```

: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 85:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptidic
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: BETA TRCP rIII, Fig. 13
US-08-487-072A-85

Query Match          97.7%; Score 168; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 5,3e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2  IHCEAVLHLRFNNGMWYTCSDKRSIAVWD 31
: |||||
Db      1  IHCEAVLHLRFNNGMWYTCSDKRSIAVWD 30

RESULT 9
US-09-177-165A-30
: Sequence 30, Application US/09177165A
: Patent No. 6426205
: GENERAL INFORMATION:
: APPLICANT: Tyets, Mike
: APPLICANT: Williams, Andrew
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
: TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
: FILE REFERENCE: 11757.100SU1
: CURRENT APPLICATION NUMBER: US/09/177,165A
: PRIORITY FILING DATE: 1998-10-22
: PRIOR APPLICATION NUMBER: 60/092,443
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: 60/063,254
: PRIORITY FILING DATE: 1997-10-24
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 30
: LENGTH: 640
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

Query Match          37.8%; Score 65; DB 4; Length 640;
Best Local Similarity 42.9%; Pred. No. 0.095;
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY      4  HCEAVLHLRFNNGMWYTCSDKRSIAVWD 31
: |||||
Db      301 HMDGVLTLQFNRYRLFTGSDYDSTIGIWD 328

RESULT 10
US-09-063-743-1
: Sequence 1, Application US/09063743
: Patent No. 6242214
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Lal, Preeti
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: APPLICANT: Paterson, Chandra
: TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
:

```

COUNTRY : USA
ZIP : 94304
COMPUTER READABLE FORM :
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cetrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0508 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEFAX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T01
CLONE: C059953
US-09-063-743-1

	Query Match	37.2%	Score 64	DB 4	Length 375
	Best Local Similarity	40.0%	Pred. No. 0.07		
	Matches 12	Conservative 7	Mismatches 9	Indels 2	Gaps 1
QY	4 HCEAVLHLEFN--NGMAYTCKSKDRSTAVWD	31			
DB	108 HSGAVMELHYNTDGSMLFSASTDRTKIVAVWD	137			

RESULT 11
 US-09-590-540-1
 Sequence 1, Application US/09590540
 Patent No. 6410267
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 Lal, Preeti
 Guegler, Karl J.
 Corley, Neil C.
 Patterson, Chandra
 TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Genomics, Inc.
 STREET: 3160 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/590,540
 FILING DATE: 08-Jun-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/063,743
 FILING DATE: April 21, 1998

ATTORNEY/AGENT INFORMATION:
NAME: David G. Streeter
REGISTRATION/DOCKET NUMBER: 43,168
REFERENCE/DOCKET NUMBER: PF-0508-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGCOT01
CLONE: 059953
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-590-540-1

Query Match	37.2%	Score 64	DB 4	Length 375
Best Local Similarity	40.0%	Pred. No. 0.07		
Matches 12	Conservative 7	Mismatches 9	Indels 2	Gaps 1
QY	4 HCEAVLHLEN--NGMMVTCSDKRLAWVD	31		
Db	108 HSGAVMELHNTDGMILFASSTDKTVAAVD	137		

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QY      4 HCEAVLHLRFN--NGMVTGSKDRSIAVWD 31
          |  ||: | : | : | : ||||
Db     108 HSGAVMELHYNTDGSMLFSASTDKTVAVWD 137
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```

RESULT 12
US-08-751-189-4
: Sequence 4, Application US/08751189
: Patent No. 5919656
: GENERAL INFORMATION:
: APPLICANT: Harrington, Lea A.
: APPLICANT: Robinson, Murray O.
: TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein
: TITLE OF INVENTION: 1
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen, Inc.
: STREET: 1840 De Havilland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320-1789
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/751,189
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Oleski, Nancy A.
: REGISTRATION NUMBER: 34,688
: REFERENCE/DOCKET NUMBER: A-433
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2629 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
:
US-08-751-189-4

Query Match 34.9%; Score 60; DB 2; Length 2629;
Best Local Similarity 39.3%; Pred. No. 3.1;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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Db 2556 HIGSVTALHVLPGLLVTASKDRDKLWE 2583

RESULT 13

US-09-060-836-4
; Sequence 4, Application US/09060836
; Patent No. 5981707
; GENERAL INFORMATION:
; APPLICANT: Harrington, Lea A.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESSES: 12
; ADDRESSEE: Amgen, Inc.
; STREET: 1840 De Havilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,836
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,189
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2629 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-060-836-4
Query Match 34.9%; Score 60; DB 2; Length 2629;
Best Local Similarity 39.3%; Pred. No. 3.1;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
QY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31
Db 2556 HIGSVTALHVLPGLLVTASKDRDKLWE 2583
RESULT 14
US-09-184-445-4
; Sequence 4, Application US/09184445
; Patent No. 6174703
; GENERAL INFORMATION:
; APPLICANT: Harrington, Lea A.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESSES: 12
; ADDRESSEE: Amgen, Inc.
; STREET: 1840 De Havilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,445
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,189
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2629 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-184-445-4
Query Match 34.9%; Score 60; DB 4; Length 2629;
Best Local Similarity 39.3%; Pred. No. 3.1;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31
Db 2556 HIGSVTALHVLPGLLVTASKDRDKLWE 2583

RESULT 15

US-09-302-769-14
; Sequence 14, Application US/09302769
; Patent No. 6323317
; GENERAL INFORMATION:
; APPLICANT: HILTON, Douglas J
; APPLICANT: ALEXANDER, Warren S
; APPLICANT: VINEY, Elizabeth M
; APPLICANT: WILSON, Tracey A
; APPLICANT: RICHARDSON, Rachael T
; APPLICANT: STARR, Robyn
; APPLICANT: NICHOLSON, Sandra E
; APPLICANT: METCALF, Donald
; APPLICANT: NICOLA, Nicos A
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
; FILE REFERENCE: 109762
; CURRENT APPLICATION NUMBER: US/09/302,769
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 08/962,560
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Mouse
US-09-302-769-14
Query Match 34.0%; Score 58.5; DB 4; Length 421;
Best Local Similarity 35.3%; Pred. No. 0.55;
Matches 12; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 LTHHCEAVLHLRF---NNGMVTCSKDRSIAVMD 31
Db 166 LVDHIEHWVDLTFAPDGSLLVSASRDKTLRWMD 199

Search completed: April 10, 2003, 12:51:18
Job time : 3.2095 secs


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RESULT 1
US-10-038-010-8
; Sequence 8, Application US/10038010
; Publication NO. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: protein-protein interactions in adipocyte cells
; FILE REFERENCE: BA767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta-TrCP1
; LOCATION: (1)..(569)
; OTHER INFORMATION:
US-10-038-010-8

Query Match          100.0%; Score 172; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,le-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LIHCEAVLIHLRFNNGMAYTCSKDRSIAYVD 31
          |||||||
Db      343 LIHCEAVLIHLRFNNGMAYTCSKDRSIAYVD 373

RESULT 2
US-10-042-417-2
; Sequence 2, Application US/10042417
; Patent No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

```

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 172; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHCFAVLHLPNGMWTGSKDRSIAVWD 31
DB 343 LHHCFAVLHLPNGMWTGSKDRSIAVWD 373

RESULT 3
US-10-060-019-30
Sequence 30, Application US/10060019
Publication No. US20030003564A1
GENERAL INFORMATION:
APPLICANT: Tyers, Mike
APPLICANT: Williams, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
FILE REFERENCE: 11/57,100S01
CURRENT APPLICATION NUMBER: US/10/060,019
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/177,165
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-060-019-30

Query Match 37.8%; Score 65; DB 9; Length 640;
Best Local Similarity 42.9%; Pred. No. 0.12;
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 HCEAVLHLPNGMWTGSKDRSIAVWD 31
DB 301 HMDGVLLQFNRYLLFTGSDYDTIGIWD 328

RESULT 4
US-10-119-932-1
Sequence 1, Application US/10119932
Patent No. US20020160488A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
Patterson, Chandra
TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Genomics, Inc.
STREET: 3160 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/119,932
FILING DATE: 09-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/590,540
FILING DATE: 08-Jun-2000
APPLICATION NUMBER: 09/063,743
FILING DATE: April 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: David G. Streeter

REGISTRATION NUMBER: 43,168
REFERENCE/DOCKET NUMBER: PF-0508-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGMOT01
CLONE: 059953

US-10-119-932-1
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 37.2%; Score 64; DB 9; Length 375;
Best Local Similarity 40.0%; Pred. No. 0.094;
Matches 12; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 4 HCEAVLHLPNGMWTGSKDRSIAVWD 31
DB 108 HSGAVMELHYNDGSMLEFSATDXTVAVWD 137

RESULT 5
US-09-213-888-7
Sequence 7, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 36.0%; Score 62; DB 9; Length 540;
Best Local Similarity 39.3%; Pred. No. 0.28;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLPNGMWTGSKDRSIAVWD 31

Db 456 HOSAVTCLQFNKNFVITSSDDGTVKLM 483

RESULT 6

US-09-213-888-10
Sequence 10, Application US/09213888A
Patent No. US20020164683A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/213,888A

CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-213-888-10

Query Match 36.0%; Score 62; DB 9; Length 540;

Best Local Similarity 39.3%; Pred. No. 0.28;

Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31

Db 456 HOSAVTCLQFNKNFVITSSDDGTVKLM 483

RESULT 7

US-09-328-877A-7
Sequence 7, Application US/09328877A
Patent No. US20020177187A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/328,877A

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-328-877A-7

Query Match 36.0%; Score 62; DB 9; Length 540;

Best Local Similarity 39.3%; Pred. No. 0.28;

Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31

Db 456 HOSAVTCLQFNKNFVITSSDDGTVKLM 483

RESULT 8

US-09-328-877A-10
Sequence 10, Application US/09328877A
Patent No. US20020177187A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/328,877A

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-328-877A-10

Query Match 36.0%; Score 62; DB 9; Length 540;

Best Local Similarity 39.3%; Pred. No. 0.28;

Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31

Db 456 HOSAVTCLQFNKNFVITSSDDGTVKLM 483

RESULT 9

US-09-213-888-6
Sequence 6, Application US/09213888A
Patent No. US20020164683A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/213,888A

CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 545

TYPE: PRT

ORGANISM: Homo sapiens

US-09-213-888-6

Query Match 36.0%; Score 62; DB 9; Length 545;

Best Local Similarity 39.3%; Pred. No. 0.28;

Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 4 HCEAVLHLRFNNGMVTCSKDRSIAVMD 31

Db 461 HOSAVTCLQFNKNFVITSSDDGTVKLM 488

RESULT 10

US-09-328-877A-6
Sequence 6, Application US/09328877A
Patent No. US20020177187A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE REFERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/328,877A

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 545

TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-6

Query Match
Best Local Similarity 36.0%; Score 62; DB 9; Length 545;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMWTCSKDRSIAVWD 31
DB 461 HOSAVTCLQFNKNFVITSSDDGTVKLMD 488

RESULT 11
US-09-213-888-5
Sequence 5, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-5

Query Match
Best Local Similarity 36.0%; Score 62; DB 9; Length 553;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMWTCSKDRSIAVWD 31
DB 469 HOSAVTCLQFNKNFVITSSDDGTVKLMD 496

RESULT 12
US-09-328-877A-5
Sequence 5, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match
Best Local Similarity 36.0%; Score 62; DB 9; Length 553;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMWTCSKDRSIAVWD 31
DB 469 HOSAVTCLQFNKNFVITSSDDGTVKLMD 496

RESULT 13
US-09-213-888-9
Sequence 9, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-9

Query Match
Best Local Similarity 36.0%; Score 62; DB 9; Length 559;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMWTCSKDRSIAVWD 31
DB 475 HOSAVTCLQFNKNFVITSSDDGTVKLMD 502

RESULT 14
US-09-328-877A-9
Sequence 9, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-9

Query Match
Best Local Similarity 36.0%; Score 62; DB 9; Length 559;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNNGMWTCSKDRSIAVWD 31
DB 475 HOSAVTCLQFNKNFVITSSDDGTVKLMD 502

RESULT 15
US-09-213-888-8
Sequence 8, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
US-09-213-888-8

```

; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-8

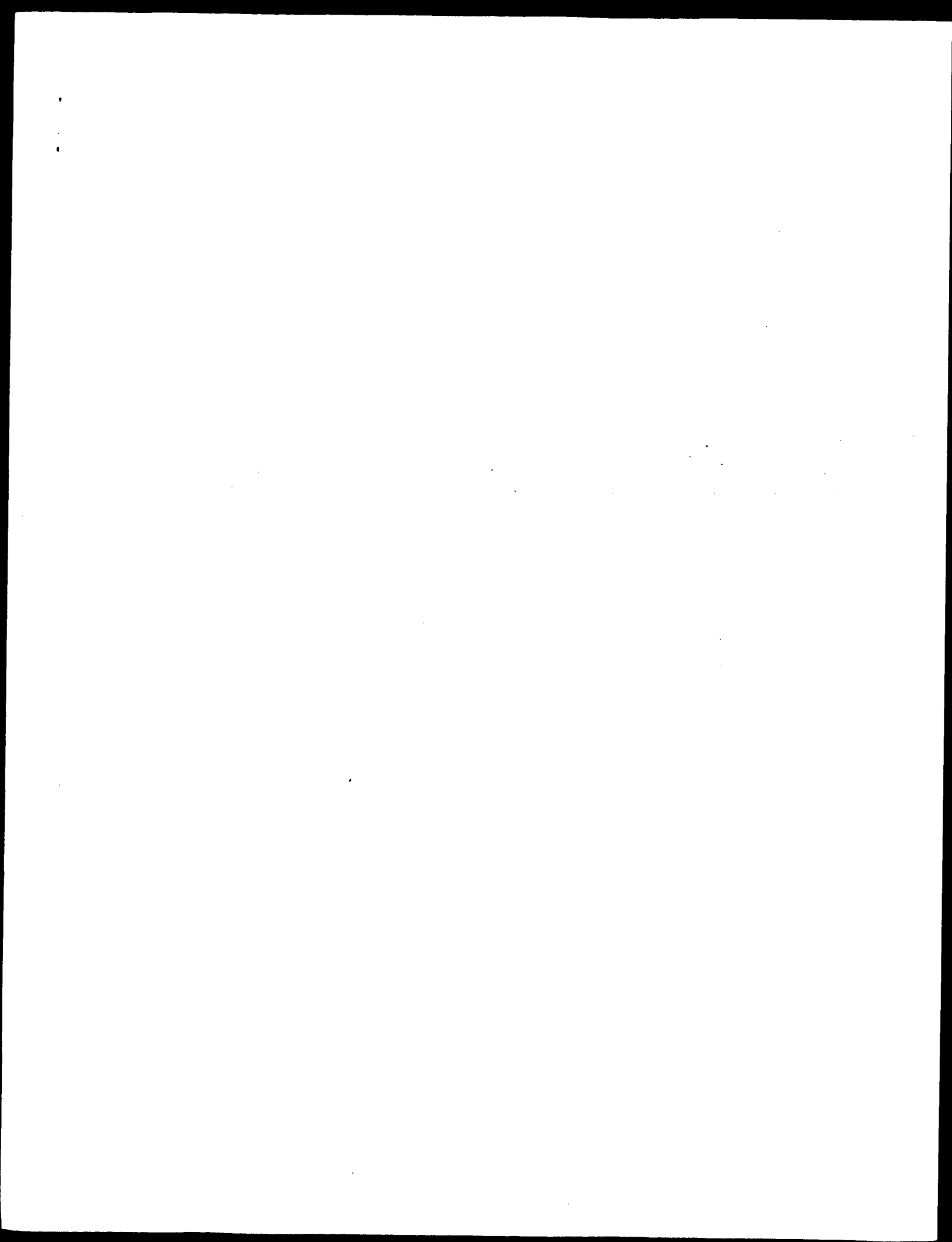
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Query Match          36.0%; Score 62; DB 9; Length 589;
Best Local Similarity 39.38; Pred. NO. 0.31;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
QY      4 HCEAVILHLPNNGMMVTCCKDRSIIVWD 31
      | | | | | | | | | | | | | | | |
Db      505 HOSAVTCLQFNKNFYITSSDDGTAKLWD 532

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Search completed: April 10, 2003, 13:16:45
 Job time : 4.17174 secs



GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.58709 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_343_373

Sequence: 172
1 LIHCEAVLHLRFNNGMMVTCSKDRSIAVWD 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	172	100.0	518	2	B48088
2	160	93.0	701	2	T16607
3	71	41.3	714	2	S56893
4	67	39.0	1893	2	T22661
5	66	38.4	331	2	T20593
6	65	37.8	640	2	S49932
7	64	37.2	659	2	S38108
8	62.5	36.3	810	2	T48835
9	62	36.0	506	2	T50211
10	62	36.0	507	2	T38653
11	61	35.5	1013	2	S51195
12	60.5	35.2	506	2	S50937
13	60	34.9	303	2	S45461
14	60	34.9	2629	2	T30987
15	59	34.3	315	2	S46046
16	59	34.3	351	2	C88082
17	59	34.3	415	2	T20335
18	59	34.3	431	2	T38471
19	58.5	34.0	421	2	T14773
20	58	33.7	1653	2	S76086
21	57.5	33.4	490	2	T37884
22	57.5	33.4	576	2	S29367
23	57	33.1	325	2	T06784
24	57	33.1	431	2	A45142
25	57	33.1	561	2	T19604
26	57	33.1	651	2	T50289
27	57	33.1	1194	2	T03818
28	57	33.1	1227	2	AE1810
29	56.5	32.8	793	2	T27133

ALIGNMENTS

30	56	32.6	64	2	T04116	GNP-binding protei
31	56	32.6	326	2	T16987	GNP-binding protei
32	56	32.6	326	2	T02340	GNP-binding regula
33	56	32.6	384	2	S46110	hypothetical prote
34	56	32.6	422	2	A56640	CD4 repeat unit-c
35	56	32.6	430	2	T41054	probable chromosom
36	56	32.6	430	2	T21482	hypothetical prote
37	56	32.6	454	2	T01337	hypothetical prote
38	56	32.6	465	2	S51295	En/Spm-like transp
39	56	32.6	465	2	T00982	hypothetical prote
40	56	32.6	515	2	S19487	hypothetical prote
41	56	32.6	629	2	T48799	Rrp9p related prot
42	56	32.6	2629	2	T32735	telomerase-associ
43	55.5	32.3	243	2	T05307	hypothetical prote
44	55	32.0	82	2	T31574	hypothetical prote
45	55	32.0	267	2	S62507	hypothetical trp-a

RESULT 1

B48088 beta-transducin repeat-containing protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000

C:Accession: B48088

R:Spavak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase

A:Reference number: A48088; MUID:9330269; PMID:8393141

A:Accession: B48088

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-518 <SPE>

A:Cross-References: GB:M98268; NID:g295542; PIDN:AAA02810.1; PID:g295543

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

C:Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match Score 172; DB 2; Length 518; Best Local Similarity 100.0%; Pred. No. 3.2e-17;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 308 LIHCEAVLHLRFNNGMMVTCSKDRSIAVWD 338

RESULT 2

T16607 hypothetical protein K10B2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16607

R:Miller, N. submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid K10B2.

A:Reference number: Z18545

A:Accession: T16607

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-701 <MULT>

A:Cross-References: EMBL:028730; NID:g860694; PID:g860695; PIDN:AAA68258.1; CESP:K10B

A:Experimental source: Strain Bristol N2

C:Genetics:

A:Gene: CESP:K10B2.1

A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3

Query Match Score 160; DB 2; Length 701; Best Local Similarity 93.5%; Pred. No. 2.4e-15;

Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	LIHHC	AVLHLR	ENGM	AVTCSK	DRSIAV	MD	31
Db	334	LIHHC	AVLHLR	FANGIM	VTCSK	DRSIAV	MD	364

RESULT 3
 S56893
 hypothetical protein YKR036c homolog YJL112w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J0802
 C:Species: Saccharomyces cerevisiae
 C:Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S56893; S56890
 R:Czapluch, C.; Kordes, E.; Pujol, A.; Taniaux, J.C.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56891
 A:Accession: S56893
 A:Molecule type: DNA
 A:Residues: 1-714 <CZI>
 A:Cross-references: EMBL:Z49387; NID:q1008299; PIDN:CAA89407.1; PID:q1008299; M
 R:Rasmussen, S.W.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56876
 A:Accession: S56890
 A:Molecule type: DNA
 A:Residues: 597-714 <RAS>
 A:Cross-references: EMBL:Z49387; MIPS:YJL112w
 C:Genetics:
 A:Gene: SGD:MDY1
 A:Cross-references: SGD:S0003648
 A:Map position: 10L
 C:Superfamily: yeast hypothetical protein YKR036c; WD repeat homology
 F:437-470/Domain: WD repeat homology <WD1>
 F:498-529/Domain: WD repeat homology <WD2>
 F:602-633/Domain: WD repeat homology <WD3>

```

QY      4 HCEAVLHLRFNNGMMVTCSKDRSIAVWD 31
      1 : : : : : : : : : : : : : :
Db      605 HTDAITSLKFDSDACLVGTSGSYDRTVRIMD 632

```

RESULT 4
 T22661
 hypothetical protein T01G1.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T22661; T24305
 R:White, S.; Mortimore, B.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19594
 A:Accession: T22661
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1893 <MIL>
 A:Cross-references: EMBL:Z82271; PIDN:CAB05214.1; GSPDB:GN00022; CESP:T01G1.1
 A:Experimental source: clone F54E12
 R:Kershaw, J.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z19872
 A:Accession: T24305
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1893 <WI2>
 A:Cross-references: EMBL:Z92811; PIDN:CAB07273.1; GSPDB:GN00022; CESP:T01G1.1
 A:Experimental source: clone T01G1
 C:Genetics:
 A:Gene: CESP:T01G1.1
 A:Map position: 4
 A:Introns: 65/3; 101/3; 194/3; 269/3; 299/3; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1; 9

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Query Match          39.0%; Score 67; DB 2; Length 1893;
Best Local Similarity 46.4%; Pseq No. 0.25;
Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY      4 HCEAVLHREFNNGMYTCSKDRSIAMD 31
      | | : | : ||| |||| : |||
Db 1571 HARGVLSVDYNEKLMYTGSKDRATKIND 1558

```

RESULT 5
 T20593
 hypochemical protein F08G12.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
 C:Accession: T20593
 R:Cottage, A.
 Submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19297
 A:Accession: T20593
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-331 <NIL>
 A:Cross-references: EMBL:Z66561; PIDD:CAA91460.1; GSPDB:GM00028; CESP:F08G12.2
 A:Experimental source: clone F08G12
 C:Genetics:
 A:Gene: CESP:F08G12.2
 A:Map position: X
 A:Introns: 6/1; 28/3; 61/3; 314/1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

OY **4** HCEAVLHLRF--NGMAMVTCSDKRSIAVMD 31
 | : | : | : | : | : | : | : | : |
Dd **80** HSGAVMDLKFTTDDSSSLVSCGTDKSVRVMD 109

RESULT 6
S49932
MEM30 protein - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein Y1905.02; protein Y1L046w
C:Species: *Saccharomyces cerevisiae*
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
C:Accession: S49932; S43750
R:Ode11, C.; Bowman, S.
submitted to the EMBL Data Library, December 1994
A:Accession: S49932
A:Molecule type: DNA
A:Residues: 1-640 <ODE>
A:Cross-references: GB:247047; EMBL:Z46861; NID:6603997; PTD:9763300; MIPS:Y1L046w
R:Thomas, D.; Cheresat, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
A:Reference number: S43750
A:Accession: S43750
A:Molecule type: DNA
A:Residues: 1-60, '1', 62-640 <THO>
A:Cross-references: EMBL:126505; NID:g432493; PID:g432494
C:Genetics:
A:Gene: SGD:MEM30
A:Cross-references: SGD:S0001308; MIPS:Y1L046w
A:Map position: 9L
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
F:298-329/Domain: WD repeat homology <WD1>
F:338-369/Domain: WD repeat homology <WD2>
F:374-409/Domain: WD repeat homology <WD3>
F:417-450/Domain: WD repeat homology <WD4>
Query Match 37.8%; Score 65; DB 2; Length 640;
Best Local Similarity 42.9%; Pred. No. 0.17;

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 2.22777 Seconds

(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_343_373
Perfect score: 172
Sequence: 1 LITHCEAVLHLEFNGMMVTCSDKSLAVMD 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	172	100.0	518	1 TRCB_XENLA	Q91854 xenopus lae
2	172	100.0	605	1 FWIA_HUMAN	Q9Y297 homo sapien
3	160	93.0	665	1 LI23_CABEL	Q09990 caenorhabdi
4	152	88.4	542	1 FWIB_HUMAN	Q9UKB1 homo sapien
5	71	41.3	714	1 YTL2_YEAST	P47025 saccharomyc
6	65	37.8	640	1 MT30_YEAST	P39014 saccharomyc
7	64	37.2	659	1 YK16_YEAST	P36130 saccharomyc
8	62	36.0	506	1 POFB_SCHPO	Q09855 schizosacch
9	60	34.9	303	1 YNA6_YEAST	P41318 saccharomyc
10	59	34.3	315	1 YB25_YEAST	P38123 saccharomyc
11	59	34.3	415	1 YLN2_CABEL	Q18964 caenorhabdi
12	59	34.3	431	1 YDPT_SCHPO	Q14021 schizosacch
13	59	34.3	1249	1 APAR_RAT	Q99P51 rattus norv
14	58.5	34.0	421	1 WSBI_HUMAN	Q9Y617 homo sapien
15	58.5	34.0	421	1 WSBI_MOUSE	Q54927 mus musculu
16	58	33.7	678	1 SCOB_EMEHI	Q00659 emeritella
17	58	33.7	1693	1 Y163_SYNY3	Q55563 synchocyst
18	57.5	33.4	490	1 YEOL_SCHPO	Q10990 schizosacch
19	57.5	33.4	576	1 PMP1_YEAST	P21304 saccharomyc
20	57	33.1	325	1 GBIP_SOYBN	Q39856 glycine max
21	57	33.1	431	1 CST1_HUMAN	Q05048 homo sapien
22	57	33.1	651	1 Y1X1_SCHPO	Q9P713 schizosacch
23	57	33.1	1248	1 APAF_HUMAN	Q14727 homo sapien
24	57	33.1	1249	1 APAF_MOUSE	Q88879 mus musculu
25	56	32.6	326	1 GBIP_NICPL	P93340 nicotiana p
26	56	32.6	326	1 GBIP_TOBAC	P49026 nicotiana t
27	56	32.6	384	1 AR41_YEAST	P38328 saccharomyc
28	56	32.6	422	1 FBW2_HUMAN	Q9UKC8 homo sapien
29	56	32.6	422	1 FBW2_MOUSE	Q60584 mus musculu
30	56	32.6	465	1 YN57_YEAST	P42841 saccharomyc
31	56	32.6	515	1 YCWI2_YEAST	P25382 saccharomyc
32	56	32.6	664	1 EMAP_LYRVA	Q9Y1C1 lytechinus
33	55	32.0	922	1 YB1C_SCHPO	P87177 schizosacch

34	54.5	31.7	446	1 GRMD_HUMAN	Q9B67 homo sapien
35	54	31.4	318	1 PEX7_MOUSE	P97865 mus musculu
36	54	31.4	325	1 GBIP_MEDSA	Q24076 medicago sa
37	54	31.4	327	1 GBIP_ARATH	Q24456 arabidopsis
38	54	31.4	327	1 GBIP_BRANA	Q29336 brassica na
39	54	31.4	339	1 CIA1_HUMAN	Q76071 homo sapien
40	54	31.4	455	1 PR17_YEAST	P40968 saccharomyc
41	54	31.4	872	1 VP2_ROTTC	P26191 porcine rot
42	53.5	31.1	349	1 YDFU_ECOLI	P76162 escherichia
43	53.5	31.1	519	1 TBL3_HUMAN	Q12788 homo sapien
44	53	30.8	318	1 GBIP_DROME	O18640 drosophila
45	53	30.8	323	1 PEX7_HUMAN	Q00628 homo sapien

ALIGNMENTS

```

RESULT 1
ID TRCB_XENLA STANDARD: PRT: 518 AA.
AC Q91854: P70037: P70038:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-TrCP (Beta-transducin repeat-containing protein).
GN FBXW1 OR BTRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330289; PubMed=8393141;
RA Spevak W., Keiper B.D., Stratowa C., Castanon M.J.;
RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
RT anaphase are rescued by Xenopus CDKs encoding N-ras or a protein
RT with beta-transducin repeats."
RL Mol. Cell. Biol. 13:4953-4966(1993).
RN [2]
RP SEQUENCE OF 302-518 FROM N.A.
RX MEDLINE=97109804; PubMed=8952061;
RA Hudson J.W., Alatron V.B., Elinson R.P.;
RT "Identification of new localized RNAs in the Xenopus oocyte by
RT differential display PCR."
RL Dev. Genet. 19:190-198(1996).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
CC MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
CC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIBLASTULA TRANSITION. DO
CC NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
CC TADPOLE EMBRIO.
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M88268; AAA02810.1; -
CC EMBL: U63921; AAB49671.1; -
CC EMBL: U63922; AAB49672.1; -
CC InterPro: IPR001810; F-box.
CC InterPro: IPR001680; WD40.
CC Pfam: PF00400; WD40; 7.

```

DR Pfam: PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR PRODOM; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat.
 KW DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.
 FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
 FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
 SQ SEQUENCE 518 AA; 59507 MW; 2A52EC19028127F3 CRC64;

Query Match 100.0%; Score 172; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2, 2e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLEFNGMVTCSKDRSTAVWD 31
 |||||||
 Db 308 LIHCEAVLHLEFNGMVTCSKDRSTAVWD 338

RESULT 2
 ID FWLA_HUMAN STANDARD; PRT; 605 AA.
 AC 09Y297; 09Y213;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-Trcp)
 GN F3KRS1kappab (PikappaBalpha-E3 receptor subunit).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RX SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=9075339; PubMed=9859996;
 RA Varon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase";
 RL Nature 396:590-594(1998).
 RN [2]
 RX SEQUENCE FROM N.A. (ISOFORM 2).
 RX TISSUE=Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940;
 RA Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.;
 RT "A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif";
 RL Mol. Cell 1:565-574(1998).
 RN [3]
 RX SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarrelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RX CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,

RA Harper J.W.;
 RT "The SCF(beta-Trcp)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and
 RT beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro";
 RL Genes Dev. 13:270-283(1999).
 CC - FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA
 CC (PIKAPPAALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR
 CC UBIQUITINATION AND DEGRADATION.
 CC - SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC - SUBCELLULAR LOCATION: Cytoplasmic.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC - SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC or send an email to license@sib-sib.ch).

DR EMBL; AF101784; AAD08702.1; -
 DR EMBL; Y14153; CAA74572.1; -
 DR EMBL; AF129530; AAF04464.1; -
 DR Genew; HGNC:1144; BTRC.
 DR MIM; 603482; -
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF004400; WD40; 7.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR PRODOM; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 190 228 F-BOX.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VANSPLC 17 52 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 605 AA; 68866 MW; 4C67F3B7E400FD37 CRC64;

Query Match 100.0%; Score 172; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLEFNGMVTCSKDRSTAVWD 31
 |||||||
 Db 379 LIHCEAVLHLEFNGMVTCSKDRSTAVWD 409

RESULT 3
 ID LI23_CAEEL STANDARD; PRT; 665 AA.
 AC 009990; 09GNM6;
 DT 15-JUN-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein lln-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxID=6239;
 [1]
 SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 MEDLINE=20515608; PubMed=11060233;
 Kipreos E.T., Gohel S.P., Hedgecock E.M.;
 "The Caenorhabditis elegans F-box/WD-repeat protein lin-23 functions
 to limit cell division during development";
 Development 127:5071-5082(2000).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=Bristol NZ;
 Miller N.;
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 [3]
 REVISIONS.
 R. Waterston R.;
 Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 cycle progression. Required to restrain cell proliferation in
 response to developmental cues. Probably recognizes and binds to
 some proteins and promotes their ubiquitination and degradation
 (by similarity).
 -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
 (by similarity).
 -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 levels in larvae. Maternal expression results in high zygotic
 levels.
 -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 -1- SIMILARITY: CONTAINS 7 WD-REPEATS (TRP-ASP DOMAINS).
 -1- SIMILARITY: STRONG. TO X.LAEVIS FBXL1.

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 EMBL; AF275253; AAG28037.1; -
 EMBL; U28730; AAA68258.2; -
 Wormpep; K10B2.1; CE28650.
 InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR PRODOM; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Developmental protein; Cell cycle; Cell division;
 Ubl conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 81 127 F-box.
 FT REPEAT 220 257 WD 1.
 FT REPEAT 260 299 WD 2.
 FT REPEAT 301 337 WD 3.
 FT REPEAT 343 380 WD 4.
 FT REPEAT 383 420 WD 5.
 FT REPEAT 423 460 WD 6.
 FT REPEAT 472 509 WD 7.
 FT DOMAIN 525 542 ALA-RICH.
 FT MUTAGEN 441 441 G->R: IN LIN-32(RH293).
 SO SEQUENCE 665 AA; 75916 MW; BF3E9AF51F1ECC6 CRC64;

```

QY      1 LTHCEAVLHLRFNNGMWVTSCKSDSIAMVD 31
        |||
Db      298 LTHCEAVLHLRFANGIMVTSCKRDSIAVMD 328
        |||

RESULT 4
FWIB_HUMAN
ID      FWIB_HUMAN          STANDARD:    PRT:       542 AA.
AC      Q9UKB1; Q9Y4C6; Q9P2S8; Q9P2S9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-trCP2).
GN      FBXW1B OR FBW1B OR BTRCP2 OR KIAA0696.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20003060; PubMed=10531035;
RX      Genclietelli C., Chisaur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA      Pagano M.;
RA      "Identification of a family of human F-box proteins.";
RL      Curr. Biol. 9:1177-1179(1999).
RN      [2]
RN      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICINGS.
RC      TISSUE=Fetal lung;
RX      MEDLINE=20160458; PubMed=10694485;
RA      Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
RA      Katoh M.;
RT      "Molecular cloning and genomic structure of the betatrcp2 gene on
RT      chromosome 5q35.1.";
RL      Biochem. Biophys. Res. Commun. 269:103-109(2000).
RN      [3]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Braint;
RX      MEDLINE=98403880; PubMed=9734811;
RX      Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA      Kotani H., Nomura N., Ohara O.;
RA      "Prediction of the coding sequences of unidentified human genes. X.
RT      The complete sequences of 100 new cDNA clones from brain which can
RT      code for large proteins in vitro.";
RL      DNA Res. 5:169-176(1998).
CC      - FUNCTION: Probably recognizes and binds to some phosphorylated
CC      proteins and promotes their ubiquitination and degradation.
CC      - SUBUNIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX.
CC      - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC      - ALTERNATIVE PRODUCTS: 3 ISOFORMS: A, B AND C (SHOWN HERE); ARE
CC      PRODUCED BY ALTERNATIVE SPLICING.
CC      - SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC      - SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC      -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib.ch).
CC      -----
DR      EMBL; AF176022; AAF04528.1; -
DR      EMBL; AB033279; BAA92329.1; -
DR      EMBL; AB033280; BAA92330.1; -
DR      EMBL; AB033281; BAA92331.1; -
DR      EMBL; AB014596; BAA31671.1; ALT_INT.
DR      Genew; HGNC:13607; FBXW1B.
DR      MIM: 605651; -.
DR      InterPro: IPR001810; F-box.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00400; WD40; 7
DR      Pfam: PF00446; F-box; 1.
DR      PRINTS: PR00320; GPROTEINBPRT.

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DR EMBL; Z6861; CAAB6905.1; -;  
DR EMDL; L26505; AAA96717.1; -;  
DR SCD; S0001308; MET30.  
DR InterPro; IPR001810; F-box.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00400; WD40; 7.  
DR Pfam; PF00646; F-box; 1.  
DR PRINTS; PR00320; GPROTEINRPT.  
DR PRODOM; PD000018; WD40; 4.  
DR SMART; SM00256; FBXX; 1.  
DR SMART; SM00320; WD40; 6.  
DR PROSITE; PS50181; FBXX; 1.  
DR PROSITE; PS00678; WD_REPEATS_1; 4.  
DR PROSITE; PS50082; WD_REPEATS_2; 6.  
DR TRANSIT; TS50294; WD_REPEATS_REGION; 1.  
KW Transcription regulation; Methionine biosynthesis;  
Cysteine biosynthesis; Repeat; WD repeat.  
FT DOMAIN  
FT REPEAT 181 227      F-BOX.  
FT REPEAT 300 328      WD 1.  
FT REPEAT 340 368      WD 2.  
FT REPEAT 380 408      WD 3.  
FT REPEAT 419 449      WD 4.  
FT REPEAT 461 499      WD 5.  
FT REPEAT 509 538      WD 6.  
FT REPEAT 550 578      WD 7.  
FT REPEAT 607 635      WD 8 (POTENTIAL).  
FT REPEAT 61             M -> I (IN REF. 1).  
SQ SEQUENCE 640 AA; 72835 MW; 5135D8BCA2E1EB97 CRC64;  
  
Query Match               37.8%; Score 65; DB 1; Length 640;  
Best Local Similarity     42.9%; Pred. No. 0.039;  
Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
  
QY 4 HCEVLIHLRFNNGMAWTCSDKRSIVAMD 31  
I :|||:::|| :: || |::|:  
DB 301 HMDDGLTLOFNRYLLFTGSYSTIGIMD 328  
  
RESULT 7  
YKJ6_YEAST  
ID YKJ6_YEAST STANDARD; PRT; 659 AA.  
AC P36130;  
DT 01-JUN-1994 (Rel. 29, Created)  
DI 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 74.7 kDa Trp-Asp repeats containing protein in DAL80-GAP1  
intergenic region.  
GN YKR036C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
CC Saccharomycetales; Saccharomycetaceae; Saccharomycos.  
OX NCBI_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A. Urrestarazu L.A., Jauniaux J.-C.;  
RA Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.  
RL -  
CC - SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).  
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DR InterPro:IPR001680; WD40.
DR Pfam:PF00400; WD40. 6.
DR PRINTS:PR00320; GPROTEINRPT.
DR ProDom:PD000018; WD40. 1.
DR SMART:SM00320; WD40. 5.
DR PROSITE:PS00678; WD_REPEATS_1; 4.
DR PROSITE:PS50082; WD_REPEATS_2; 5.
DR PROSITE:PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein: Repeat; WD repeat.
FT REPEAT 333 364 WD 1.
FT REPEAT 376 407 WD 2.
FT REPEAT 438 466 WD 3.
FT REPEAT 503 531 WD 4.
FT REPEAT 543 571 WD 5.
FT REPEAT 582 610 WD 6.
SQ SEQUENCE 659 AA; 74709 MW; 13959354C56DD37 CRC64;

Oy 4 HCEAVLHLEFNGMMWTCSDKRSIAVWD 31
Db 544 HTDGITSLKFEDEKLTGSGMDSNRVIMD 571

RESULT 8
POFB_SCHPO STANDARD: PRT; 506 AA.
AC 009855; O9P7VL;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein profilin.
GN PF011 OR SPAC29E6.01 OR SPAC30.05.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 111
RP SEQUENCE FROM N.A.
RA Harrison C.L., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in fission yeast.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=18484401; PubMed=11859360;
RA Wood V., Gwilliam R., Ralandream M.A., Lyne M., Lyne R., Stewart A., Brooks K., Brown D., Brown S., Chillingworth T., Churchman S., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., Mclean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Gymnietz B., Wellens I., Vansteelt E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moselt D., Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M., Beer P., Zimmermann W., Medler H., Wambut R., Purnelle B., Goffeau A., Cadieu E., Dreno S., Gloux S., Jelaire V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

```

RA Shpakovski G.V., Usersty D., Barrell B.G., Nurse P.;
 RT "the genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: CONTAINS 1 P-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB061694; BAB55543.1; -
 CC EMBL: AL136538; CAB6464.1; -
 CC EMBL: Z66525; CAA91423.1; -
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF00400; WD40; 7.
 CC Pfam: PF00646; F-box; 1.
 CC PRINTS: PR00320; GPROTEINBRPT.
 CC PRODOM: PD000018; WD40; 3.
 CC SMART: SM00256; FBOX; 1.
 CC SMART: SM00320; WD40; 8.
 CC PROSITE: PS50181; FBOX; 1.
 CC PROSITE: PS00678; WD_REPEATS_1; 3.
 CC PROSITE: PS50082; WD_REPEATS_2; 6.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat: WD repeat.
 FT DOMAIN 70 116 F-BOX.
 FT REPEAT 219 256 WD 1.
 FT REPEAT 259 298 WD 2.
 FT REPEAT 301 338 WD 3.
 FT REPEAT 345 386 WD 4.
 FT REPEAT 388 426 WD 5.
 FT REPEAT 427 464 WD 6.
 FT REPEAT 468 505 WD 7.
 SQ SEQUENCE 506 AA; 58257 MW; CEF34D4EFFBC2E10 CRC64;
 Query Match 36.0%; Score 62; DB 1; Length 506;
 Best Local Similarity 38.5%; Pred. No. 0.086;
 Matches 10; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
 QY 6 EAVLHRENGMAMVTCCKRSTAYWD 31
 DB 222 DSVYCVQYDDEIMVSQSKRTVSWD 247
 ID YNA6_YEAST STANDARD; PRT; 303 AA.
 AC P41318;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 34.0 kDa Trp-Asp repeats containing protein in SISI-MRPL2
 DE intergenic region.
 DE YNL006W OR N2005.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=95076713; PubMed=7985421;
 RA Verhasselt P., Aert R., Voet M., Volckaert G.;
 RT "Nucleotide sequence analysis of an 8887 bp region of the left arm of
 RL yeast chromosome XIV, encompassing the centromere sequence.";
 RN [2]
 RP SEQUENCE FROM N.A.

RA Dolignon F., Crouzet M.;
 RL Submitted (Mar-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X77114; CAA54380.1; -
 CC EMBL: Z71282; CAA95865.1; -
 CC PIR: S45123; S45123.
 CC PIR: S45461; S45461.
 CC SGD: S0004951; YNL006W.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF00400; WD40; 7.
 CC PRINTS: PR00320; GPROTEINBRPT.
 CC PRODOM: PD000018; WD40; 2.
 CC SMART: SM00320; WD40; 6.
 CC PROSITE: PS00678; WD_REPEATS_1; 4.
 CC PROSITE: PS50082; WD_REPEATS_2; 5.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat: WD repeat.
 FT REPEAT 73 103 WD 1.
 FT REPEAT 114 144 WD 2.
 FT REPEAT 157 187 WD 3.
 FT REPEAT 205 235 WD 4.
 FT REPEAT 248 278 WD 5.
 SQ SEQUENCE 303 AA; 34034 MW; 536AA1DB8E815F0 CRC64;
 Query Match 34.9%; Score 60; DB 1; Length 303;
 Best Local Similarity 38.5%; Pred. No. 0.099;
 Matches 10; Conservative 7; Mismatches 7; Indels 2; Gaps 1;
 QY 6 EAVLHRENGMAMVTCCKRSTAYWD 31
 DB 121 EVVHHP--NOGELLSCDRDGRIRWD 144
 ID YB25_YEAST STANDARD; PRT; 315 AA.
 AC P38123;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 34.8 kDa Trp-Asp repeats containing protein in SMY2-RPS6B
 DE intergenic region.
 DE YBR175W OR YBR1237.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
 RA Niegemann E., Schenk-Groening R., Servos J., Wehner E.,
 RA Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
 RA Gruenbein R., Hedges D., Klesau P., Korol S., Krems B., Proft M.,
 RA Slegers K., Baur A., Boles E., Miosga T.,
 RA Schait-Gerstenschlaeger I., Zimmermann F.K.;
 RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
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Query Match Similarity	34.3%	Score 59	DB 1	Length 315
Best Local Similarity	40.6%	Pred. No. 0.15		
Matches 13	Conservative 4	Mismatches 13	Indels 2	Gaps 1
QY	2	IHCCEAVLHFRN--NGMAVTCSDKRSIAVMD	31	
Db	93	IGHTAPVISTLFRKGNLLFTSSMDISIIWMD	124	

Query Match 34.3%; Score 59; DB 1; Length 415;
Best Local Similarity 36.7%; Pred. No. 0.2;
Matches 11; Conservative 7; Mismatches 12; Indels 0; Gaps 0.

RESULT	12
YDPI_SCHPO	
ID	YDPI_SCHPO
AC	014021
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Hypothetical WD-repeat protein C29A4.18 in chromosome I
GN	SPAC29A4.18

OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN-9720
RX MEDLINE-9720 PubMed-11859360.
RA Wood V., Gilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Squires J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymopre B.,
RA Welljens I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S.,
RA Gabriel C., Fuchs M., Filicz C., Holzner E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Egger P., Zimmermann W., Wedler H., Wambolt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Motlier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revelleta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Szpakowski G.V., Usersty D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1-SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -1-SIMILARITY: BELONGS TO THE HIFI FAMILY OF WD-REPEAT PROTEINS.

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Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Brain;
 RA MEDLINE-21154917; PubMed-11230166;
 RA Wiemann S., Weill B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansoorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Ottenwälder B., Obermaier B., Tampe J., Heubner D.,
 RA Wamboldt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hypothalamus;
 RX MEDLINE-20402571; PubMed-10931946;
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
 RT axis and full-length cDNA cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Pituitary;
 RA Song H., Peng Y., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G.,
 RA Luo M., Chen J., Hu R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Colon;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: CONTAINS 1 SOCS BOX DOMAIN.
 CC
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 CC
 DR EMBL; AF072880; AAD28808.1; -
 DR EMBL; AF069313; AAD20954.2; -
 DR EMBL; AF240696; AAF82746.1; -
 DR EMBL; AL110243; CAB53693.1; -
 DR EMBL; AF112205; AAF17193.1; -
 DR EMBL; AF106683; AAD43036.1; -
 DR EMBL; BC021110; AAH21110.1; -
 DR InterPro: IPR001496; SOCS.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 2.
 DR SMART: SM00253; SOCS; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR PROSITE: PS50225; SOCS; 1.
 KW Repeat; WD repeat; Alternative splicing.
 FT REPEAT 32 71 WD 1.
 FT REPEAT 124 165 WD 2.
 FT REPEAT 168 208 WD 3.
 FT REPEAT 212 251 WD 4.
 FT REPEAT 254 293 WD 5.

FT REPEAT 309 346 WD 6.
 FT DOMAIN 372 421 SOCS BOX.
 FT VARSPLIT 14 159 MISSING (IN ISOFORM 2).
 FT CONFLICT 16 16 L -> S (IN REF. 3 AND 4).
 FT CONFLICT 178 178 F -> L (IN REF. 5).
 FT CONFLICT 231 231 S -> P (IN REF. 5).
 SQ SEQUENCE 421 AA; 47432 MW; 650d4942e97d4b8d CRC64;
 Query Match 34.0%; Score 58.5; DB 1; Length 421;
 Best Local Similarity 35.3%; Pred. No. 0.24;
 Matches 12; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
 Qy 1 LHHCEAVLHREF--NNGMWTCSKDRSLAVWD 31
 Db 166 LVDTHEVVRDLTFAPDGSLLVLSASRDKTLRWMD 199
 ID WSB1_MOUSE STANDARD; PRT; 421 AA.
 WSBI_MOUSE
 AC 054927;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE WD repeat and SOCS box containing protein 1 (WSB-1).
 GN WSB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss;
 RX MEDLINE=98081836; PubMed=9419338;
 RA Hilton D.J., Richardson R.T., Alexander W.S., Viney E.M.,
 RA Wilson T.A., Sprigg N.S., Starr R., Nicholson S.E., Metcalfe D.,
 RA Nicola N.A.;
 RT "Twenty proteins containing a C-terminal SOCS box form five structural
 RT classes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:114-119(1998).
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: CONTAINS 1 SOCS BOX DOMAIN.
 CC
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 CC
 DR EMBL; AF033186; AAB96647.1; -
 DR InterPro: IPR001496; SOCS.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 2.
 DR SMART: SM00253; SOCS; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR PROSITE: PS50225; SOCS; 1.
 KW Repeat; WD repeat.
 FT REPEAT 124 165 WD 1.
 FT REPEAT 168 208 WD 2.
 FT REPEAT 212 251 WD 3.
 FT REPEAT 254 293 WD 4.
 FT REPEAT 309 346 WD 5.
 FT DOMAIN 372 421 SOCS BOX.
 SQ SEQUENCE 421 AA; 47065 MW; 4003d1ffe7a9a2ef CRC64;
 Query Match 34.0%; Score 58.5; DB 1; Length 421;

Best Local Similarity 35.3%; Pred. No. 0.24;
Matches 12; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

Qy 1 LIHCEAVLHLRF--NNGMMVTCCKDRSIAVWD 31
| | | | | : : : | | |
Db 166 LVDHTEWVRDLTFAPDGSLLIVSASRDKTLRWMD 199

Search completed: April 10, 2003, 13:19:35
Job time : 3.22777 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 7.32521 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168B-2_COPY_343_373

Sequence: 1 LIHCEAVLHLRFNNGMMVTCSKDRSIAVVD 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : SPTREMBL_21:*

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.ornanella:*
9:  sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteria:*
17: sp.archaea:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	172	100.0	122	13	08UN03	08un03 xenopus lae
2	172	100.0	510	5	044382	044382 drosophila
3	172	100.0	510	5	09VDE3	09vde3 drosophila
4	172	100.0	559	11	0927159	092159 mus musculus
5	172	100.0	559	11	090015	090015 mus musculus
6	167	97.1	559	11	09R167	09r167 mus musculus
7	157	91.3	430	5	09B054	09b054 heterodera
8	152	88.4	252	11	092227	092227 mus musculus
9	152	88.4	553	11	0923H0	0923H0 mus musculus
10	70	40.7	524	3	09P7C0	09p7c0 schizosacch
11	69	40.1	280	5	08SR25	08sr25 enccephalito
12	68	39.5	637	5	09VM11	09vm11 drosophila
13	67	39.0	442	3	096V17	096v17 pneumocystis
14	67	39.0	1609	5	09GRC3	09grc3 caenorhabdi
15	67	39.0	1893	5	017887	017887 caenorhabdi
16	66	38.4	331	5	Q19211	Q19211 caenorhabdi

17	66	38.4	436	5	Q9VAK0	Q9VAK0	drosohilla
17	65	37.8	573	11	Q9QXW2	Q9QXW2	mus musculus
18	64	37.2	310	4	Q75938	Q75938	homo sapien
19	64	37.2	357	4	Q95320	Q95320	homo sapien
20	64	37.2	357	4	Q95320	Q95320	homo sapien
21	64	37.2	357	4	Q96D17	Q96D17	homo sapien
22	64	37.2	370	11	Q9DCX3	Q9DCX3	mus musculus
23	64	37.2	414	5	Q8SM59	Q8SM59	encephallito
24	64	37.2	566	4	Q9H6A8	Q9H6A8	homo sapien
25	64	37.2	566	4	Q969U6	Q969U6	homo sapien
26	64	36.9	456	4	Q9NV62	Q9NV62	homo sapien
27	63.5	36.9	449	5	Q9HAD4	Q9HAD4	homo sapien
28	63.5	36.9	942	5	Q96611	Q96611	dictyostell
29	63	36.6	299	10	Q94AH2	Q94AH2	arabidopsis
30	63	36.6	343	10	Q9FGG0	Q9FGG0	arabidopsis
31	62.5	36.3	810	3	Q9P6V7	Q9P6V7	neurospora
32	62.5	36.3	1326	5	Q9VZF4	Q9VZF4	drosophila
33	62	36.0	357	11	Q9D0K7	Q9D0K7	mus musculus
34	62	36.0	360	4	Q9C069	Q9C069	homo sapien
35	62	36.0	360	4	Q9CEE3	Q9CEE3	homo sapien
36	62	36.0	360	11	Q8R2U0	Q8R2U0	mus musculus
37	62	36.0	421	4	Q96MH3	Q96MH3	homo sapien
38	62	36.0	507	3	Q9UT85	Q9UT85	schizosacch
39	62	36.0	553	4	Q9NUX6	Q9NUX6	homo sapien
40	62	36.0	561	4	Q96R12	Q96R12	homo sapien
41	62	36.0	589	4	Q96LE0	Q96LE0	homo sapien
42	62	36.0	627	4	Q96A16	Q96A16	homo sapien
43	62	36.0	629	11	Q8VHP4	Q8VHP4	mus musculus
44	62	36.0	629	11	Q8VBV4	Q8VBV4	mus musculus
45	62	36.0	707	4	Q969H0	Q969H0	homo sapien

ALIGNMENTS

RESULT 1		PRELIMINARY:		PRT:	122 AA.
OBUN3					
ID	OBUN3				
AC	OBUN3				
DT	01-MAR-2002 (TrEMBLref. 20, Created)				
DT	01-MAR-2002 (TrEMBLref. 20, Last sequence update)				
DT	01-JUN-2002 (TrEMBLref. 21, Last annotation update)				
DE	Beta-TRCP protein (Fragment).				
GN	Beta-TRCP.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Carnevali F.;				
RN	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RA	Ballarino M.;				
RT	"Analisi strutturale e funzionale del gene beta-TRCP in Xenopus				
RT	laevis.";				
RL	Thesis (2001).				
RL	Department of Genetics and Molecular Biology "Charles Darwin",				
RL	University of Rome La Sapienza, Rome, Italy.				
DR	EMBL; AJ428938; CAD1935.1; -.				
DR	InterPro; IPR001680; WD40.1.				
DR	Pfam; PF004400; WD40.3.				
DR	PRINTS; PR00320; GPROTEINRPT.				
DR	ProDom; PD000018; WD40.2.				
DR	SMART; SM00320; WD40.3.				
DR	PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.				
DR	PROSITE; PS50082; WD_REPEATS_2; 3.				
DR	PROSITE; PS50294; WD_REPEATS_REGION. 1.				
FT	NON_TER 1				
FT	NON_TER 122				
SEQ	SEQUENCE 122 AA: 13682 MW: 3666B6B39ACBF5387 CRC64:				

Query Match 100.0%; Score 172; DB 13;
 Best Local Similarity 100.0%; Pred. No. 4.9e-19;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLRFNNGMMVTCSDRSIAVMD 31
 DB 13 LIHCEAVLHLRFNNGMMVTCSDRSIAVMD 43

RESULT 2

ID 044382 PRELIMINARY; PRT; 510 AA.

AC 044382; 01-JUN-1998 (TREMUREL. 06, Created)

DT 01-JUN-1998 (TREMUREL. 06, Last sequence update)

DE 01-MAR-2002 (TREMUREL. 20, Last annotation update)

SLMB SLMB OR SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

SEQUENCE FROM N.A.

RA MEDLINE=98121115; PubMed=9461217;

RT Regulation of the Hedgehog and Wingless signalling pathways by the F-box/WD40-repeat protein Slmb."

RL Nature 391:493-496(1998).

CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).

DR EMBL: AF032878; AAC38652.1;

DR InterPro: IPR001810; F-box.

DR Pfam: PF00646; F-box; 1.

DR PRINTS: PR00400; WD40; 7.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00256; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

SEQUENCE 510 AA; 58952 MM; DB024303730A5E8 CRC64;

Query Match 100.0%; Score 172; DB 5; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.3e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLRFNNGMMVTCSDRSIAVMD 31

DB 286 LIHCEAVLHLRFNNGMMVTCSDRSIAVMD 316

RESULT 3

ID 09VDE3 PRELIMINARY; PRT; 510 AA.

AC 09VDE3; 01-MAY-2000 (TREMUREL. 13, Created)

DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)

DE 01-MAR-2002 (TREMUREL. 20, Last annotation update)

SLMB protein (SLMB).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

SEQUENCE FROM N.A.
 STRAIN=BERKELEY;

RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayant A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Korell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kul D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacלב J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J., Zou X., Zhou X., Zhou Q., Zhou L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).

RT independent transcription of wingless in all limb discs, and induce

RT decapentaplegic transcription linked to imaginal disc regeneration.";

RT Mech. Dev. 93:15-26(2000).

CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).

DR EMBL: AE003733; AAF55853.1;

DR EMBL: AF222924; AAF63214.1;

DR EMBL: AF222923; AAF63213.1;

DR FLYBASE: FBgn0023423; slmb.

DR InterPro: IPR001810; F-box.

DR Pfam: PF00646; F-box; 1.

DR PRINTS: PR00320; GPROTEINRPT.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00256; FBOX; 1.

DR PROSITE: PS50181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; 5.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

Repeat; WD repeat.

SEQUENCE 510 AA; 58952 MM; F4D5DF126F58A012 CRC64;

Query Match 100.0%; Score 172; DB 5; Length 510;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHCEAVLHLRFNNGMMVTCSDRSIAVMD 31

Db 286 LIHCEAVLHLRFNNGMVTCSKDRSLAVWD 316

RESULT 4

ID 092159 PRELIMINARY: PRT: 569 AA.

AC 092159; 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-transducin repeat containing protein.
 GN BTRC.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=99145465; PubMed=9990853;

RA Spencer E., Jiang J., Chen Z.J.,

RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein

SLIMB/beta-TrCP."

RL Genes Dev. 13:284-294(1999).

CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL: AF112979; AAD04181.1;

DR MGD: MGI:1338871; Btrc.

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001680; WD40.

DR Pfam: PF00646; F-box; 1.

DR PRINTS: PR00320; GPROTEINBRPT.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00256; FBOX; 1.

DR SMART: SM00320; WD40; 7.

DR PROSITE: PS0181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

DR Repeat: WD repeat.

KW Repeat: WD repeat.

SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;

Query Match 100.0%; Score 172; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHCEAVLHLRFNNGMVTCSKDRSLAVWD 31
 Db 343 LIHCEAVLHLRFNNGMVTCSKDRSLAVWD 373

RESULT 5
 Q90U15 PRELIMINARY: PRT: 569 AA.

AC 090U15; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Ubiquitin ligase FWD1 (Beta-transducin repeat containing protein)

DE (F-box-WD40 repeat protein 1).

GN BTRC OR FBXW1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=99199275; PubMed=10097128;

RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,

Hattori K., Higashi H., Nakano H., Okumura K., Ono K., Good R.A.,

Nakayama K.-I.,

RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a

ubiquitin ligase Skp1/Cul 1/F-box protein FWD1."

GN BTRC.

Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).

[2]
 SEQUENCE FROM N.A.

RX MEDLINE=99075339; PubMed=9859996;

RA Yaron A., Hatzudai A., Davis M., Lavon I., Amit S., Manning A.M.,

Andersen J.S., Mann M., Mercutio F., Ben-Neriah Y.,

RT "Identification of the receptor component of the IkappaBalpha-

ubiquitin ligase."

RL Nature 396:590-594(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [4]
 RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RX MEDLINE=21601157; PubMed=11735228;

RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,

Nakayama K.-I.;

RT "Characterization of a Mouse Gene (fbxw6) That Encodes a Homologue of

Caenorhabditis elegans SEL-10."

RL Genomics 78:214-222(2001).

CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

DR EMBL: AF081887; AAD17755.1;

DR EMBL: AF099932; AAD08701.1;

DR EMBL: BC003989; AAD03989.1;

DR EMBL: AF391190; AAL40929.1;

DR EMBL: AF391178; AAL40929.1; JOINED.

DR EMBL: AF391179; AAL40929.1; JOINED.

DR EMBL: AF391180; AAL40929.1; JOINED.

DR EMBL: AF391181; AAL40929.1; JOINED.

DR EMBL: AF391182; AAL40929.1; JOINED.

DR EMBL: AF391183; AAL40929.1; JOINED.

DR EMBL: AF391184; AAL40929.1; JOINED.

DR EMBL: AF391185; AAL40929.1; JOINED.

DR EMBL: AF391186; AAL40929.1; JOINED.

DR EMBL: AF391187; AAL40929.1; JOINED.

DR EMBL: AF391188; AAL40929.1; JOINED.

DR EMBL: AF391189; AAL40929.1; JOINED.

DR MGD: MGI:1338871; Btrc.

DR InterPro: IPR001810; F-box.

DR InterPro: IPR001680; WD40.

DR Pfam: PF00646; F-box; 1.

DR Pfam: PF00400; WD40; 7.

DR PRINTS: PR00320; GPROTEINBRPT.

DR PRODOM: PD000018; WD40; 4.

DR SMART: SM00256; FBOX; 1.

DR SMART: SM00320; WD40; 7.

DR PROSITE: PS0181; FBOX; 1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.

DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

DR Repeat: WD repeat.

KW Repeat: WD repeat.

SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match 100.0%; Score 172; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHCEAVLHLRFNNGMVTCSKDRSLAVWD 31
 Db 343 LIHCEAVLHLRFNNGMVTCSKDRSLAVWD 373

RESULT 6
 Q9RIG7 PRELIMINARY: PRT: 569 AA.

AC 09RIG7; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Beta-transducin repeat-containing protein.

GN BTRC.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Winston J., Ellledge S.J., Harper J.W.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF110396; AAD41025.1; -.
 DR MGD: MGI:135871; Btcc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;

Query Match 97.1%; Score 167; DB 11; Length 569;
 Best Local Similarity 96.8%; Pred. No. 1.6e-17;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHCEAVLHLRFNNGMVTCKSKDRSIAYWD 31
 Db 343 LHHCEAVLHLRFNNGMVTCKSKDRSIAYWD 373

RESULT 7
 Q9BJ54 PRELIMINARY; PRT; 430 AA.
 AC Q9BJ54;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-transducin repeat-containing protein (Fragment).
 OS Heterodera glycyines (Soybean cyst nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
 OX NCBI_TaxID=51029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kovalova E.S., Yakovlev A.G., Master E.P.;
 RT "Plant parasitic nematode b-TGCP.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF339101; AAK26376.1; -.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER
 SQ SEQUENCE 430 AA; 47916 MW; 4ABC3FFD2FE3A50B CRC64;

Query Match 91.3%; Score 157; DB 5; Length 430;
 Best Local Similarity 87.1%; Pred. No. 4.2e-16;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHCEAVLHLRFNNGMVTCKSKDRSIAYWD 31
 Db 167 LVHHCFAVLHLRFNNGMVTCKSKDRSIAYWD 197

RESULT 8
 Q922C7 PRELIMINARY; PRT; 252 AA.
 AC Q922C7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Similar to f-box and WD-40 domain protein 1B (Fragment).
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: BC008552; AAO8352.1; -.
 DR MGD: MGI:2144023; FBXW1B.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40; 3.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER
 SQ SEQUENCE 252 AA; 28424 MW; F71737CHD7A9F75F CRC64;

Query Match 88.4%; Score 152; DB 11; Length 252;
 Best Local Similarity 90.3%; Pred. No. 1.4e-15;
 Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHCEAVLHLRFNNGMVTCKSKDRSIAYWD 31
 Db 26 LHHCEAVLHLRFNNGMVTCKSKDRSIAYWD 56

RESULT 9
 Q923H0 PRELIMINARY; PRT; 563 AA.
 AC Q923H0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE F-box/WD40 repeat-containing protein HOS.
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
 RT "Mouse homolog of HOS (mHOS) is overexpressed in skin tumors and
 implicated in constitutive activation of NF-kappaB.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AY038079; AAK72095.1; -.
 DR MGD: MGI:2144023; FBXW1B.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR Prodom: PD000018; WD40; 4.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AE003612; AAF52336.1; -;
 DR FLYbase: FBgn001773; CG9144.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; F-box; 1.
 DR SMART: SM00320; WD40; 2.
 DR PROSITE: PS0181; F-box; 1.
 DR PROSITE: PS50082; WD_REPEATS_2; 2.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
 KW Repeat; WD repeat.
 SQ SEQUENCE 627 AA; 71908 MW; 11A2E2FEF4DE433 CRC64;

Query Match 39.5%; Score 68; DB 5; Length 627;
 Best Local Similarity 43.3%; Pred. No. 0.046;
 Matches 13; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

OY 4 HCEAVLHFR--NNGMAYTCSDRSIAVWD 31
 DB 128 HTHQVLHVSFAHNGEMFATCSKDGVIITWN 157

RESULT 13
 OY 096V17 PRELIMINARY; PRT; 442 AA.
 AC 096V17;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Probable nuclear migration protein.
 OS *Pneumocystis carinii*.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 NC NCBITaxID=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PNEUMOCYSTIS CARINII F. SP. CARINII;
 RA Murphy L., Quail M., Harris D., Hall N., Wakefield A., Smulian A.G.,
 RA Cushion M.T., Stringer J.R., Keely S.P., Barrett B.G.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AL592382; CAC43453.1; -;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRODOM: PD000018; WD40; 2.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 442 AA; 49914 MW; 0B16704A217BC123 CRC64;

Query Match 39.0%; Score 67; DB 3; Length 442;
 Best Local Similarity 40.6%; Pred. No. 0.045;
 Matches 13; Conservative 7; Mismatches 8; Indels 4; Gaps 1;

OY 4 HCEAVLHFR--NNGMAYTCSDRSIAVWD 31
 DB 156 HTKAVLDIEFTFSDSCLVSCSSDLTIKIMD 187

RESULT 14
 ID 09GRC3 PRELIMINARY; PRT; 1609 AA.
 AC 09GRC3;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Kinesin like protein KLP-12.
 GN KLP-12.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 NC NCBITaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA All M.Y., Siddiqui S.S.;
 RT "C. elegans Kinesin Like Protein, klp-12";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AB035591; BAB16763.1; -;
 DR HSP: P17119; 3KAR.
 DR InterPro: IPR001752; kinesin_motor.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00225; kinesin; 1.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR PRODOM: PD000018; WD40; 1.
 DR SMART: SM00129; KISC; 1.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 DR PROSITE: PS50067; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE: PS50082; WD_REPEATS_2; 2.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW ATP-binding; Coiled coil; Microtubules; Motor protein; Repeat;
 KW WD repeat.
 SQ SEQUENCE 1609 AA; 179646 MW; 5F710B840B4E9416 CRC64;

Query Match 39.0%; Score 67; DB 5; Length 1609;
 Best Local Similarity 46.4%; Pred. No. 0.18;
 Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 4 HCEAVLHFRNNGMAYTCSDRSIAVWD 31
 DB 1287 HARGVLSVDVNEKLVTCGSKDRTAKIMD 1314

RESULT 15
 OY 017887 PRELIMINARY; PRT; 1693 AA.
 AC 017887; 018007;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE T01G1.1 protein.
 DE T01G1.1 protein.
 GN T01G1.1.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 NC NCBITaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kerstow J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,
 RA Gardner M., Dear S., Du Z., Durbin R., Pavello A., Fulton L.,
 RA Craxton A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kerstow J., Kirsten J., Laister N., Latelle P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaison N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wellstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";

RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA White S., Mortimore B.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: 292811; CAB07273.1; -
 DR EMBL: 282271; CAB07273.1; JOINED.
 DR EMBL: 282271; CAB05214.1; -
 DR EMBL: 292811; CAB05214.1; JOINED.
 DR HSSP: P17119; 3KAR.
 DR InterPro: IPR001752; kinesin_motor.
 DR InterPro: IPR001441; UPP_synth.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00225; kinesin; 1.
 DR Pfam: PF01255; UPP_synthetase; 1.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR ProDom: PD000018; WD40; 1.
 DR ProDom: PD003461; UPP_synth; 1.
 DR SMART: SM00129; KISC; 1.
 DR SMART: SM00320; WD40; 3.
 DR TIGRFAMs: TIGR00055; upps; 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE: PS50657; KINESIN_MOTOR_DOMAIN2; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE: PS50082; WD_REPEATS_2; 2.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR ATP-binding; Coiled coil; Microtubules; Motor protein; Repeat;
 KM WD repeat.
 SQ SEQUENCE 1893 AA; 212825 MW; 166B7477C1BD810C CRC64;

Query Match 39.0%; Score 67; DB 5; Length 1893;
 Best Local Similarity 46.4%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 4 HCEAVLHLRFNGMAMVTCSDRSIAVWD 31
 Db 1571 HARGVLSDVNEKIMVTGSKDRITAKLWD 1598

Search completed: April 11, 2003, 11:51:36
 Job time : 9.32521 secs

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2.

3.

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 ; Search time 8.93666 Seconds
(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_387_415

Perfect score: 151
Sequence: 1 VGHRAAVNVDFDDKTYVSASGDRITKVM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_101002:*
2: /SID2/gcgdata/geneseq/genesep-emb1/AA1980.DAT.*
3: /SID2/gcgdata/geneseq/genesep-emb1/AA1981.DAT.*
4: /SID2/gcgdata/geneseq/genesep-emb1/AA1982.DAT.*
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23: /SID2/gcgdata/geneseq/genesep-emb1/AA2001.DAT.*
24: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	151	100.0	517	16 AAR85852	WD-40 domain-contg
2	151	100.0	542	21 AAY96696	Human E3 ubiquitin
3	151	100.0	542	22 AAM79127	Human protein SFO
4	151	100.0	542	22 AAM40208	Human polypeptide
5	151	100.0	550	22 AAM41994	Human polypeptide
6	151	100.0	569	20 AAY24054	A human beta-trans
7	151	100.0	569	21 AAB12812	Mouse ubiquitin 11
8	151	100.0	569	21 AAB12813	Human beta-transdu
9	151	100.0	569	21 AAY96697	Human beta-TrCP.
10	151	100.0	569	21 AAY83041	F-box protein FBP-

11	151	100.0	569	21 AAY83250	F-box protein hbet
12	151	100.0	569	21 AAY83254	F-box protein FMD1
13	151	100.0	569	21 AAY44249	Human cell signal
14	151	100.0	569	22 AAB48298	Human ZF1 protein
15	151	100.0	579	22 AAM78583	Human protein SFO
16	151	100.0	590	22 AAM00847	Human bone marrow
17	151	100.0	605	22 AAM78582	Human protein SFO
18	151	100.0	608	22 AAM00960	Human bone marrow
19	151	100.0	632	22 AAM78584	Human protein SFO
20	151	100.0	654	22 AAM79566	Human protein SFO
21	151	100.0	654	22 AAM79567	Human protein SFO
22	151	100.0	654	22 AAM79568	Human protein SFO
23	151	100.0	654	22 AAM79569	Human protein SFO
24	147	97.4	510	22 AAR84938	Peptide r1V from a
25	82	54.3	17	21 AAY96714	Drosophila melanog
26	78	51.7	1326	22 ABB67237	Drosophila melanog
27	78	51.7	1326	22 ABB67238	Drosophila melanog
28	78	51.7	1326	22 ABB67239	Drosophila melanog
29	76	50.3	514	16 AAR85881	Human polypeptide
30	75	49.7	513	22 AAM40282	Human protein sequ
31	75	49.7	513	22 AAB93194	Human GTP-binding
32	75	49.7	513	22 AAB68510	Human polypeptide
33	75	49.7	525	22 AAM42068	Amino acid sequenc
34	75	49.7	587	20 AAY03204	Drosophila melanog
35	75	49.7	860	22 ABB62502	Peptide r1V from
36	74	49.0	33	16 AAR84944	Stronglyocentrotus
37	74	49.0	690	21 AAY49948	Human prostate can
38	74	49.0	744	21 AAB56769	WD-40 domain-contg
39	74	49.0	906	16 AAR85853	Arabidopsis thalia
40	73	48.3	234	21 AAG23335	Arabidopsis thalia
41	73	48.3	244	21 AAG23334	Arabidopsis thalia
42	73	48.3	310	21 AAG42208	Arabidopsis thalia
43	73	48.3	311	21 AAG04819	Arabidopsis thalia
44	73	48.3	311	21 AAG04819	Arabidopsis thalia
45	73	48.3	316	21 AAG28460	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ID AAR85852 standard: peptide: 517 AA.
XX AAR85852:
XX 13-SEP-1996 (first entry)
XX WD-40 domain-contg. beta-TRCP protein.
XX DE
XX WD40 repeat region: beta-transducin: protein-protein interaction: drug;
XX intracellular signalling: protein kinase C; homology: motif: modulator;
XX receptors of activated protein kinase: enzyme activity: isozyme: human.
XX OS
XX Synthetic.
XX PN
XX W09521252-A2.
XX 10-AUG-1995.
XX PD
XX 31-JAN-1995; 95WO-US01210.
XX PF
XX 01-FEB-1994; 94US-0190802.
XX PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX PA
XX Mochly-Rosen D, Ron D;
XX PI
XX WPI: 1995-283772/37.
XX DR
XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
XX activity of a protein, eg. protein kinase C, which interacts with a
XX protein contg. a WD-40 region.
XX PT

XX Example 5; Page 80-82; 351pp; English.
XX
CC Proteins AAR8551-92 are protein which contain at least one WD-40 (also
CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR8580). Proteins AAR8581-82 were isolated based
CC on homology with beta-transducin, whereas proteins AAR8582-92 were
CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
CC The proteins were used to construct the peptides AAR4928-R85063 and
CC AAR85786-R85842. The peptides can be used to identify target proteins
CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC proteins involved in protein-protein interaction and to screen for drugs
CC that will affect protein-protein interaction involving WD-40 domains.
XX
SQ Sequence 517 AA:
Query Match 100.0%; Score 151; DB 16; Length 517;
Best Local Similarity 100.0%; Pred. No. 2,9e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGHRAAVNVDPDDKITYASASGDRITIKYW 29
DB 351 VGHRAAVNVDPDDKITYASASGDRITIKYW 379
RESULT 2
ID AAY6696
ID AAY6696 standard; Protein: 542 AA.
AC AAY6696;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human E3 ubiquitin ligase.
XX
KM E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KM nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KM anti-inflammatory; immunosuppressive; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200034447-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US29371.
XX
PR 10-DEC-1998; 98US-0210060.
XX
PA (SIGNS) STGMAL PHARM INC.
XX (YISS) YISSUM RES & DEV CO.
XX
PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
PI Layon I, Yaron A;
XX
DR WPI: 2000-431294/37.
DR N-PSDB: AAK51228.
XX
PT Polypeptide enhancing phosphorylated I-kappa-B ubiquitination useful for
PT treating disorder associated with NF-kappa-B activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant
XX
PS Claim 1; Page 70-72; 77pp; English.
XX
CC This is human E3 ubiquitin ligase (E3), which is homologous to human
CC beta-TrCP, an F-box/WD protein family member. E3 enhances ubiquitination
CC of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor
CC kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the
CC ubiquitin pathway is useful for identifying modulators of this process

CC for use in treating diseases associated with activation of NF-kappa-B. In
CC vitro analysis suggests that deletion of the F-box results in a protein
CC that functions as a dominant negative molecule in vivo. Transient
CC over-expression of delta-beta-TrCP (a deletion mutant) inhibited the
CC degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells,
CC resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be
CC used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP
CC can be used to modulate NF-kappa-B to treat inflammatory diseases,
CC autoimmune diseases, cancer and viral infections.
XX
SQ Sequence 542 AA:
Query Match 100.0%; Score 151; DB 21; Length 542;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGHRAAVNVDPDDKITYASASGDRITIKYW 29
DB 360 VGHRAAVNVDPDDKITYASASGDRITIKYW 388
RESULT 3
ID AAM79127
ID AAM79127 standard; Protein: 542 AA.
AC AAM79127;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1789.
XX
KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB: AAK52260.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 4147-4148; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM0020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 542 AA:

Query Match 100.0%; Score 151; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 3.1e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
 |||||
 Db 360 VGHRAAVNVDPDDKYIVSASGDRITKW 388

RESULT 4
 AAM40208
 ID AAM40208 standard; Protein; 542 AA.

XX AC AAM40208;
 XX DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3353.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US4263.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

XX PR 19-OCT-2000; 2000US-0693036.

XX PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PT Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI: 2001-442253/47.

XX DR N-PSDB: AAI59364.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders
 XX such as central nervous system injuries -
 XX Example 5; SEQ ID NO 3353; 10078pp; English.
 XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activity/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 542 AA:

Query Match 100.0%; Score 151; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 3.1e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
 |||||
 Db 360 VGHRAAVNVDPDDKYIVSASGDRITKW 388

RESULT 5
 AAM41994
 ID AAM41994 standard; Protein; 550 AA.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6925.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US4263.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

XX PR 19-OCT-2000; 2000US-0693036.

XX PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PT Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI: 2001-442253/47.

XX DR N-PSDB: AAI61150.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders
 XX such as central nervous system injuries -
 XX Example 2; SEQ ID NO 6925; 10078pp; English.
 XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with noctropic.

DR WPI; 2000-485550/43.

DR N-PSDB; AAA73131.
 XX F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin
 XX
 PS Claim 2: Page 9-10; 19pp; Japanese.
 XX
 CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 CC
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 151; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VGHRAAVNVVDFDDKRYIVSASGDRITKXW 29
 Db 387 VGHRAAVNVVDFDDKRYIVSASGDRITKXW 415
 |||||
 RESULT 8
 AAB12813
 ID AAB12813 standard; protein; 569 AA.
 AC AAB12813:
 XX 27-NOV-2000 (first entry)
 DT
 XX Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
 DE
 XX Ubiquitin ligase SCF complex: F-box protein; ubiquitination; Ikappab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FMD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-TrCP.
 XX
 OS Homo sapiens.
 XX
 PN JP2000166542-A.
 PD 20-JUN-2000.
 PF 02-DEC-1998; 98JP-0343437.
 XX
 PR 02-DEC-1998; 98JP-0343437.
 XX
 PA (KAGAKU GIJUTSU SHINKO JIGYODAN.
 DR WPI: 2000-485550/43.
 DR N-PSDB; AAA73132.
 XX
 PT F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin
 PS Claim 3: Page 10-12; 19pp; Japanese.
 XX
 CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 CC

SQ Sequence 569 AA:
 Query Match 100.0%; Score 151; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VGHRAAVNVVDFDDKRYIVSASGDRITKXW 29
 Db 387 VGHRAAVNVVDFDDKRYIVSASGDRITKXW 415
 |||||
 RESULT 9
 AAY96697
 ID AAY96697 standard; protein; 569 AA.
 AC AAY96697:
 XX 26-SEP-2000 (first entry)
 DT
 XX Human beta-TrCP.
 DE
 XX E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
 KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
 KW anti-inflammatory; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200034447-A2.
 PD 15-JUN-2000.
 PF 10-DEC-1999; 99WO-US29371.
 XX
 PR 10-DEC-1998; 98US-0210060.
 XX
 PA (SIGMA) SIGNAL PHARM INC.
 PA (YISS) YISSUM RES & DEV CO.
 PI
 PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
 PI Lavon I, Yaron A;
 DR WPI: 2000-431294/37.
 DR N-PSDB; AAA51229.
 XX
 PT polypeptide enhancing phosphorylated Ikappab ubiquitination useful for
 PT treating disorder associated with NF-kappa-B activation e.g. cancer,
 PT comprising amino acid sequence of human E3 ubiquitin ligase or its
 PT variant
 PS Claim 21: Page 72-74; 77pp; English.
 XX
 CC Human beta-TrCP, an F-box/WD protein family member, has been shown to
 CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
 CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
 CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
 CC degradation via the ubiquitin pathway is useful for identifying
 CC modulators of this process for use in treating diseases associated with
 CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
 CC the F-box results in a protein that functions as a dominant negative
 CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a
 CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
 CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
 CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
 CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
 CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
 CC
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 151; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VGHRAAVNVVDFDDKRYIVSASGDRITKXW 29

PT Human cell signaling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders
 XX
 PS Claim 1; Page 77-78; 90pp; English.
 XX
 CC The present sequence is cell signalling protein-12 (CSIGP-12) encoded
 CC by cDNA obtained from Incyte clone 3239149 of COLAUCT01 library. It is
 CC expressed in musculoskeletal, gastrointestinal and nervous tissues and is
 CC found to be homologous to beta transducin repeats containing
 CC protein. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 151; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGHRAAVNVDPDKYIVSASGDRITKW 29
 DB 387 VGHRAAVNVDPDKYIVSASGDRITKW 415
 RESULT 14
 AAB48298
 ID AAB48298 standard; protein; 569 AA.
 AC AAB48298;
 XX
 XX 02-APR-2001 (first entry)
 DT
 XX
 DE Human ZF11 protein.
 XX
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.
 OS Homo sapiens.
 OS
 XX MO200075184-A1.
 PN
 XX 14-DEC-2000.
 PD
 XX 05-JUN-2000; 2000WO-US15449.
 PF
 XX 04-JUN-1999; 99US-0137494.
 PR
 XX (UYYA) UNIV YALE.
 PA
 XX Zhang H, Tsvetkov LM, Kondo T;
 PI WPI: 2001-061703/07.
 DR N-PSDB: AAC84610.
 DR
 XX
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 PS Claim 3; Page 130-132; 162pp; English.
 XX
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for

CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 151; DB 22; Length 569;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGHRAAVNVDPDKYIVSASGDRITKW 29
 DB 387 VGHRAAVNVDPDKYIVSASGDRITKW 415
 RESULT 15
 AAM78583
 ID AAM78583 standard; Protein; 579 AA.
 AC AAM78583;
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX
 DE Human protein SEQ ID NO 1245.
 DE
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 OS
 XX WO200157190-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US04098.
 PF
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R.
 PI
 XX WPI: 2001-476283/51.
 DR N-PSDB: AAK51716.
 DR
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 PS Claim 20; Page 3504-3505; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

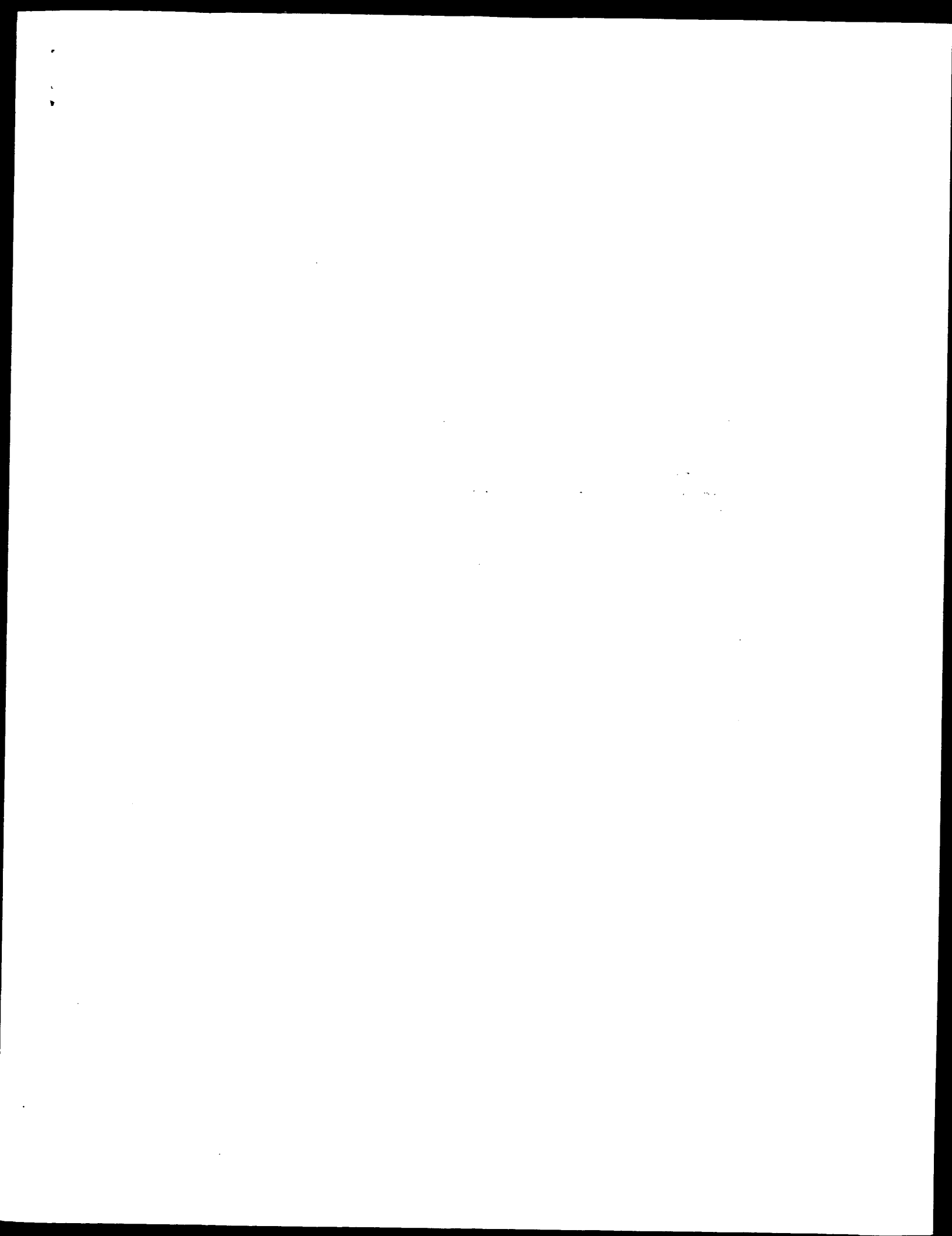
CC (AAM60020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 579 AA;

Query Match 100.0%; Score 151; DB 22; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.3e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVVDFDDKYIVSASGDRITKW 29
 ||||||||||||||||||
 Db 397 VGHRAAVNVVDFDDKYIVSASGDRITKW 425

Search completed: April 11, 2003, 11:48:16
 Job time : 9.93666 secs



GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.00244 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168B-2_COPY_387_415

Perfect score: 151
Sequence: 1 VGHRAAVNVDPDDKIVSASGDRITKW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	151	100.0	517	1 US-08-190-802A-30	Sequence 30, Appl
2	151	100.0	517	4 US-08-477-346-30	Sequence 30, Appl
3	151	100.0	517	4 US-08-473-089-30	Sequence 30, Appl
4	151	100.0	517	4 US-08-487-072A-30	Sequence 86, Appl
5	147	97.4	29	1 US-08-190-802A-86	Sequence 86, Appl
6	147	97.4	29	4 US-08-477-346-86	Sequence 86, Appl
7	147	97.4	29	4 US-08-473-089-86	Sequence 86, Appl
8	147	97.4	29	4 US-08-487-072A-86	Sequence 86, Appl
9	82	54.3	1146	4 US-08-914-999-6	Sequence 6, Appl
10	80	53.0	732	4 US-08-914-999-8	Sequence 6, Appl
11	76	50.3	514	1 US-08-190-802A-66	Sequence 66, Appl
12	76	50.3	514	4 US-08-477-346-66	Sequence 66, Appl
13	76	50.3	514	4 US-08-473-089-66	Sequence 66, Appl
14	75	50.3	514	4 US-08-487-072A-66	Sequence 66, Appl
15	75	49.7	209	3 US-08-899-578-6	Sequence 2, Appl
16	75	49.7	209	3 US-08-899-578-2	Sequence 2, Appl
17	74	49.0	33	1 US-08-190-802A-92	Sequence 92, Appl
18	74	49.0	33	4 US-08-473-089-92	Sequence 92, Appl
19	74	49.0	33	4 US-08-487-072A-92	Sequence 92, Appl
20	74	49.0	33	4 US-08-487-072A-10	Sequence 10, Appl
21	74	49.0	253	4 US-09-724-884-10	Sequence 2, Appl
22	74	49.0	253	4 US-09-724-884-2	Sequence 2, Appl
23	74	49.0	690	4 US-09-291-170A-2	Sequence 2, Appl
24	74	49.0	690	4 US-09-724-884-2	Sequence 31, Appl
25	74	49.0	906	1 US-08-190-802A-31	Sequence 31, Appl
26	74	49.0	906	4 US-08-477-346-31	Sequence 31, Appl
27	74	49.0	906	4 US-08-473-089-31	Sequence 31, Appl

28	74	49.0	906	4 US-08-487-072A-31	Sequence 31, Appl
29	72	47.7	640	4 US-09-177-165A-30	Sequence 30, Appl
30	72	47.7	2627	2 US-08-751-189-3	Sequence 3, Appl
31	72	47.7	2627	2 US-09-060-836-3	Sequence 3, Appl
32	72	47.7	2627	2 US-09-184-445-3	Sequence 4, Appl
33	72	47.7	2629	2 US-08-751-189-4	Sequence 4, Appl
34	71	47.0	2629	2 US-09-060-836-4	Sequence 4, Appl
35	71	47.0	2629	4 US-09-184-445-4	Sequence 4, Appl
36	70	46.4	798	1 US-08-190-802A-64	Sequence 64, Appl
37	70	46.4	798	1 US-08-190-802A-68	Sequence 64, Appl
38	70	46.4	798	2 US-08-308-818-2	Sequence 2, Appl
39	70	46.4	798	4 US-08-477-346-64	Sequence 64, Appl
40	70	46.4	798	4 US-08-477-346-68	Sequence 64, Appl
41	70	46.4	798	4 US-08-473-089-64	Sequence 64, Appl
42	70	46.4	798	4 US-08-473-089-68	Sequence 64, Appl
43	70	46.4	798	4 US-08-487-072A-64	Sequence 64, Appl
44	70	46.4	798	4 US-08-487-072A-68	Sequence 64, Appl
45	69	45.7	29	1 US-08-190-802A-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-0 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R. 33, 875
REGISTRATION NUMBER: 8600-0139
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
AMTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-190-802A-30

Query Match 100.0%; Score 151; DB 1; Length 517;
Best local Similarity 100.0%; Pred. NO. 3.5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VGHRAAVNVDPDDKIVSASGDRITKW 29

DB 351 VGHRAAVNVDFDDKXIVSASGDRITKW 379

RESULT 2

US-08-477-346-30
Sequence 30, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeotf
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match 100.0%; Score 151; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDFDDKXIVSASGDRITKW 29
DB 351 VGHRAAVNVDFDDKXIVSASGDRITKW 379

RESULT 3

US-08-473-089-30
Sequence 30, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeotf
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 100.0%; Score 151; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDFDDKXIVSASGDRITKW 29
DB 351 VGHRAAVNVDFDDKXIVSASGDRITKW 379

RESULT 4

US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeotf
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 100.0%; Score 151; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 3,5e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDDKTYIVSASGDRITIKW 29
Db 351 VGHRAAVNVDFDDKTYIVSASGDRITIKW 379

RESULT 5
US-08-190-802A-86
Sequence 86, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP RIV, Fig. 13
US-08-190-802A-86

Query Match 97.4%; Score 147; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKTYIVSASGDRITIKW 29

Db 1 GHRAAVNVDFDDKTYIVSASGDRITIKW 28
|||||

RESULT 6
US-08-477-346-86
Sequence 86, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP RIV, Fig. 13
US-08-477-346-86

Query Match 97.4%; Score 147; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKTYIVSASGDRITIKW 29
Db 1 GHRAAVNVDFDDKTYIVSASGDRITIKW 28

RESULT 7
US-08-473-089-86
Sequence 86, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rIV, Fig. 13
US-08-473-089-86

Query Match 97.4%; Score 147; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4,6e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHRAAVNVVDFDDKTYIVASGDRITIKYW 29
|||||
DB 1 GHRAAVNVVDFDDKTYIVASGDRITIKYW 28

RESULT 8
US-08-487-072A-86
Sequence 86, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rIV, Fig. 13
US-08-487-072A-86

Query Match 97.4%; Score 147; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4,6e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHRAAVNVVDFDDKTYIVASGDRITIKYW 29
|||||
DB 1 GHRAAVNVVDFDDKTYIVASGDRITIKYW 28

RESULT 9
US-08-914-999-6
Sequence 6, Application US/08914999
Patent No. 6346406
GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey G.
APPLICANT: Halt, William N.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
TITLE OF INVENTION: AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Dictyostellium discoideum
US-08-914-999-6

Query Match 54.3%; Score 82; DB 4; Length 1146;
Best Local Similarity 55.2%; Pred. No. 0.00035;
Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDPDDKTYIVASGDRITKYM 29
DB 951 VGHTEVNCVNAEKYLFSCSYDKITKYM 979

RESULT 10
US-08-914-999-8
Sequence 8, Application US/08914999
Patent No. 6346406
GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey G.
APPLICANT: Pavur, Karen S.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
TITLE OF INVENTION: AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Dictyostellium discoideum
US-08-914-999-8
Query Match 53.0%; Score 80; DB 4; Length 732;
Best Local Similarity 53.6%; Pred. No. 0.00042;
Matches 15; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
OY 2 GHRRAAVNVDPDDKTYIVASGDRITKYM 29
DB 540 GHDKPVHTVLNDKTYLFSSGSDKITKYM 567
RESULT 11
US-08-190-802A-66
Sequence 66, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION/DOCKET NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: YCM2 PROTEIN, Fig. 49
US-08-190-802A-66
Query Match 50.3%; Score 76; DB 1; Length 514;
Best Local Similarity 56.7%; Pred. No. 0.0011;
Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
OY 2 GHRRAAVNVDF--DDKTYIVASGDRITKYM 29
DB 400 GHOKLVNHVAFSPDGRYIVASFSFMSIKLM 429
RESULT 12
US-08-477-346-66
Sequence 66, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: YCW2 PROTEIN, Fig. 49
US-08-477-346-66

Query Match 50.3%; Score 76; DB 4; Length 514;
Best Local Similarity 56.7%; Pred. No. 0.0011;
Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIVASGDRITKYW 29
||: ||| | | : ||||| | : ||: |
Db 400 GHOKLVNHVAFSPDGRYIVASAFDINSIKLM 429

RESULT 13
US-08-473-089-66
Sequence 66, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: YCW2 PROTEIN, Fig. 49
US-08-473-089-66

Query Match 50.3%; Score 76; DB 4; Length 514;

Best Local Similarity 56.7%; Pred. No. 0.0011;
Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
OY 2 GHRAAVNVDF--DDKYIVASGDRITKYW 29
||: ||| | | : ||||| | : ||: |
Db 400 GHOKLVNHVAFSPDGRYIVASAFDINSIKLM 429

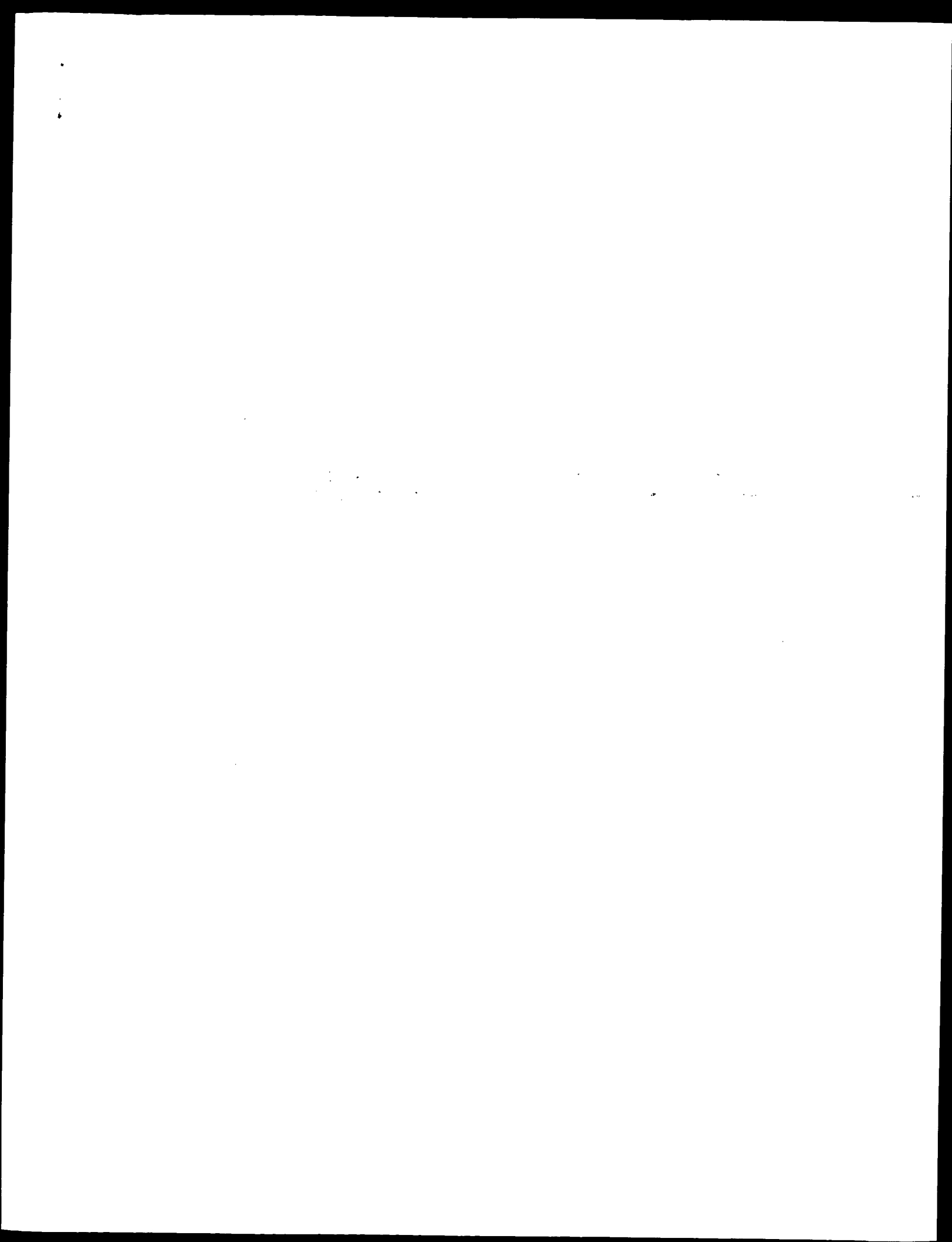
RESULT 14
US-08-487-072A-66
Sequence 66, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: YCW2 PROTEIN, Fig. 49
US-08-487-072A-66

Query Match 50.3%; Score 76; DB 4; Length 514;
Best Local Similarity 56.7%; Pred. No. 0.0011;
Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIVASGDRITKYW 29
||: ||| | | : ||||| | : ||: |
Db 400 GHOKLVNHVAFSPDGRYIVASAFDINSIKLM 429

RESULT 15
US-08-899-578-6
Sequence 6, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP



Fri Apr 11 13:31:11 2003

us-09-601-168b-2_copy_387_415.rapb

Page 1

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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 2.96711 Seconds
(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_387_415
Sequence: 1 VGHRAAVNVDPDDKYIVSASGDRITIKW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	569	9 US-10-038-010-8	Sequence 8, Appl1
2	151	100.0	569	12 US-10-042-417-2	Sequence 2, Appl1
3	83	55.0	678	10 US-09-801-368-314	Sequence 14, App
4	82	54.3	1146	9 US-09-832-292-10	Sequence 10, Appl
5	82	54.3	1146	10 US-09-994-485-6	Sequence 6, Appl1
6	80	53.0	732	10 US-09-994-485-8	Sequence 8, Appl1
7	77	51.0	296	9 US-10-083-357-1300	Sequence 1300, Ap
8	76	50.3	732	9 US-09-832-292-12	Sequence 12, Appl
9	74	49.0	744	10 US-09-925-300-1347	Sequence 1347, Ap
10	72	47.7	485	9 US-10-132-744A-6	Sequence 6, Appl1
11	72	47.7	640	9 US-10-060-019-30	Sequence 30, Appl
12	70	46.4	422	12 US-10-042-417-4	Sequence 4, Appl1
13	69	45.7	159	9 US-09-774-639-247	Sequence 247, App
14	69	45.7	159	9 US-09-969-730-345	Sequence 345, App
15	69	45.7	261	9 US-10-132-744A-4	Sequence 4, Appl1
16	69	45.7	484	9 US-10-132-744A-2	Sequence 2, Appl1
17	69	45.7	540	9 US-09-213-888-7	Sequence 7, Appl1
18	69	45.7	540	9 US-09-213-888-10	Sequence 10, Appl
19	69	45.7	540	9 US-09-328-877A-7	Sequence 7, Appl1

20	69	45.7	540	9 US-09-328-877A-10	Sequence 10, Appl
21	69	45.7	545	9 US-09-213-888-6	Sequence 6, Appl1
22	69	45.7	545	9 US-09-328-877A-6	Sequence 6, Appl1
23	69	45.7	553	9 US-09-213-888-5	Sequence 5, Appl1
24	69	45.7	553	9 US-09-328-877A-5	Sequence 5, Appl1
25	69	45.7	559	9 US-09-213-888-9	Sequence 9, Appl1
26	69	45.7	559	9 US-09-328-877A-9	Sequence 8, Appl1
27	69	45.7	589	9 US-09-213-888-8	Sequence 8, Appl1
28	69	45.7	589	9 US-09-328-877A-8	Sequence 4, Appl1
29	69	45.7	592	9 US-09-213-888-4	Sequence 4, Appl1
30	69	45.7	592	9 US-09-328-877A-4	Sequence 21, Appl
31	69	45.7	626	9 US-09-213-888-21	Sequence 21, Appl
32	69	45.7	626	9 US-09-328-877A-21	Sequence 21, Appl
33	69	45.7	627	9 US-09-213-888-3	Sequence 3, Appl1
34	69	45.7	627	9 US-09-328-877A-3	Sequence 3, Appl1
35	69	45.7	666	9 US-09-213-888-27	Sequence 27, Appl
36	69	45.7	666	9 US-09-328-877A-27	Sequence 27, Appl
37	69	45.7	669	9 US-09-213-888-25	Sequence 25, Appl
38	69	45.7	669	9 US-09-328-877A-25	Sequence 25, Appl
39	69	45.0	521	10 US-09-764-853-449	Sequence 449, App
40	68	45.0	779	9 US-10-060-019-29	Sequence 29, Appl
41	67.5	44.7	372	10 US-09-967-552A-10	Sequence 10, Appl
42	67	44.4	1356	9 US-10-077-111-10	Sequence 10, Appl
43	66	43.7	114	9 US-09-796-692-1445	Sequence 1445, Ap
44	66	43.7	114	9 US-09-796-692-1541	Sequence 1541, Ap
45	66	43.7	114	9 US-09-796-692-1895	Sequence 1895, Ap

ALIGNMENTS

RESULT 1
US-10-038-010-8
Sequence 8, Application US/10038010
Publication No. US2003040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038, 010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259, 377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Beta-Trip1
LOCATION: (1)..(569)
OTHER INFORMATION:
US-10-038-010-8
Query Match 100.0% Score 151; DB 9; Length 569;
Best Local Similarity 100.0% Pred No. 2, 9e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VGHRAAVNVDPDDKYIVSASGDRITIKW 29
Db 387 VGHRAAVNVDPDDKYIVSASGDRITIKW 415
RESULT 2
US-10-042-417-2
Sequence 2, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pasano, M
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 151; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 2,9e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
Db 387 VGHRAAVNVDPDDKYIVSASGDRITKW 415

RESULT 3
US-09-801-368-314
Sequence 314, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 314
LENGTH: 678
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-801-368-314

Query Match 55.0%; Score 83; DB 10; Length 678;
Best Local Similarity 50.0%; Pred. No. 0.00011;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 GHRAAVNVDPDDKYIVSASGDRITKW 29
Db 387 GHRAAVNVDPDDKYIVSASGDRITKW 414

RESULT 4
US-09-832-292-10
Sequence 10, Application US/09832292
Patent No. US20020177205A1
GENERAL INFORMATION:
APPLICANT: Ryzanov, Alexey
APPLICANT: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF

FILE REFERENCE: 601-1-098CIP
CURRENT APPLICATION NUMBER: US/09/832,292
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/632,131
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 1146
TYPE: PRT
ORGANISM: Dictyostelium discoideum
US-09-832-292-10

Query Match 54.3%; Score 82; DB 9; Length 1146;
Best Local Similarity 55.2%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
Db 951 VGHTEGVNCVANKYILFSCSYDKITKW 979

RESULT 5
US-09-994-485-6
Sequence 6, Application US/09994485
Patent No. US20020142429A1
GENERAL INFORMATION:
APPLICANT: Ryzanov, Alexey G.
Halt, William N.
Pavur, Karen S.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/994,485
FILING DATE: 27-NO. US20020142429A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Dictyostelium discoideum
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-994-485-6

Query Match 54.3%; Score 82; DB 10; Length 1146;
Best Local Similarity 55.2%; Pred. No. 0.00029;
Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDDKXYIVSASGDRITKW 29
||| | : : : : :
Db 951 VGHTEVNCVANEKYLFCSDYDKITKW 979

RESULT 6
US-09-994-485-8
; Sequence 8, Application US/09994485
; Patent No. US20020142429A1

GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey G.
Halt, William N.
Pavur, Karen S.

TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/994,485
FILING DATE: 27-NO. US20020142429A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5600
TELEFAX: 201-487-1684

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Dictyostelium discoideum
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-994-485-8

Query Match 53.0%; Score 80; DB 10; Length 732;
Best Local Similarity 53.6%; Pred. No. 0.00035;
Matches 15; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKXYIVSASGDRITKW 29
||| | : : : : :
Db 540 GHDKPVTHVLNDKYLFGSSSDKITKW 567

RESULT 7
US-10-083-357-1300
; Sequence 1300, Application US/10083357
; Publication No. US20030054370A1

GENERAL INFORMATION:
APPLICANT: Oidong zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1300
LENGTH: 296
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae

US-10-083-357-1300

Query Match 51.0%; Score 77; DB 9; Length 296;
Best Local Similarity 50.0%; Pred. No. 0.00035;
Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKXYIVSASGDRITKW 29
||| | : : : : :
Db 182 GHRAVLGLGLSDKFLVSVSDGIRCW 209

RESULT 8
US-09-832-292-12
; Sequence 12, Application US/09832292
; Patent No. US20020177205A1

GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey
TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
THERAPEUTIC USES THEREOF
FILE REFERENCE: 601-1-098CIP
CURRENT APPLICATION NUMBER: US/09/832,292
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/632,131
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 732
TYPE: PRT
ORGANISM: Dictyostelium discoideum

US-09-832-292-12

Query Match 50.3%; Score 76; DB 9; Length 732;
Best Local Similarity 53.6%; Pred. No. 0.0014;
Matches 15; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKXYIVSASGDRITKW 29
||| | : : : : :
Db 540 GHDKPVTHVLNDKYLFGSSSDKITKW 567

RESULT 9
US-09-925-300-1347
; Sequence 1347, Application US/09925300
; Patent No. US20020151681A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
Steve Ruden,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1347
LENGTH: 744
TYPE: PRT
ORGANISM: Homo sapiens

US-09-925-300-1347

Query Match 50.0%; Score 77; DB 9; Length 296;
Best Local Similarity 50.0%; Pred. No. 0.00035;
Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKXYIVSASGDRITKW 29
||| | : : : : :
Db 540 GHDKPVTHVLNDKYLFGSSSDKITKW 567

RESULT 9
US-09-925-300-1347
; Sequence 1347, Application US/09925300
; Patent No. US20020151681A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
Steve Ruden,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1347
LENGTH: 744
TYPE: PRT
ORGANISM: Homo sapiens

US-09-925-300-1347

TYPE: PRT
ORGANISM: *Saccharomyces cerevisiae*

147-600-4110

Matches 14; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

QY 2 GHRAAVNVDF--DKYIVSASGDRTIKW 29

Db 72 GHQALINQVLFSPDSRIVASASFDKSIKLM 101

```

RESULT 14
US-09-969-730-345
; Sequence 345, Application US/09969730
; Publication No. US20030054443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 345

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; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (63)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-969-730-345

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Query Match 45.7%; Score 69; DB 9; Length 159;
Best Local Similarity 46.7%; Pred. No. 0.0029;
Matches 14; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

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Qy 2 GHRAAVNVDF--DDKYIVASGDRITKW 29

Db 72 GHQALINQVLFSPDSRIVASASFDKSIKLM 101

```

RESULT 15
US-10-132-744A-4
; Sequence 4, Application US/10132744A
; Publication No. US20030027261A1
; GENERAL INFORMATION:
; APPLICANT: Utku, Nalan
; TITLE OF INVENTION: No. US20030027261A1 genes Tzap7/A, Tzap7/B and Tzap7 involve
; FILE REFERENCE: Utku-4 CON
; CURRENT APPLICATION NUMBER: US/10/132,744A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: PCT/EP00/10670
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/185,016
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/162,675
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-744A-4

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Query Match 45.7%; Score 69; DB 9; Length 261;
Best Local Similarity 46.7%; Pred. No. 0.0052;
Matches 14; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

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Qy 2 GHRAAVNVDF--DDKYIVASGDRITKW 29

Db 146 GHQALINQVLFSPDSRIVASASFDKSIKLM 175

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Search completed: April 10, 2003, 13:16:46
Job time : 3.96711 secs

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1. The first part of the document is a list of names and addresses of the members of the committee.

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.35566 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_387_415
Perfect score: 151
Sequence: 1 VGHRAAVNVVDFDDKIIVSASGDRITIKVW 29

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pIR:73:*
2: pIR1:*
3: pIR3:*
4: pIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	100.0	518	2 B48088	beta-transducin re
2	148	98.0	701	2 T16607	hypothetical prote
3	85	56.3	650	2 T46660	sulfur controller
4	83	55.0	934	2 AG1889	WD-40 repeat prote
5	82	54.3	1146	2 A55532	myosin-heavy chain
6	81	53.6	925	2 T29585	hypothetical prote
7	79	53.3	1551	2 AB2410	WD-repeat protein
8	77	51.7	1747	2 AC1842	WD-40 repeat prote
9	77	51.0	185	2 S50566	hypothetical prote
10	77	51.0	319	2 S54578	hypothetical prote
11	76	50.3	515	2 S19487	hypothetical prote
12	75	49.7	530	2 T20360	hypothetical prote
13	75	49.7	571	2 T20359	hypothetical prote
14	75	49.7	579	2 T22703	hypothetical prote
15	75	49.7	1258	2 A12155	WD-repeat protein
16	74	49.0	535	2 S48268	probable membrane
17	74	49.0	906	2 S35342	Golgi-associated p
18	74	49.0	906	2 S35312	coatomer complex b
19	74	49.0	1189	2 AH2154	WD-repeat protein
20	74	49.0	1711	2 AD1842	WD-40 repeat prote
21	73	48.3	267	2 S62507	hypothetical lrp-a
22	73	48.3	325	2 T06784	GTP-binding protei
23	73	48.3	325	2 T09613	probable GTP-bind
24	73	48.3	327	2 S48839	guanine nucleotide
25	73	48.3	506	2 T50211	WD-repeat protein
26	72	47.7	334	2 T03764	protein RMD - rice
27	72	47.7	640	2 S49932	Mer130 protein - ye
28	72	47.7	876	2 T51507	WD0-repeat protei
29	71	47.0	303	2 S45461	hypothetical prote

30	71	47.0	473	2 T33805	hypothetical prote
31	71	47.0	943	2 S59317	DIP2 protein - yea
32	71	47.0	1683	2 AF2071	WD-40 repeat prote
33	71	47.0	1693	2 S76086	beta transducin-li
34	71	47.0	2629	2 T30987	telomerase-associa
35	71	47.0	2629	2 T32735	telomerase-associa
36	70	46.4	290	2 T02300	GTP-binding regula
37	70	46.4	316	2 S57839	CPC2 protein - Neu
38	70	46.4	317	2 T46032	WD-40 repeat regul
39	70	46.4	372	2 T15181	hypothetical prote
40	70	46.4	559	2 AB2202	hypothetical prote
41	70	46.4	586	2 T38992	WD-40 repeat regul
42	70	46.4	798	2 S34023	TATA box-binding p
43	70	46.4	889	2 B55123	coatomer complex b
44	70	46.4	1269	2 T00443	hypothetical prote
45	70	46.4	1389	2 H84914	probable WD-40 rep

ALIGNMENTS

RESULT 1
B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trop
C:Species: Xenopus laevis (African clawed frog)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; M01D:93330289; PMID:8393141
A:Accession: B48088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SP>
A:Cross-references: GB:098268; NID:9295542; PIDN:AAA02810.1; PID:9295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <MD1>

Query Match 100.0%; Score 151; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VGHRAAVNVVDFDDKIIVSASGDRITIKVW 29
Db 352 VGHRAAVNVVDFDDKIIVSASGDRITIKVW 380

RESULT 2

T16607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16607
R:Miller, N.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: Z18545
A:Accession: T16607
A:Status: preliminary; translated from GH/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-701 <MD1>
A:Cross-references: EMBL:U28730; NID:9860694; PID:9860695; PIDN:AAA68258.1; CESP:K10B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.1
A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
Query Match 98.0%; Score 148; DB 2; Length 701;
Best Local Similarity 96.6%; Pred. No. 1.1e-13;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDDKYIVSASGDRITKW 29
 DB 378 VGHRAAVNVDFDDKYIVSASGDRITKW 406

RESULT 3

T46660
 C:Species: Neurospora crassa
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
 C:Accession: T46660
 R:Kumar, A.; Paletta, J.V.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
 A:Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a
 A:Accession: T46660
 A:Reference number: 223121; MUID:95241499; PMID:7724564
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-650 <KUR>
 A:Cross-references: EMBL:U17251; NID:g806757; PIDN:AAA68968.1; PID:g806758
 C:Genetics:
 A:Gene: scon-2
 A:Map position: 3
 A:Introns: 75/3; 319/1; 354/1
 C:Function:
 A:Description: negatively regulates sulfur structural gene expression
 A:Note: scon-2+ expression is dependent on Cys3 function and the binding of Cys3 to the
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 56.3%; Score 85; DB 2; Length 650;
 Best Local Similarity 51.7%; Pred. No. 0.0002;
 Matches 15; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDDKYIVSASGDRITKW 29
 DB 331 VGHTRAGIRALQFPDSKILSGSDHTIKW 359

RESULT 4

AGI889
 WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AGI889
 R:Kaneoko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AGI889
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-934 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA872622.1; PID:917130010; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al10664

Query Match 55.0%; Score 83; DB 2; Length 934;
 Best Local Similarity 56.7%; Pred. No. 0.00059;
 Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRRAAVNVDFDDKYIVSASGDRITKW 29
 DB 530 GHONGVNVSTFSPDGKLIATASGDRITKW 559

RESULT 5
 A55532
 myosin-heavy-chain kinase (EC 2.7.1.129) A - slime mold (Dictyostelium discoideum)
 C:Species: Dictyostelium discoideum

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000
 C:Accession: A55532
 R:Fuley, L.M.; Medley, Q.G.; Cole, G.P.; Egelhoff, T.T.
 J. Biol. Chem. 270, 523-529, 1995
 A:Title: Structural analysis of myosin heavy chain kinase A from Dictyostelium. Evid
 the beta-subunit of heterotrimeric G proteins.
 A:Reference number: A55532; MUID:95122486; PMID:7822274
 A:Accession: A55532
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1146 <FUT>
 A:Cross-references: GB:U16856; NID:g608519; PIDN:AAA66070.1; PID:g608520
 C:Genetics:
 A:Introns: #status absent
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

C:Keywords: autophosphorylation; coiled coil; multimer; phosphoprotein; phosphotransf
 F:865-898/Domain: WD repeat homology <MD1>
 F:950-981/Domain: WD repeat homology <MD2>
 F:991-1022/Domain: WD repeat homology <MD3>
 F:1031-1062/Domain: WD repeat homology <MD4>
 F:1071-1102/Domain: WD repeat homology <MD5>
 F:1112-1143/Domain: WD repeat homology <MD6>

Query Match 54.3%; Score 82; DB 2; Length 1146;
 Best Local Similarity 55.2%; Pred. No. 0.001;
 Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDDKYIVSASGDRITKW 29
 DB 951 VGHTEVNCVAVNEKYLFCSDYDRTIKW 979

RESULT 6

T29585
 hypothetical protein F55F8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
 C:Accession: T29585
 R:Gatung, S.; Scheet, P.; Kemp, K.
 submitted to the EMBL data library, November 1996
 A:Description: The sequence of C. elegans cosmid F55F8.
 A:Reference number: Z20647
 A:Accession: T29585
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-925 <GAT>
 A:Cross-references: EMBL:U060447; PIDN:AA837807.1; GSPDB:GN00019; CESP:F55F8.3
 A:Experimental source: strain Bristol N2; clone F55F8
 C:Genetics:
 A:Gene: CESP:F55F8.3
 A:Map position: 1
 A:Introns: 6/3; 44/2; 76/1; 109/2; 159/2; 204/3; 327/1; 469/3; 617/1; 775/1; 825/3; 8
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 53.6%; Score 81; DB 2; Length 925;
 Best Local Similarity 50.0%; Pred. No. 0.0011;
 Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHRRAAVNVDFDDKYIVSASGDRITKW 29
 DB 486 GHESAIISSIDHGNHIVSGSMRTIKW 513

RESULT 7

AB2410
 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AB2410
 R:Kaneoko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2410
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1551 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA076533.1; PID:g17133971; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4834

Query Match 52.3%; Score 79; DB 2; Length 1551;
Best Local Similarity 46.7%; Pred. No. 0.004;
Matches 14; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIYASGDRITIKW 29
DB 1484 GHRGAVRSISIPDQYIATASDDRTVKLM 1513

RESULT 8

WD:40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC1842
R:Ranko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC1842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1747 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA077807.1; PID:g17135261; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0283

Query Match 51.7%; Score 78; DB 2; Length 1747;
Best Local Similarity 53.3%; Pred. No. 0.0064;
Matches 16; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIYASGDRITIKW 29
DB 1135 GHRGAVNVAVSFDPGKYLASASDDRTVKLM 1164

RESULT 9

S50569
hypothetical protein YER066w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C:Accession: S50569
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A:Reference number: S50427

A:Accession: S50569
A:Molecule type: DNA
A:Residues: 1-185 <DIE>
A:Cross-references: EMBL:U01813; NID:g1381127; PIDN:AAB64602.1; PID:g603302; MIPS:YER066

C:Genetics:
A:Cross-references: SGD:S0000868

A:Map position: 5R
C:Superfamily: Saccharomyces hypothetical protein YER066w; WD repeat homology

C:Keywords: duplication
F:7-40/Domain: WD repeat homology <WD1>
F:69-100/Domain: WD repeat homology <WD2>

Query Match 51.0%; Score 77; DB 2; Length 185;

Best Local Similarity 50.0%; Pred. No. 0.00077;
Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHRAAVNVDFDDKYIYASGDRITIKW 29
DB 71 GHRALVGLISLSDKFLVASVDSISRCW 98

RESULT 10

S54578
hypothetical protein YMR16c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YMR16c; YMR16c; hypothetical protein YMR16c.15c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 26-May-2000
C:Accession: S54578; S54577

R:Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54510

A:Accession: S54578
A:Molecule type: DNA
A:Residues: 1-319 <HUN>
A:Cross-references: EMBL:Z49702; NID:g817859; PIDN:CAA89754.1; PID:g817876; MIPS:YMR1

A:Experimental source: strain AB972

A:Accession: S54577
A:Molecule type: DNA
A:Residues: 221-319 <HUN>
A:Cross-references: EMBL:Z49702; NID:g817859; PIDN:CAA89753.1; PID:g817875; MIPS:YMR1

A:Experimental source: strain AB972

C:Genetics:
A:Gene: SGD:BEL1
A:Cross-references: SGD:S0004722; MIPS:YMR16c

A:Map position: 13R
A:Introns: 179/3

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

F:13-47/Domain: WD repeat homology <WD1>
F:61-94/Domain: WD repeat homology <WD2>

F:103-136/Domain: WD repeat homology <WD3>
F:144-183/Domain: WD repeat homology <WD4>

F:192-225/Domain: WD repeat homology <WD5>
F:235-265/Domain: WD repeat homology <WD6>

F:283-315/Domain: WD repeat homology <WD7>

Query Match 51.0%; Score 77; DB 2; Length 319;
Best Local Similarity 54.8%; Pred. No. 0.0014;
Matches 17; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

OY 1 VGHRAVNVDFDDK--YIVSASGDRITIKW 29
DB 104 VGHKSDVMSVDIDDKKASMIISGRDKTITKW 134

RESULT 11

S19487
hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 19-Apr-2002
C:Accession: S19487; S26557
R:Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sanz, E.

submitted to the Protein Sequence Database, March 1992
A:Reference number: S19486

A:Accession: S19487
A:Molecule type: DNA
A:Residues: 1-484, 1,486, 1,490, 492-515 <BAL1>

A:Cross-references: EMBL:X59720; MIPS:YCR072c
A:Note: this sequence has been revised in reference S26557

submitted to the Protein Sequence Database, October 1992
A:Reference number: S26587

A:Accession: S26557
A:Molecule type: DNA

A:Residues: 481-503 <BAL2>
A:Cross-references: EMBL:X59720; MIPS:YCR072c

C:Genetics:

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A:Cross-references: SCD:S0000668
A:Map position: 3R
E:Superfamily: unassigned WD repeat proteins; WD repeat homology
F:182-215/Domain: WD repeat homology <MD2>
F:223-265/Domain: WD repeat homology <MD3>
F:274-306/Domain: WD repeat homology <MD4>
F:398-431/Domain: WD repeat homology <MD5>
F:440-473/Domain: WD repeat homology <MD6>

Query Match      50.3%; Score 76; DB 2; Length 515;
Best Local Similarity 56.7%; Pred. No. 0.0033;
Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1

OY 2 GHRAAVNVDF--DDKYIVASGDRITKW 29
   || | | | | | | | | | | | | | |
Db 400 GHQKLVNHVAFSPDGRYIVASFSDNSIKIM 429

RESULT 12
T20360
hypothetical protein D2030.9b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20360
R:Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19261
A:Accession: T20360
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-530 <MIL>
A:Cross-references: EMBL:Z73906; PIDN:CAB54209.1; GSPDB:GN00019; CESP:D2030.9b
A:Experimental source: Clone D2030
C:Gene: CESP:D2030.9b
A:Map position: 1
A:Introns: 13/3; 60/3; 144/1; 226/2; 296/3; 356/3; 427/1; 462/3

Query Match      49.7%; Score 75; DB 2; Length 530;
Best Local Similarity 53.3%; Pred. No. 0.0048;
Matches 16; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIVASGDRITKW 29
   || | | | | | | | | | | | | | |
Db 316 GHRDGVTHVDSQDERYLISKSQTIKW 345

RESULT 13
T20359
hypothetical protein D2030.9a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20359
R:Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19261
A:Accession: T20359
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-571 <MIL>
A:Cross-references: EMBL:Z73906; PIDN:CAA98121.1; GSPDB:GN00019; CESP:D2030.9a
A:Experimental source: clone D2030
C:Gene: CESP:D2030.9a
A:Map position: 1
A:Introns: 29/1; 54/3; 101/3; 185/1; 267/2; 337/3; 397/3; 468/1; 503/3

Query Match      49.7%; Score 75; DB 2; Length 571;
Best Local Similarity 53.3%; Pred. No. 0.0052;
Matches 16; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

OY 2 GHRAAVNVDF--DDKYIVASGDRITKW 29
   || | | | | | | | | | | | | | |

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Db      357  GHRDGVTHVDSRQDERYLLTNSKDOTIKW 386

RESULT 14
T22703
hypothetical protein F55B12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22703
R:Sim, M.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19602
A:Accession: T22703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-579 <MULT>
A:Cross-references: EMBL:Z79757; PIDN:CA802129.1; GSPDB:GN00023; CESP:F55B12.3
C:Genetics:
A:Experimental source: clone F55B12
A:Gene: CESP:F55B12.3
A:Map position: 5
A:Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1

Query Match      49.7%; Score 75; DB 2; Length 579;
Best Local Similarity 50.0%; Pred. No. 0.0053;
Matches 14; Conservative 3; Mismatches 11; Gaps 0; Indels 0;

QY      2  GHRAAVNVDFDDKRYIVASGDRTRIKW 29
      ||||| ||| ||| ||| |||
Db      368  GHHAARVCGVFDGTTIVSGGYDFYKIKW 395

RESULT 15
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
A:12155
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: A12155
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyama, N.; Shimpo, S.; Sugimoto, M.; Takezawa, M.; Yamada, M.; Yasuda, M.; Tabatake, N.; Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takezawa, M.; Yamada, M.; Yasuda, M.; Tabatake, N.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Nostoc sp. strain PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1258 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAE74499.1; PID:q17131893; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2800

Query Match      49.7%; Score 75; DB 2; Length 1258;
Best Local Similarity 48.4%; Pred. No. 0.012;
Matches 15; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

QY      1  VGHRAAVNVDF--DDKRYIVASGDRTRIKW 29
      || | | : | | ||| ||| |||
Db      849  IGHITNSVSYIAVSPDSKILVSGSDRTIKLW 879

Search completed: April 10, 2003, 13:23:03
Job time : 3.35566 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model1

Run on: April 10, 2003, 12:51:26 ; Search time 2.08404 Seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_387_415

Perfect score: 151
Sequence: 1 VGHRAAVNVVDFDDKYIVASGDRLTKVW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_40:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	518	1 TRCB_XENLA	Q91854 xenopus lae
2	151	100.0	542	1 FM1B_HUMAN	Q9ukb1 homo sapien
3	151	100.0	605	1 FM1A_HUMAN	Q9y297 homo sapien
4	148	98.0	665	1 LI23_CAEEL	Q09990 caenorhabdi
5	85	56.3	650	1 SCOB_NEUCR	Q01277 neurospora
6	83	55.0	678	1 SCOB_EMENT	Q00659 ementella
7	82	54.3	1146	1 KHALDICTI	P42527 dictyosteli
8	81	53.6	910	1 PMW2_CAEEL	P91341 caenorhabdi
9	80	53.0	732	1 KMBB_DICDI	P40042 dictyosteli
10	77	51.0	185	1 YEP6_YEAST	P38011 saccharomyc
11	77	51.0	319	1 GBLP_YEAST	P23382 saccharomyc
12	76	50.3	515	1 YCWL_YEAST	P90794 caenorhabdi
13	75	49.7	571	1 YR1Q_CAEEL	Q93794 caenorhabdi
14	75	49.7	579	1 SET10_CAEEL	O62621 dictyosteli
15	75	49.7	914	1 COPP_DROME	Q8YLC2 anabadena sp
16	75	49.7	1258	1 YS00_ANASP	P38262 saccharomyc
17	74	49.0	535	1 SIR2_YEAST	O35142 rattus norv
18	74	49.0	904	1 COPP_RAT	P35605 bos taurus
19	74	49.0	905	1 COPP_BOVIN	P35606 homo sapien
20	74	49.0	905	1 COPP_HUMAN	O55029 mus musculu
21	74	49.0	905	1 COPP_MOUSE	O24076 medicago sa
22	73	48.3	325	1 GBLP_MEDSA	Q34836 glycyline max
23	73	48.3	325	1 GBLP_SOYBN	Q34456 arabidopsis
24	73	48.3	327	1 GBLP_ARATH	Q33336 brassica na
25	73	48.3	327	1 GBLP_BRANA	O09855 schizosacch
26	73	48.3	506	1 PORB_SCHPO	P53699 candida alb
27	73	48.3	684	1 CC4_CANAL	P49027 oryza sativ
28	72	47.7	640	1 GBLP_ORYSA	P39014 saccharomyc
29	72	47.7	640	1 MT30_YEAST	P43138 saccharomyc
30	71	47.0	303	1 YNA6_YEAST	Q12220 saccharomyc
31	71	47.0	943	1 DIP2_YEAST	O8YV57 anabadena sp
32	71	47.0	1683	1 YL24_ANASP	Q55563 synecocyst
33	71	47.0	1693	1 Y163_SYNY3	

34	70	46.4	316	1 GBLP_NEUCR	Q01369 neurospora
35	70	46.4	422	1 FBW2_HUMAN	Q9ukb1 homo sapien
36	70	46.4	586	1 TU12_SCHPO	Q9uug8 schizosacch
37	70	46.4	798	1 T2D4_YEAST	P38129 saccharomyc
38	70	46.4	889	1 COPP_YEAST	P41811 saccharomyc
39	69	45.7	715	1 DOA1_YEAST	P36037 saccharomyc
40	68.5	45.4	525	1 COZ2_HUMAN	Q92828 homo sapien
41	68	45.0	604	1 RCO1_NEUCR	P78706 neurospora
42	68	45.0	605	1 RCO1_NEUCR	P87053 schizosacch
43	68	45.0	614	1 TU11_SCHPO	O09715 schizosacch
44	68	45.0	651	1 Y1X1_SCHPO	O9p713 schizosacch
45	68	45.0	703	1 POP2_SCHPO	O14170 schizosacch

ALIGNMENTS

RESULT 1
ID TRCB_XENLA STANDARD: PRT; 518 AA.
AC Q91854: P70037: P70038:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-TRCP (beta-transducin repeat-containing protein).
GN FBXW1 OR BTCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330289; PubMed=8393141;
RA Spevak W., Keiper B.D., Stratawa C., Castanon M.J.;
RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
RT anaphase are rescued by Xenopus CDNs encoding N-ras or a protein
RT with beta-transducin repeats."
RL Mol. Cell. Biol. 13:4953-4966(1993).
RN [2]
RP SEQUENCE OF 302-518 FROM N.A.
RX MEDLINE=97109804; PubMed=8952061;
RA Hudson J.W., Alarcon V.B., Ellinson R.P.;
RT "Identification of new localized RNAs in the Xenopus oocyte by
RT differential display PCR."
RL Dev. Genet. 19:190-198(1996).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
CC MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
CC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
CC NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
CC TADPOLE EMBRYO.
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 FD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
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CC
CC EMBL: M98268: AAA02810.1; -
CC EMBL: U63921: AAB49671.1; -
CC EMBL: U63922: AAB49672.1; -
CC InterPro: IPR001810; F-box.
CC InterPro: IPR001680; WD40.
CC Pfam: PF00400; WD40; 7.

DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat: WD repeat.
 KW Ubl conjugation pathway; Repeat: WD repeat.
 FT DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.
 FT REPEAT 502 510 WD 7.
 FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
 FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
 SO SEQUENCE 518 AA; 59507 MW; 2A52EC19028127F3 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDFDKYIVSASGDRITKVV 29
 DB 352 VGHRAAVNVDFDKYIVSASGDRITKVV 380

RESULT 2

FWIB_HUMAN STANDARD; PRT; 542 AA.
 AC Q9YKBL; Q9YKBL; Q9P2S8; Q9P2S9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP2).
 GN FBXW1B OR FBXW1 OR BTCP2 OR KIAA0696.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RT Pagano M.;
 RL "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Fetal lung;
 RX MEDLINE=20160458; PubMed=10694485;
 RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katoh M.;
 RT "Molecular cloning and genomic structure of the betaTRCP2 gene on
 RT chromosome 5q35.1.";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AND C (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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DR EMBL: AF176022; AAF04528.1; -;
 DR EMBL: AB033279; BAA92329.1; -;
 DR EMBL: AB033280; BAA92330.1; -;
 DR EMBL: AB033281; BAA92331.1; -;
 DR EMBL: AB014596; BAA31671.1; ALT_INIT.
 DR Genew: HGNC:13607; FBXW1B.
 DR MIM: 605651; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat: WD repeat; Alternative splicing.
 FT DOMAIN 129 157 F-BOX.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPIC 16 49 WD 7.
 FT VARSPIC 16 48 MISSING (IN ISOFORM A).
 FT VARSPIC 16 48 CSVPSRLMLGCAIVESKALCSLOSMPVRCVCL -> NTSV
 MEDONEDSPKRLTM (IN ISOFORM B).
 SO SEQUENCE 542 AA; 62090 MW; 7CD40087EFAA5C8A CRC64;

Query Match 100.0%; Score 151; DB 1; Length 542;
 Best Local Similarity 100.0%; Pred. No. 6e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

FWIA_HUMAN STANDARD; PRT; 605 AA.
 AC Q9Y297; Q9Y213;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP)
 DE (E3RSIKappab) (pikappabalpha-E3 receptor subunit).
 GN FBXW1A OR FBW1A OR BTCP OR BTCP.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996;

RA Varon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the I-kappaBalpha-
 RT ubiquitin ligase.";
 RL Nature 396:590-594(1998).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940;
 RA Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.;
 RT "A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif.";
 RL Mol. Cell 1:565-574(1998).
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN (4)
 RP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
 RA Harper J.W.;
 RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and
 RT beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
 RL Genes Dev. 13:270-283(1999).
 CC -1- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKR ALPHA
 CC (PIKAPPAALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR
 CC UBIQUITINATION AND DEGRADATION.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: AF101784; AAD08702.1; -
 CC EMBL: Y14153; CAA74572.1; -
 CC EMBL: AF129530; AAF04464.1; -
 CC Genew: HGNC:1144; BTRC.
 DR MIM: 603482; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 KW DOMAIN 190 228
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT

FT REPEAT 553 590 WD 7.
 FT VARSPIC 17 52 MISSING (IN ISOFORM 2).
 SO SEQUENCE 605 AA: 68866 MW: 4667F3B7EA00FD37 CRC64:
 Query Match 100.0%; Score 151; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 6.8e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGHRAAVNVDFDDKIVYSASGDTIKVW 29
 DB 423 VGHRAAVNVDFDDKIVYSASGDTIKVW 451
 RESULT 4
 ID LI23_CAEEL STANDARD; PRT; 665 AA.
 AC Q09990; Q9GNN6;
 DT 15-JUL-1998 (Rel. 36, Created)
 DR 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein lin-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RX MEDLINE=20515608; PubMed=11060233;
 RA Kipreos E.T., Gohel S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein lin-23 functions
 RT to limit cell division during development.";
 RL Development 127:5071-5082(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 CC cycle progression. Required to restrain cell proliferation in
 CC response to developmental cues. Probably recognizes and binds to
 CC some proteins and promotes their ubiquitination and degradation
 CC (By similarity).
 CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 CC levels in larvae. Maternal expression results in high zygotic
 CC levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO X.LAEVIS PAX1.
 CC -----
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 CC -----
 CC EMBL: AF275253; AAG28037.1; -
 CC EMBL: U28730; AAA68258.2; -
 CC WormPep: K10B2.1; CE28600.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.


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FT DOMAIN 178 224 F-BOX.
FT REPEAT 347 375
FT REPEAT 387 415 WD 1.
FT REPEAT 427 455 WD 2.
FT REPEAT 466 496 WD 3.
FT REPEAT 508 543 WD 4.
FT REPEAT 553 595 WD 5.
FT REPEAT 607 635 WD 6.
FT REPEAT 647 675 WD 7.
FT REPEAT 675 695 WD 8.
SQ SEQUENCE 678 AA; 76070 MM; D840D452E37B4C53 CRC64;

Query Match 55.0%; Score 83; DB 1; Length 678;
Best Local Similarity 50.0%; Pred. No. 0.00012;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 2 GHRAAVNVDPDDKYIVASAGDRTIKYW 29
Db 387 GHESGICRLCPDDTKLISGMDRTIKYW 414

RESULT 7
KMH_A_DICDI STANDARD; PRT; 1146 AA.
ID KMH_A_DICDI
AC P42527;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Myosin heavy chain kinase A (EC 2.7.1.129) (MHCK A).
GN MHKA OR MHCKA.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=AX3.
RX MEDLINE=95122486; PubMed=7822274;
RA Futey L.M., Medley O.G., Cote G.P., Eggehoff T.T.;
RT "Structural analysis of myosin heavy chain kinase A from
RT Dictyostellum. Evidence for a highly divergent protein kinase domain,
RT an amino-terminal coiled-coil domain, and a domain homologous to the
RT beta-subunit of heterotrimeric G proteins.";
RL J. Biol. Chem. 270:523-529(1995).
RN [2]
RP CHARACTERIZATION OF THE CATALYTIC DOMAIN.
RC STRAIN=AX3;
RX MEDLINE=97207233; PubMed=9054368;
RA Cote G.P., Luo X., Murphy M.B., Eggehoff T.T.;
RT "Mapping of the novel protein kinase catalytic domain of
RT Dictyostellum myosin II heavy chain kinase A.";
RL J. Biol. Chem. 272:6846-6849(1997).
CC -1- FUNCTION: PHOSPHORYLATES THREONINE IN THE C-TERMINAL TAIL REGION
CC OF MYOSIN II HEAVY CHAIN. THIS PHOSPHORYLATION IS CRITICAL IN
CC REGULATING THE ASSEMBLY AND DISASSEMBLY OF MYOSIN II FILAMENT.
CC REQUIRES AUTOHOSPHORYLATION FOR ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + [myosin heavy-chain] = ADP + [myosin
CC heavy-chain] phosphate.
CC -1- COFACTOR: MAGNESIUM OR MANGANESE.
CC -1- SUBUNIT: OLIGOMER.
CC -1- DOMAIN: CONSISTS OF AN N-TERMINAL DOMAIN WITH PROBABLE COILED COIL
CC STRUCTURE, A CENTRAL NONREPETITIVE CATALYTIC DOMAIN, AND A C-
CC TERMINAL DOMAIN WITH SEVEN WD REPEATS.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE MHCK / EF-2 PROTEIN KINASE FAMILY.
CC -----
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DR EMBL: U016856; AAA66070.1: -.
DR DictDb: DD01086; mhkA.
DR InterPro: IPR004166; MCKC_EF2_Kinase.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR02816; MCKC_EF2_Kinase; 1.
DR ProDom: PD000018; GPROTEINRPT.
DR SMART: SM00320; WD40; 3.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS00682; WD_REPEATS_2; 5.
DR PROSITE: PS00294; WD_REPEATS_REGION; 1.
DR TransEsterase_Serine/threonine-protein kinase; ATP-Binding; Repeat;
KW WD Repeat; Phosphorylation; Coiled coil.
FT DOMAIN 100 120 COILED COIL (POTENTIAL).
FT DOMAIN 144 148 POLY-GLN.
FT DOMAIN 175 181 POLY-GLY.
FT DOMAIN 187 241 COILED COIL (POTENTIAL).
FT DOMAIN 297 502 COILED COIL (POTENTIAL).
FT DOMAIN 345 348 POLY-SER.
FT DOMAIN 438 441 POLY-LEU.
FT DOMAIN 500 551 PSEUDOSUBSTRATE/AUTOINHIBITORY DOMAIN
(POTENTIAL).
FT FT 552 852 CATALYTIC.
FT NP_BIND 778 783 ATP (POTENTIAL).
FT REPEAT 867 897 WD 1.
FT REPEAT 910 938 WD 2.
FT REPEAT 952 980 WD 3.
FT REPEAT 993 1021 WD 4.
FT REPEAT 1033 1061 WD 5.
FT REPEAT 1073 1101 WD 6.
FT REPEAT 1114 1142 WD 7.
SQ SEQUENCE 1146 AA; 128945 MW; 98D831F7948B5573 CRC64;

Query Match 54.3%; Score 82; DB 1; Length 1146;
Best Local Similarity 55.2%; Pred. No. 0.00031;
Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 VGHRAAVNVYDEDDPKYIVASGDRIRKYW 29
||| ||| ::||| :||| ||| ||| |||
Db 951 VGHTEGVNCAVNAEKYLFSCSYDKIRKYW 979

RESULT 8
PMP2_CAEEL
ID PMP2_CAEEL STANDARD: PRT; 910 AA.
AC P91341.
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Periodic tryptophan protein 2 homolog.
GN F55F8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxId=6239;
OX [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Scheet P., Kemp K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 14 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: BELONGS TO THE PMP2 FAMILY OF WD-REPEAT PROTEINS.
CC -----
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DR EMBL: U18813; AAB64602.1; -
 DR SGD: S0000868; YER066W.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 3.
 DR ProDom: PD000018; WD40; 1.
 DR SMART: SM00320; WD40; 2.
 DR PROSITE: PS00678; WD_REPEATS_1; 1.
 DR PROSITE: PS50082; WD_REPEATS_2; 2.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 9 48 WD 1.
 FT REPEAT 71 108 WD 2.
 FT REPEAT 111 148 WD 3.
 SQ SEQUENCE 185 AA; 20686 MW; A07DCE8B3CA30399 CRC64;
 Query Match 51.0%; Score 77; DB 1; Length 185;
 Best Local Similarity 50.0%; Pred. No. 0.00022;
 Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHRAAVNVDFDCKYIVSASGDKTIKW 29
 Db 71 GHRALVGLGLGSDKFLVSASVDSIRCW 98
 ||||| : ||||| : ||| :
 GBLP_YEAST STANDARD; PRT; 319 AA.
 ID GBLP_YEAST
 AC P38011;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Guanine nucleotide-binding protein beta subunit-1-like protein.
 GN ASCL OR YMR16C OR YMR718.15C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RA Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 54-62.
 RC STRAIN=5288C; PubMed=7895733;
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RT Voipe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 database";
 RT Electrophoresis 15:1466-1486(1994).
 RN [3]
 RP SEQUENCE OF 63-70 AND 138-149.
 RC STRAIN=ATCC 44827 / SKQ2N;
 RA MEDLINE=97190279; PubMed=9038161;
 RA Norbeck J., Blomberg A.;
 RT "Metabolic and regulatory changes associated with growth of
 Saccharomyces cerevisiae in 1.4 M NaCl. Evidence for osmotic
 induction of glycerol dissimilation via the dihydroxyacetone
 pathway";
 RT J. Biol. Chem. 272:5544-5554(1997).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 DR EMBL: 249702; CAAB9754.1; -
 DR SGD: S0004722; ASCL.

DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT REPEAT 15 46 WD 1.
 FT REPEAT 63 93 WD 2.
 FT REPEAT 105 135 WD 3.
 FT REPEAT 146 182 WD 4.
 FT REPEAT 194 224 WD 5.
 FT REPEAT 235 264 WD 6.
 FT REPEAT 284 314 WD 7.
 SQ SEQUENCE 319 AA; 34805 MW; B9A5DA959A3C54FB CRC64;
 Query Match 51.0%; Score 77; DB 1; Length 319;
 Best Local Similarity 54.8%; Pred. No. 0.0004;
 Matches 17; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 GHRAAVNVDFDCKYIVSASGDKTIKW 29
 Db 104 VGHRSDVMSYDIDKKASMIISGRDRTIKW 134
 ||||| : ||||| : ||||| :
 YCW2_YEAST STANDARD; PRT; 515 AA.
 ID YCW2_YEAST
 AC P25382;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 57.0 kDa Trp-Asp repeats containing protein in CPR4-SSK22
 DE Intergenic region.
 GN YCR072C OR YCR72C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
 RA Sanz E.;
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RA Jimenez A.;
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
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 DR EMBL: X59720; CAA42270.1; -
 DR PIR: S19487; S19487.
 DR SGD: S0000668; YCR072C.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 8.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 6.
 DR SMART: SM00320; WD40; 8.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 141 172 WD 1.

FT REPEAT 184 214 WD 2.
 FT REPEAT 227 264 WD 3.
 FT REPEAT 276 305 WD 4.
 FT REPEAT 318 387 WD 5.
 FT REPEAT 400 430 WD 6.
 FT REPEAT 442 472 WD 7.
 FT REPEAT 484 514 WD 8.
 SQ SEQUENCE 515 AA; 57040 MW; DFE03B79BF8530A CRC64;

Query Match 50.3%; Score 76; DB 1; Length 515;
 Best Local Similarity 56.7%; Pred. No. 0.00098;
 Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 2 GHRAAVNVDF--DDKYIVASGDRITIKVW 29
 DB 400 GHOKLVNHVAFSPDGRIYASAFDNSTIKW 429

RESULT 13
 YRIO_CAEEL STANDARD; PRT: 571 AA.
 AC P90794;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 65.2 kDa Trp-Asp repeats containing protein D2030.9 in chromosome 1.
 GN D2030.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
 OC Rhabdilitidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE LEC14B FAMILY OF WD-REPEAT PROTEINS.
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 CC -----
 DR EMBL; Z73906; CAA98121.1;
 DR WormPep; D2030.9; CE09086.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 5.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM00320; WD40; 5.
 DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
 DR PROSITE; PS50082; WD_REPEATS_2; 3.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 309 340 WD 1.
 FT REPEAT 357 387 WD 2.
 FT REPEAT 439 470 WD 3.
 FT REPEAT 482 512 WD 4.
 SQ SEQUENCE 571 AA; 65170 MW; 521932753C6F8FC4 CRC64;

Query Match 49.7%; Score 75; DB 1; Length 571;
 Best Local Similarity 53.3%; Pred. No. 0.0016;
 Matches 16; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 2 GHRAAVNVDF--DDKYIVASGDRITIKVW 29
 DB 357 GHRCGVTHVDSKODERILNSKDDITIKW 386

RESULT 14
 SE10_CAEEL STANDARD; PRT: 579 AA.
 AC Q93794;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE sel-10 protein.
 GN sel-10 OR F55B12.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
 OC Rhabdilitidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RA Jones S.J.M.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z79757; CAB02129.1;
 DR WormPep; F55B12.3; CE16120.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 5.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 3.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT DOMAIN 113 159 F-BOX.
 FT REPEAT 245 274 WD 1.
 FT REPEAT 286 316 WD 2.
 FT REPEAT 328 356 WD 3.
 FT REPEAT 368 396 WD 4.
 FT REPEAT 408 438 WD 5.
 FT REPEAT 453 481 WD 6.
 FT REPEAT 493 522 WD 7.
 SQ SEQUENCE 579 AA; 64275 MW; 0647245AF5964663 CRC64;

Query Match 49.7%; Score 75; DB 1; Length 579;
 Best Local Similarity 50.0%; Pred. No. 0.0016;
 Matches 14; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 GHRAAVNVDFDDKYIVASGDRITIKVW 29
 DB 368 GHHAAYRCVQFDCTTYVSGGYDTYKIV 395

RESULT 15
 COPP_DROME STANDARD; PRT: 914 AA.
 ID COPP_DROME
 AC 062621;
 DT 16-OCT-2001 (Rel. 40, Created)

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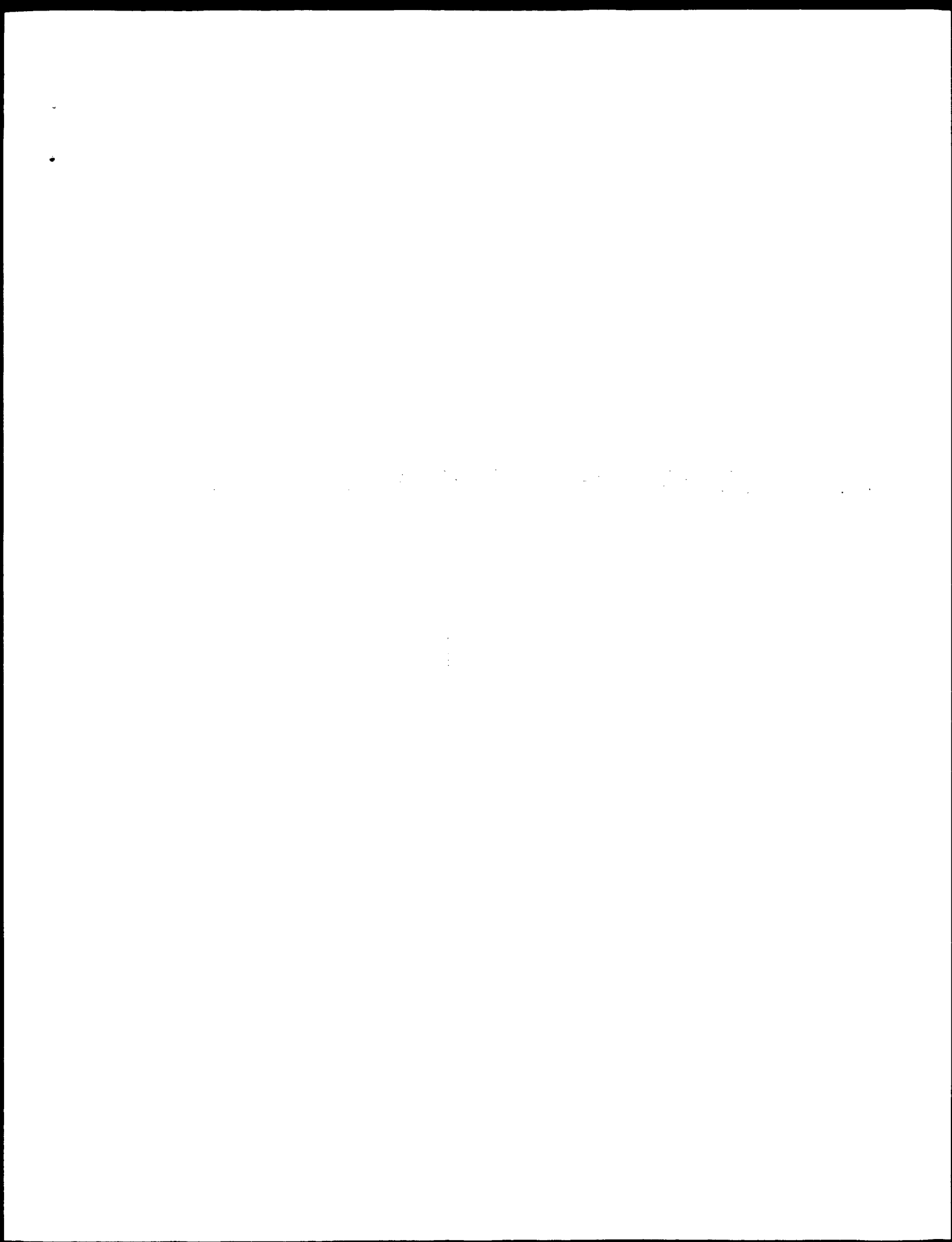
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP).
GN BETA'-COP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Merdes G., Heid H.W., Mechler B.M.;
RT *Cloning and characterization of the Drosophila coatomer subunit
RT beta'*.
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSIST OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AJ006524; CAA07085.1; -.
DR EMBL; AJ006523; CAA07084.1; -.
DR Flybase; FBgn025724; Beta'-COP.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Transport; Protein transport; Golgi stack; Membrane; Repeat;
KW WD repeat; Endoplasmic reticulum.
FT REPEAT 13 43 WD 1.
FT REPEAT 55 85 WD 2.
FT REPEAT 97 127 WD 3.
FT REPEAT 140 171 WD 4.
FT REPEAT 183 215 WD 5.
FT REPEAT 227 257 WD 6.
SO SEQUENCE 914 AA; 102697 MW; C7AA25FAE5426695 CRC64;

Query Match 49.7%; Score 75; DB 1; Length 914;
Best Local Similarity 40.6%; Pred. No. 0.0026;
Matches 13; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

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QY 2 GHRRAVNVDF---DDKYIVSAGDRTIKW 29
 DB 183 GHEKGVNCVYTHGGDKPYLISGADDLVKIW 214

Search completed: April 10, 2003, 13:19:36
 Job time : 3.08404 secs



GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

```
Run on:      April 11, 2003, 11:23:10 ; Search time 6.85262 Seconds
              (without alignments)
              871.983 Million cell updates/sec
```

Title:	US-09-601-168B-2_COPY_387_415
Perfect score:	151
Sequence:	1 VGHRAVNVYDFDDKYLVSASGDRITIKW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters:  671580
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	151	100.0	122	13	Q8UNN3	Q8UNN3 xenopus lae
2	151	100.0	252	11	Q922C7	Q922C7 mus musculus
3	151	100.0	569	11	Q9L1G7	Q9L1G7 mus musculus
4	151	100.0	569	11	Q9L1S9	Q9L1S9 mus musculus
5	151	100.0	569	11	Q9QU15	Q9QU15 mus musculus
6	147	97.4	510	5	Q44382	Q44382 drosophila
7	147	97.4	510	5	Q9VDE3	Q9VDE3 drosophila
8	144	95.4	430	5	Q9B5E4	Q9B5E4 heterodera
9	133	88.1	563	11	Q923H0	Q923H0 mus musculus
10	83	55.0	934	16	Q8Y2J1	Q8Y2J1 anabaena sp
11	81	55.6	423	5	Q8SSJ1	Q8SSJ1 encaphalito
12	79	52.3	1376	3	Q8X1P2	Q8X1P2 podospora a
13	79	52.3	1551	16	Q8YMU3	Q8YMU3 anabaena sp
14	78	51.7	1326	5	Q9VZF4	Q9VZF4 drosophila
15	78	51.7	1747	16	Q8C020	Q8C020 anabaena sp
16	76	50.3	513	11	Q9D1I8	Q9D1I8 mus musculus

ALIGNMENTS

17	75	49.7	196	13	Q8GUG0	Q8gu0 melanochrom
18	75	49.7	196	13	Q8GXT9	Q8glt1 astatocliap
19	75	49.7	196	13	Q8GXT8	Q8glt1 labidochrom
20	75	49.7	196	13	Q8GXT7	Q8glt7 tropheus du
21	75	49.7	196	13	Q8GXT6	Q8glt6 spathodus e
22	75	49.7	196	13	Q8GXT5	Q8glt5 cyprichromi
23	75	49.7	196	13	Q8GXT4	Q8glt4 xenotiliapia
24	75	49.7	196	13	Q8GXT3	Q8glt3 neolamproid
25	75	49.7	196	13	Q8GXT2	Q8glt2 altolamprol
26	75	49.7	196	13	Q8GXT1	Q8glt1 neolampirolo
27	75	49.7	196	13	Q8GXT0	Q8glt0 steatocranu
28	75	49.7	196	13	Q8GXS9	Q8gxs9 iliapia but
29	75	49.7	196	13	Q8GXS8	Q8gxs8 oreochromis
30	75	49.7	503	11	Q9CY96	Q9cy96 mus musculu
31	75	49.7	513	4	Q9BU59	Q9bu59 homo sapien
32	75	49.7	513	4	Q9NVD1	Q9nvd1 homo sapien
33	75	49.7	513	11	Q9J9M63	Q9j9m63 rattus norv
34	75	49.7	513	11	Q9J9J70	Q9jjj70 mus musculu
35	75	49.7	530	5	Q9U3K9	Q9u3k9 caenorhabdi
36	75	49.7	585	5	Q9S2T0	Q9s2t0 caenorhabdi
37	75	49.7	587	5	Q440B3	Q440b3 caenorhabdi
38	75	49.7	690	5	Q9VJZ0	Q9vjz0 drosophila
39	74	49.0	690	5	Q615B5	Q615b5 strongyloce
40	74	49.0	1189	16	Q8YRDI1	Q8yrdi1 anaabaena sp
41	74	49.0	1711	16	Q8Z0I9	Q8zdi9 anaabaena sp
42	73	48.3	326	10	Q9LYZ8	Q9lyz8 arabidopsis
43	73	48.3	326	10	Q9C4Z6	Q9cz46 arabidopsis
44	73	48.3	849	5	Q9U5J8	Q9u5j8 trypanosoma
45	72	47.7	689	10	Q93ZT0	Q93zt0 arabidopsis

RESULT 1

ID	ORGUN3:	PRELIMINARY:	PRT:	122 AA.
AC	080UN3:			
DT	01-MAR-2002 (TtEMBLrel.	20, Created)		
DT	01-MAR-2002 (TtEMBLrel.	20, last sequence update)		
DT	01-JUN-2002 (TtEMBLrel.	21, last annotation update)		
DE	Beta-TrCP protein (Fragment).			
GN	Beta-TrCP.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Carnevali F.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ballarino M.;			
RT	"Analisi strutturale e funzionale del gene beta-TrCP in Xenopus			
RT	laevis.";			
RL	Thesis (2001).			
RL	Department of Genetics and Molecular Biology "Charles Darwin",			
RL	University of Rome La Sapienza, Rome, Italy.			
DR	EMBL; AJ428938; CAD21955.1; .			
DR	InterPro; IPR001680; WD40.			
DR	Pfam; PF00400; WD40; 3.			
DR	PRINTS; PR00320; GPXOTENBRPT.			
DR	Prodom; PD000018; WD40; 2.			
DR	SMART; SM00320; WD40; 3.			
DR	PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.			
DR	PROSITE; PS50082; WD_REPEATS_2; 3.			
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.			
FT	NON_TER	1	122	
FT	NON_TER	1	122	
SO	SEQUENCE	122 AA;	13682 MW;	36BB6B39AC8F5387 CRC64;

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Query Match          100.0%; Score 151; DB 13; Length 122;
Best Local Similarity 100.0%; Pred. No. 6,7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 57 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 85

RESULT 2
O922C7 PRELIMINARY; PRT; 252 AA.
AC O922C7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to f-box and WD-40 domain protein 1B (Fragment).
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC008552; AA08552.1;
DR MGD; MGI:2144023; Fbxw1b.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER
SQ SEQUENCE 252 AA; 28424 MW; F7173CBD7A9F75F CRC64;

Query Match          100.0%; Score 151; DB 11; Length 252;
Best Local Similarity 100.0%; Pred. No. 1,6e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 70 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 98

RESULT 3
O9RIG7 PRELIMINARY; PRT; 569 AA.
AC O9RIG7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-transducin repeat-containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF110396; AAD41025.1;
DR MGD; MGI:1338871; BTRC.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.

Query Match          100.0%; Score 151; DB 13; Length 122;
Best Local Similarity 100.0%; Pred. No. 6,7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 57 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 85

RESULT 2
O922C7 PRELIMINARY; PRT; 252 AA.
AC O922C7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to f-box and WD-40 domain protein 1B (Fragment).
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC008552; AA08552.1;
DR MGD; MGI:2144023; Fbxw1b.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER
SQ SEQUENCE 252 AA; 28424 MW; F7173CBD7A9F75F CRC64;

Query Match          100.0%; Score 151; DB 11; Length 252;
Best Local Similarity 100.0%; Pred. No. 1,6e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 70 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 98

RESULT 3
O9RIG7 PRELIMINARY; PRT; 569 AA.
AC O9RIG7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-transducin repeat-containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF110396; AAD41025.1;
DR MGD; MGI:1338871; BTRC.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.

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DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D51D9D CRC64;

Query Match          100.0%; Score 151; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4,5e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 387 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 415

RESULT 5
O90U15 PRELIMINARY; PRT; 569 AA.
AC O90U15;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

Query Match          100.0%; Score 151; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4,5e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 29
    |||||
DB 387 VGHRAAVNVVDFDDKTYIVSASGDRITKIV 415

RESULT 5
O90U15 PRELIMINARY; PRT; 569 AA.
AC O90U15;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

```

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Ubiquitin ligase FWD1 (beta-transducin repeat containing protein)
 GN (F-box-WD40 repeat protein 1).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9919275; PubMed=10097128;
 RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
 RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
 RA Nakayama K., I.
 RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a
 RT ubiquitin ligase Skp1/Cul1/F-box protein FWD1."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99075339; PubMed=9859996;
 RA Yaron A., Hatzubal A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase."
 RL Nature 396:590-594(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21601157; PubMed=11735228;
 RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
 RA Nakayama K., I.
 RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
 RT Caenorhabditis elegans SEL-10."
 RL Genomics 78:214-223(2001).
 CC -1 SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF081887; AADI7755.1; -;
 DR EMBL: AF099932; AAD08701.1; -;
 DR EMBL: BC003989; AAH03989.1; -;
 DR EMBL: AF391190; AAL40929.1; -;
 DR EMBL: AF391178; AAL40929.1; JOINED.
 DR EMBL: AF391179; AAL40929.1; JOINED.
 DR EMBL: AF391180; AAL40929.1; JOINED.
 DR EMBL: AF391181; AAL40929.1; JOINED.
 DR EMBL: AF391182; AAL40929.1; JOINED.
 DR EMBL: AF391183; AAL40929.1; JOINED.
 DR EMBL: AF391184; AAL40929.1; JOINED.
 DR EMBL: AF391185; AAL40929.1; JOINED.
 DR EMBL: AF391186; AAL40929.1; JOINED.
 DR EMBL: AF391187; AAL40929.1; JOINED.
 DR EMBL: AF391188; AAL40929.1; JOINED.
 DR EMBL: AF391189; AAL40929.1; JOINED.
 DR MGI: MGI:1338871; Btcc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ligase; Repeat; WD repeat.
 SQ SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match 100.0%; Score 151; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 4.5e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
 DB 387 VGHRAAVNVDPDDKYIVSASGDRITKW 415

RESULT 6
 044382 PRELIMINARY; PRT; 510 AA.

AC 044382;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE SLIMB.
 GN SLIMB OR SLIMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Query Match 97.4%; Score 147; DB 5; Length 510;
 Best Local Similarity 96.6%; Pred. No. 1.6e-13;

Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDPDDKYIVSASGDRITKW 29
 DB 330 VGHRAAVNVDPDDKYIVSASGDRITKW 358

RESULT 7
 09YDE3 PRELIMINARY; PRT; 510 AA.

AC 09YDE3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE SLIMB protein (SLIMB).
 GN SLIMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Borchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dooson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wattarman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster.",
 RL Science 287:2185-2195(2000).
 [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY, AND IMAGINAL DISC;
 RX MEDLINE-20245299; PubMed-10781936;
 RA Miletich I., Limbourg-Bouchon B.,
 RT "Drosophila null slimb clones transiently deregulate Hedgehog-
 RT independent transcription of wingless in all limb discs, and induce
 RT decapentaplegic transcription linked to imaginal disc regeneration.",
 RL Mech. Dev. 93:15-26(2000).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF003733; AAF5853.1; -
 DR EMBL: AF222924; AAF63214.1; -
 DR EMBL: AF222923; AAF63213.1; -
 DR Flybase: FBgn0023423; slimb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS50678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58552 MW; F4D5DF126F58A012 CRC64;

Query Match 97.4%; Score 147; DB 5; Length 510;
 Best Local Similarity 96.6%; Pred. No. 1,6e-13;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VGHRAAVNVDPDDKITYSASGDRITKYM 29
 DB 330 VGHRAAVNVDPDDKITYSASGDRITKYM 358

RESULT 8
 ID 09BJ54 PRELIMINARY; PRT; 430 AA.
 AC 09BJ54;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-transducin repeat-containing protein (fragment).
 OS Heterodera glycines (Soybean cyst nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchida; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchida; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 NX NCBL:Taxid=51029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kovaleva E.S., Yakovlev A.G., Masler E.P.,
 RT "Plant parasitic nematode b-TIRCP".
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF339101; AAK26376.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER
 SQ SEQUENCE 430 AA; 47916 MW; 4ABC3CF2DFE3A50B CRC64;
 Query Match 95.4%; Score 144; DB 5; Length 430;
 Best Local Similarity 96.6%; Pred. No. 3,6e-13;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 VGHRAAVNVDPDDKITYSASGDRITKYM 29
 DB 211 VGHRAAVNVDPDDKITYSASGDRITKYM 239

RESULT 9
 ID 0923H0 PRELIMINARY; PRT; 563 AA.
 AC 0923H0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE F-box/WD40 repeat-containing protein HOS.
 GN FBXW1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBL:Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FVB/N;
 RA Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
 RT "Mouse homolog of HOS (mHOS) is overexpressed in skin tumors and
 RT implicated in constitutive activation of NF-kappaB".
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AY038079; AAK72095.1; -
 DR MGD: MGI:2144023; Fbxw1b.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRODOM: PD000018; WD40; 4.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS50678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.

DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 563 AA; 64741 MW; 9AB5623FF5E3496 CRC64;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 2.2e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 RAAVNVVDFDDKIVYASGDRITIKW 29
 DB 384 RAAVNVVDFDDKIVYASGDRITIKW 409
 RESULT 10
 OY 08Y223 PRELIMINARY; PRT; 934 AA.
 AC 08Y223;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE WD-40 repeat protein.
 GN ALU0664.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iiguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003583; BAB72622.1; -
 DR InterPro: IPR001680; WD40.14.
 DR Pfam: PF00400; WD40.14.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR SMART: SM00320; WD40.14.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 13.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Complete proteome.
 SQ SEQUENCE 934 AA; 104389 MW; D371F162040DFB3 CRC64;
 Query Match
 Best Local Similarity 56.7%; Score 83; DB 16; Length 934;
 Matches 17; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
 OY 2 GHRAAVNVDF--DDKIVYASGDRITIKW 29
 DB 530 GHGQVNSVTFSPDGKLIATASGDRITIKW 559
 RESULT 11
 OY 08SSJ1 PRELIMINARY; PRT; 423 AA.
 AC 08SSJ1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE WD-repeat protein similar to cell division control protein 4 / SEL10
 DE protein.
 GN ECU01_1300.
 OS Enecephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Enecephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 DE WD-repeat protein.
 GN Genoscope;

RL submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1.
 RX MEDLINE=21576510; PubMed=11719806;
 RA Kallinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Presnier G., Barbe V., Peyretilade E., Brotier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 Enecephalitozoon cuniculi.";
 RL Nature 414:450-453(2001).
 DR EMBL: AL391737; CAD25003.1; -
 SQ SEQUENCE 423 AA; 47791 MW; 661672B1621620CF CRC64;
 Query Match
 Best Local Similarity 53.6%; Score 81; DB 5; Length 423;
 Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 OY 1 VGHRAAVNVVDFDDKIVYASGDRITIKW 29
 DB 151 VGHKGVWTFMFNDKIVSGSTDKTARIW 179
 RESULT 12
 OY 08X1P2 PRELIMINARY; PRT; 1376 AA.
 AC 08X1P2;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta transducin-like protein HET-D2Y.
 GN HET-D.
 OS Podospira anserina.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Lasiosphaeriaceae; Podospira.
 OX NCBI_TaxID=5145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Espagne E., Balhadere P., Bequeret J., Turcq B.;
 RT "A new family of WD40 proteins implicated in vegetative
 incompatibility: evidence for a major role of WD40 repeat domain in
 the specificity of het-e and het-d genes.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF323585; AAL37301.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40.12.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR Prodom: PD000018; WD40.9.
 DR SMART: SM00320; WD40.12.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_11.
 DR PROSITE: PS50082; WD_REPEATS_2; 11.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 SQ SEQUENCE 1376 AA; 152068 MW; 2191826A5C62D97 CRC64;
 Query Match
 Best Local Similarity 53.3%; Score 79; DB 3; Length 1376;
 Matches 16; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
 OY 2 GHRAAVNVDF--DDKIVYASGDRITIKW 29
 DB 1123 GHGQVNSVAFSPDSKMWASGSDRTIKITW 1152
 RESULT 13
 OY 08YMU3 PRELIMINARY; PRT; 1551 AA.
 AC 08YMU3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE WD-repeat protein.
 GN ALU4834.

OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Matanabe A., Iritani M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003597; BAB76533.1;
 DR InterPro: IPR000408; Reg_chit_condens.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 14.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR SMART: SM00320; WD40; 14.
 DR PROSITE: PS00626; RC01_2; UNKNOWN_1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_9.
 DR PROSITE: PS50082; WD_REPEATS_2; 14.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Complete proteome.
 SQ SEQUENCE 1551 AA; 176680 MW; 8FEB62B3BA727317 CRC64;

Query Match 52.3%; Score 79; DB 16; Length 1551;
 Best Local Similarity 46.7%; Pred. No. 0.01;
 Matches 14; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

QY 2 GHRAAVNVDF--DDKYIVASGDRRTIKW 29
 Db 1484 GHKAVKSIISPPDGYATATASDDRTIKW 1513

RESULT 14
 QYVZFA PRELIMINARY; PRT; 1326 AA.
 ID QYVZFA;
 AC QYVZFA;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CG15010 protein (LD21322p) (LD30271p).
 GN AGO OR CG15010.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burks K.C., Bussem D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Abmayyan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacled J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Abmayyan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Frise E., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacled J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AE003480; AAC22246.1; -;
 DR EMBL: AY061300; AA128848.1; -;
 DR EMBL: AY075401; AA168231.1; -;
 DR FlyBase: FBgn0041171; ago.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR Pfam: PF000018; WD40; 2.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 1326 AA; 141360 MW; 3F42C873CFA3027F CRC64;

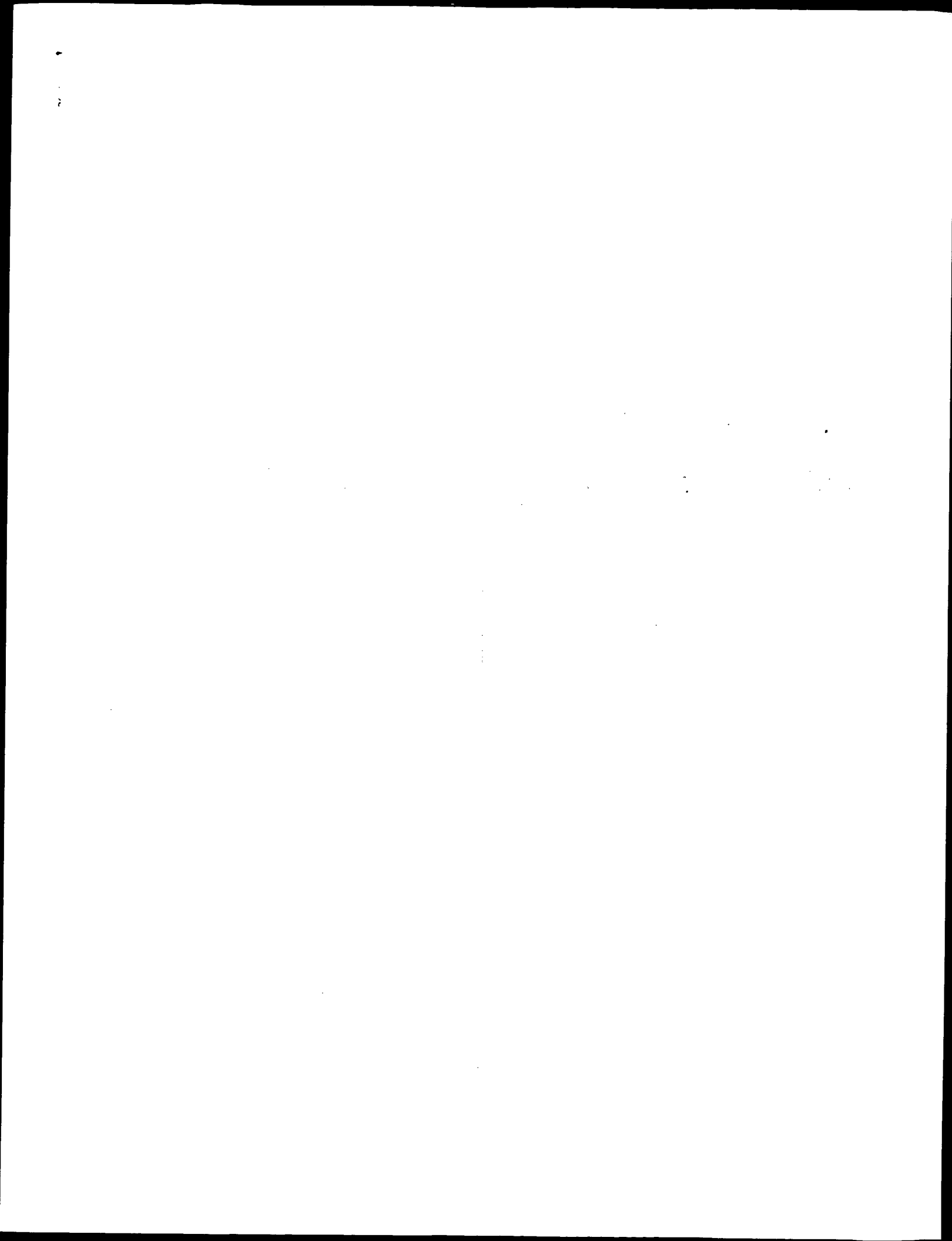
Query Match 51.7%; Score 78; DB 5; Length 1326;
 Best Local Similarity 51.7%; Pred. No. 0.012;
 Matches 15; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGHRAAVNVDFDDKYIVASGDRRTIKW 29
 Db 1112 VGHAAVRCVQYDGLKLVGAYDYMKW 1140

RESULT 15
 Q8Z020 PRELIMINARY; PRT; 1747 AA.
 ID Q8Z020;
 AC Q8Z020;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	WD40 repeat protein.
GN	ALLO283.
OS	Anabaena sp. (strain PCC 7120).
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX	NCBI_TaxID=103690;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21595285; PubMed=11759840;
RA	Kaneko T., Nakamura Y., Molk C.P., Kunitz T., Sasamoto S.,
RA	Matsumoto A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA	Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA	Yasuda M., Tabata S.;
RT	"Complete genomic sequence of the filamentous nitrogen-fixing
RT	Cyanobacterium Anabaena sp. strain PCC 7120.";
RL	DNA Res. 8:205-213(2001).
DR	EMBL; AP003581; BAB7807.1; -
DR	InterPro; IPR001680; WD40.
DR	Pfam; PF00400; WD40; 14.
DR	PRINTS; PR00320; GPROTEINRPT.
DR	SMART; SM00320; WD40; 14.
DR	PROSITE; PS00678; WD_REPEATS_1; UNKNOWN-5.
DR	PROSITE; PS50082; WD_REPEATS_2; 12.
DR	PROSITE; PS50094; WD_REPEATS_REGION; 1.
KW	Complete proteome.
SO	SEQUENCE 1747 AA; 192610 MW; 27DC1CF2DCC8BDACA CRC64;
QY	Query Match 51.7%; Score 78; DB 16; Length 1747;
DB	Best Local Similarity 53.3%; Pred. No. 0.017;
Matches	16; Conservative 3; Mismatches 9; Indels 2; Gaps 1;
QY	2 GHRAAVNVDF--DDKIYVASCGRDTIKW 29
DB	1135 GHAQGVNAVSPDGRKVLASASDDRVKLM 1164

Search completed: April 11, 2003, 11:51:44
Job time : 14.8526 secs



GenCore version 5.1.4-P5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 ; Search time 8.93666 Seconds
(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_427_455

Perfect score: 156
Sequence: 1 NGRKRGICLOYRDLRVSSGSDNTIRLM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	517	16 AAR85852	WD-40 domain-contg
2	156	100.0	542	21 AAY96696	Human E3 ubiquitin
3	156	100.0	542	21 AAM79127	Human protein SEQ
4	156	100.0	542	22 AAM40208	Human polypeptide
5	156	100.0	550	22 AAM41994	Human polypeptide
6	156	100.0	569	20 AAY24054	A human beta-trans
7	156	100.0	569	21 AAB12812	Mouse ubiquitin 11
8	156	100.0	569	21 AAB12813	Human beta-transdu
9	156	100.0	569	21 AAY96697	Human beta-TRCP.
10	156	100.0	569	21 AAY83041	F-box protein FBP-

11	156	100.0	569	21 AAY83250	F-box protein hbet
12	156	100.0	569	21 AAY83254	F-box protein FWD1
13	156	100.0	569	21 AAY44249	Human cell signa11
14	156	100.0	569	22 AAB48298	Human ZF1 protein
15	156	100.0	579	22 AAB48363	Human protein SEQ
16	156	100.0	590	22 AAM00847	Human bone marrow
17	156	100.0	605	22 AAM78582	Human protein SEQ
18	156	100.0	608	22 AAM00960	Human bone marrow
19	156	100.0	632	22 AAM78584	Human protein SEQ
20	156	100.0	654	22 AAM79566	Human protein SEQ
21	156	100.0	654	22 AAM79567	Human protein SEQ
22	156	100.0	654	22 AAM79568	Human protein SEQ
23	152	97.4	510	22 AAB59857	Drosophila melanog
24	152	96.2	29	16 AAR84939	Peptide r1 from a
25	150	55.8	34	16 AAR84935	Peptide r1 from a
26	83	53.2	1326	22 ABB67237	Drosophila melanog
27	83	53.2	1326	22 ABB67238	Drosophila melanog
28	83	53.2	1326	22 ABB70051	Drosophila melanog
29	82.5	52.9	28	16 AAR84936	Peptide r1 from a
30	80	51.3	694	21 AAY99661	Human GTPase assoc
31	79	50.6	357	23 ABB90392	Human polypeptide
32	79	50.6	438	21 AAG07498	Arabidopsis thailia
33	79	50.6	438	21 AAG53870	Human polypeptide
34	79	50.6	540	20 AAY22465	Human polypeptide
35	79	50.6	540	20 AAY22468	Human polypeptide
36	79	50.6	540	20 AAB59197	Human polypeptide
37	79	50.6	540	22 AAB59200	Human polypeptide
38	79	50.6	545	20 AAY22464	Human polypeptide
39	79	50.6	545	22 AAB59196	Human polypeptide
40	79	50.6	553	20 AAY22463	Human polypeptide
41	79	50.6	553	22 AAB93475	Human polypeptide
42	79	50.6	553	22 AAB59195	Human polypeptide
43	79	50.6	559	22 AAY22467	Human polypeptide
44	79	50.6	559	22 AAB59199	Human polypeptide
45	79	50.6	589	20 AAY22466	Human polypeptide

ALIGNMENTS

RESULT 1
ID AAR85852 standard; peptide: 517 AA.
XX AAR85852:
AC AAR85852:
XX 13-SEP-1996 (first entry)
DE WD-40 domain-contg. beta-TRCP protein.
XX
XX WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signalling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme activity; isozyme; human.
XX
XX Synthetic.
OS
XX W09521252-A2.
PN
XX 10-AUG-1995.
PD
XX 31-JAN-1995; 95MO-US01210.
PF
XX 01-FEB-1994; 94US-0190802.
PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX Mochly-Rosen D, Ron D;
PI
XX WDI: 1995-283772/37.
DR
XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

XX Example 5; Page 80-82; 351pp; English.

PS Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.

SQ Sequence 517 AA:

Query Match 100.0%; Score 156; DB 16; Length 517;
 Best Local Similarity 100.0%; Pred. No. 2,2e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGACIQLYRDLVVGSSDNTIRLM 29
 DB 391 NGHKGACIQLYRDLVVGSSDNTIRLM 419

RESULT 2
 AAY96696
 ID AAY96696 standard; Protein; 542 AA.

AC AAY96696;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Human E3 ubiquitin ligase.
 XX
 KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
 KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
 KW anti-inflammatory; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200034447-A2.
 XX
 PD 15-JUN-2000.
 XX
 PF 10-DEC-1999; 99WO-US29371.
 XX
 PR 10-DEC-1998; 98US-0210060.
 XX
 PA (SIGN-) SIGNAL PHARM INC.
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Manning AM, Mercurio F, Amlt S, Ben-eriah Y, Davis M, Hatzubai A,
 PI Lavon I, Yaron A;
 XX
 DR WPI: 2000-431294/37.
 XX
 DR N-PSDB; AAK51228.
 XX
 PT Polypeptide enhancing phosphorylated I-kappaB ubiquitination useful for
 PT treating disorder associated with NF-kappaB activation e.g. cancer,
 PT comprising amino acid sequence of human E3 ubiquitin ligase or its
 PT variant
 XX
 PS Claim 1; Page 70-72; 77pp; English.

CC This is human E3 ubiquitin ligase (E3), which is homologous to human
 CC beta-TrCP, an F-box/WD protein family member. E3 enhances ubiquitination
 CC of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor
 CC kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the
 CC ubiquitin pathway is useful for identifying modulators of this process

CC for use in treating diseases associated with activation of NF-kappa-B. In
 CC vitro analysis suggests that deletion of the F-box results in a protein
 CC that functions as a dominant negative molecule in vivo. Transient
 CC over-expression of delta-beta-TrCP (a deletion mutant) inhibited the
 CC degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells,
 CC resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be
 CC used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP
 CC can be used to modulate NF-kappa-B to treat inflammatory diseases,
 CC autoimmune diseases, cancer and viral infections.

SQ Sequence 542 AA:

Query Match 100.0%; Score 156; DB 21; Length 542;
 Best Local Similarity 100.0%; Pred. No. 2,3e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGACIQLYRDLVVGSSDNTIRLM 29
 DB 400 NGHKGACIQLYRDLVVGSSDNTIRLM 428

RESULT 3
 AAM79127
 ID AAM79127 standard; Protein; 542 AA.

AC AAM79127;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1789.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI: 2001-476283/51.
 XX
 DR N-PSDB; AAK52260.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 4147-4148; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK60020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

CC Sequence 542 AA:

Query Match 100.0%; Score 156; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 2.3e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKRGIAQLQYRDRLVSGSSDNTIRLM 29
 |||||
 Db 400 NGHKRGIAQLQYRDRLVSGSSDNTIRLM 428

RESULT 4
 ID AAM40208 standard; Protein; 542 AA.

XX AAM40208:

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3353.

XX Human: neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

PD 26-DEC-2000; 2000MO-US34263.

XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSEQ-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.
 DR N-PSDB: AAI59364.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX Example 5; SEQ ID NO 3353; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

CC Sequence 542 AA:

Query Match 100.0%; Score 156; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 2.3e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKRGIAQLQYRDRLVSGSSDNTIRLM 29
 |||||
 Db 400 NGHKRGIAQLQYRDRLVSGSSDNTIRLM 428

RESULT 5
 ID AAM41994 standard; Protein; 550 AA.

XX AAM41994:

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6925.

XX Human: neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

PD 26-DEC-2000; 2000MO-US34263.

XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSEQ-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.
 DR N-PSDB: AAI61150.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX Example 2; SEQ ID NO 6925; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

CC Sequence 550 AA;

Query Match 100.0%; Score 156; DB 22; Length 550;
 Best Local Similarity 100.0%; Pred. No. 2,3e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKGACIACQYRDLVSSGSDNTIRLW 29
 ||||||||||||||||||
 Db 408 NGHKGACIACQYRDLVSSGSDNTIRLW 436

RESULT 6
 ID AAY24054 standard; Protein; 569 AA.
 XX
 AC AAY24054;

XX 30-SEP-1999 (first entry)

DE A human beta-transducin repeat containing protein.

XX
 KW Beta-transducin repeat containing protein; beta-Trcp; Skp1p;
 KW proteasome degradation pathway; Vpu protein; beta-catenin;
 KW human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;
 KW ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
 KW antiviral; antitumour; cell cycle regulation; protein degradation;
 KW and anti-inflammatory; osteo-articular inflammation; acute inflammation;
 KW tumour necrosis factor.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Region 147..191 /note= "F box sequence"

FT Region 259..292 /note= "WD motif"

FT Region 304..332 /note= "WD motif"

FT Region 343..372 /note= "WD motif"

FT Region 387..415 /note= "WD motif"

FT Region 427..455 /note= "WD motif"

FT Region 467..492 /note= "WD motif"

FT Region 516..544 /note= "WD motif"

FT Region

XX MO9938969-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-FR00196.

XX 09-DEC-1998; 98PR-0015545.

XX 30-JAN-1998; 98FR-0001100.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR.

XX Arenzana Seisdedos F; Benarous R, Concordet J, Durand H;

XX Kroll M, Margottin F;

XX WPI: 1999-469329/39.

XX N-PSDB; AAX86501.

XX Claim 1; Page 60-61; 71pp; French.

XX The present sequence represents a human beta-transducin repeat containing
 CC protein (beta-Trcp). The protein directs proteins to the proteasome
 CC degradation pathways. The protein is able to interact with the Vpu
 CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
 CC Ikappab or beta-catenin (bc) and/or protein Skp1p. The protein controls
 CC ubiquitinylation of phosphorylated proteins and thus their targeting to
 CC proteasomes for degradation. Depending on whether the process is
 CC inhibited or promoted, the result may be delayed breakdown of CD4 (in
 CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
 CC activity of NFkappab) and increased degradation of mutant bc in tumour
 CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
 CC patients. The beta-Trcp protein, and its active peptide fragments, or its
 CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
 CC antitumour agents that disrupt cell cycle regulation or protein
 CC degradation in human tumour cells, and anti-inflammatory agents that
 CC disrupt activation by NFkappab. Fragments of the protein are also
 CC useful for treating osteo-articular inflammation or acute inflammation
 CC associated with release of tumour necrosis factor.

SO Sequence 569 AA;

Query Match 100.0%; Score 156; DB 20; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2,4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKGACIACQYRDLVSSGSDNTIRLW 29
 ||||||||||||||||||
 Db 427 NGHKGACIACQYRDLVSSGSDNTIRLW 455

RESULT 7

AAAB12812 standard; protein; 569 AA.

XX AAAB12812;

XX 27-NOV-2000 (first entry)

DE Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

XX Ubiquitin ligase SCF complex; F-box protein; ubiquitinylation; Ikappab;
 KW beta-catenin; Skp1; Cul1; F-box motif; WD40 repeat motif; FWD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-Trcp.

XX Mus musculus.

XX JP200016542-A.

XX 20-JUN-2000.

XX 02-DEC-1998; 98JP-0343437.

XX 02-DEC-1998; 98JP-0343437.

XX (KAGA-) KAGAKU GIYUSU SHINKO JIGYODAN.

XX WPI: 2000-485550/43.

DR N-PSDB; AAA73131.
 XX F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin
 XX
 PS Claim 2; Page 9-10; 19pp; Japanese.
 XX
 CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NGHRRGIACLOYRDLRVVSGSSDNTIRLM 29
 Db 427 NGHRRGIACLOYRDLRVVSGSSDNTIRLM 455
 RESULT 8
 AAB12813
 ID AAB12813 standard; protein; 569 AA.
 XX
 AC AAB12813:
 XX
 DT 27-NOV-2000 (first entry)
 XX
 DE Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
 XX
 KW Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WPA0 repeat motif; FMD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-TrCP.
 XX
 OS Homo sapiens.
 XX
 PN JP2000166542-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 02-DEC-1998; 98JP-0343437.
 XX
 PR 02-DEC-1998; 98JP-0343437.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI: 2000-485550/43.
 XX
 DR N-PSDB; AAA73132.
 XX
 PT F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikappab or beta-catenin
 XX
 PS Claim 3; Page 10-12; 19pp; Japanese.
 XX
 CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikappab or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 XX

SQ Sequence 569 AA:
 Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NGHRRGIACLOYRDLRVVSGSSDNTIRLM 29
 Db 427 NGHRRGIACLOYRDLRVVSGSSDNTIRLM 455
 RESULT 9
 AAY96697
 ID AAY96697 standard; Protein; 569 AA.
 XX
 AC AAY96697:
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Human beta-TrCP.
 XX
 KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
 KW nuclear factor kappa B; NF-kappa-B; degradation; modulator; anti-viral;
 KW anti-inflammatory; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200034447-A2.
 XX
 PD 15-JUN-2000.
 XX
 PF 10-DEC-1999; 99WO-US29371.
 XX
 PR 10-DEC-1998; 98US-0210060.
 XX
 PA (SIGN-) SIGNAL PHARM INC.
 PA (YISS) YISSUM RES & DEV CO.
 PI Manning AM, Mercurio F, Amit S, Ben-zuriah Y, Davis M, Hatzubai A;
 PI Lavon I, Yaron A;
 XX
 DR WPI: 2000-431294/37.
 XX
 DR N-PSDB; AAA51229.
 XX
 PT Polypeptide enhancing phosphorylated Ikappab ubiquitination useful for
 PT treating disorder associated with NF-kappa-B activation e.g. cancer,
 PT comprising amino acid sequence of human E3 ubiquitin ligase or its
 PT variant
 XX
 PS Claim 21; Page 72-74; 77pp; English.
 XX
 CC Human beta-TrCP, an F-box/WD protein family member, has been shown to
 CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
 CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
 CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
 CC degradation via the ubiquitin pathway is useful for identifying
 CC modulators of this process for use in treating diseases associated with
 CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
 CC the F-box results in a protein that functions as a dominant negative
 CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a
 CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
 CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
 CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
 CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
 CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NGHRRGIACLOYRDLRVVSGSSDNTIRLM 29

Db 427 NGHKGIACTQYRDRLVVGSSDNTIRLM 455

RESULT 10

ID AAY83041 standard; Protein; 569 AA.

AC AAY83041;

DT 16-AUG-2000 (first entry)

DE F-box protein FBP-1.

KW F-box protein; FBP; diagnosis; treatment; screening; agonist;
 KW antagonist; proliferative disorder; differentiative disorder;
 KW breast cancer; prostate cancer; ovarian cancer; cancer;
 KW small cell lung carcinoma; immune disorder; cardiovascular disorder;
 KW inflammatory disorder; human.

OS Homo sapiens.

PN WO200012679-A1.

PD 09-MAR-2000.

PF 27-AUG-1999; 99WO-US19560.

PR 28-AUG-1998; 98US-0098355.

PR 03-FEB-1999; 99US-0118568.

PR 15-MAR-1999; 99US-0124449.

XX (UYNY) UNIV NEW YORK STATE.

PI Chiaux DS, Pagano M, Latres E;

DR WPI; 2000-256635/22.

DR N-PSDB; AA293350.

XX Novel nucleic acid for screening compounds useful for treating

PT proliferative and differentiative disorders such as cancer and immune

PT disorders comprises sequences encoding ubiquitin ligases

XX Disclosure: Figure 3a; 245pp; English.

XX Nucleic acids encoding substrate-targeting subunits of ubiquitin
 CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 CC of proliferative and differentiated related disorders by measuring
 CC FBP gene expression. Cells expressing such proteins or
 CC their fragments are useful for screening compounds. The compounds
 CC are agonists or antagonists, which are useful for treating a
 CC proliferative or differentiative disorder in a mammal such as
 CC breast, ovarian and prostate cancer and small cell lung carcinoma
 CC and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein,
 CC analogs, derivatives and their subsequences, anti-FBP antibodies
 CC are also useful in diagnosis of the disorders.

XX Sequence 569 AA:

Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGIACTQYRDRLVVGSSDNTIRLM 29

Db 427 NGHKGIACTQYRDRLVVGSSDNTIRLM 455

RESULT 11

ID AAY83250 standard; Protein; 569 AA.

AC AAY83250;

XX 16-AUG-2000 (first entry)

DE F-box protein hBetaTrcp.

KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human.

OS Homo sapiens.

PN WO200022110-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23705.

PR 09-OCT-1998; 98US-0103787.

PR (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR WPI; 2000-317970/27.

DR N-PSDB; AA293710.

PT Targeting degradation of polypeptide useful for treating cancer and
 PT other proliferative disorders. Involves conjugating polypeptide with
 PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 PT compound

XX Claim 9; Page 171; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

XX Sequence 569 AA:

Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGIACTQYRDRLVVGSSDNTIRLM 29

Db 427 NGHKGIACTQYRDRLVVGSSDNTIRLM 455

RESULT 12

ID AAY83254 standard; Protein; 569 AA.

AC AAY83254;

DT 16-AUG-2000 (first entry)

DE F-box protein FWD1p.

PT Human cell signalling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders -
 XX
 PS Claim 1; Page 77-78; 90pp; English.
 CC The present sequence is cell signalling protein-12 (CSIGP-12) encoded
 CC by cDNA obtained from Incyte clone 3239149 of COLAUC01 library. It is
 CC expressed in musculoskeletal, gastrointestinal and nervous tissues and is
 CC found to be homologous to beta-transducin repeats containing
 CC protein. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 156; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 NGHKGRIACLOYRDRLVSGSSDNTIRLM 29
 427 NGHKGRIACLOYRDRLVSGSSDNTIRLM 455
 RESULT 14
 AAB48298
 ID AAB48298 standard; protein; 569 AA.
 AC AAB48298;
 XX
 DT 02-APR-2001 (first entry)
 DE Human zfp11 protein.
 XX
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.
 XX
 OS Homo sapiens.
 PA WO200075184-A1.
 PN 14-DEC-2000.
 PD
 XX
 PF 05-JUN-2000; 2000MO-US15449.
 XX
 PR 04-JUN-1999; 990US-0137494.
 XX
 PA (UYVA) UNIV VALE.
 PI Zhang H, Tsvetkov LM, Kondo T;
 DR WPI; 2001-061703/07.
 DR N-PSDB; AAC84610.
 XX
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 XX
 PS Claim 3; Page 130-132; 162pp; English.
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for

CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 XX
 SQ Sequence 569 AA:
 Query Match 100.0%; Score 156; DB 22; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 NGHKGRIACLOYRDRLVSGSSDNTIRLM 29
 427 NGHKGRIACLOYRDRLVSGSSDNTIRLM 455
 RESULT 15
 AAM78583
 ID AAM78583 standard; protein; 579 AA.
 AC AAM78583;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 1245.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 PA WO200157190-A2.
 PN 09-AUG-2001.
 PD
 XX
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51716.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3504-3505; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78133-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation.
 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

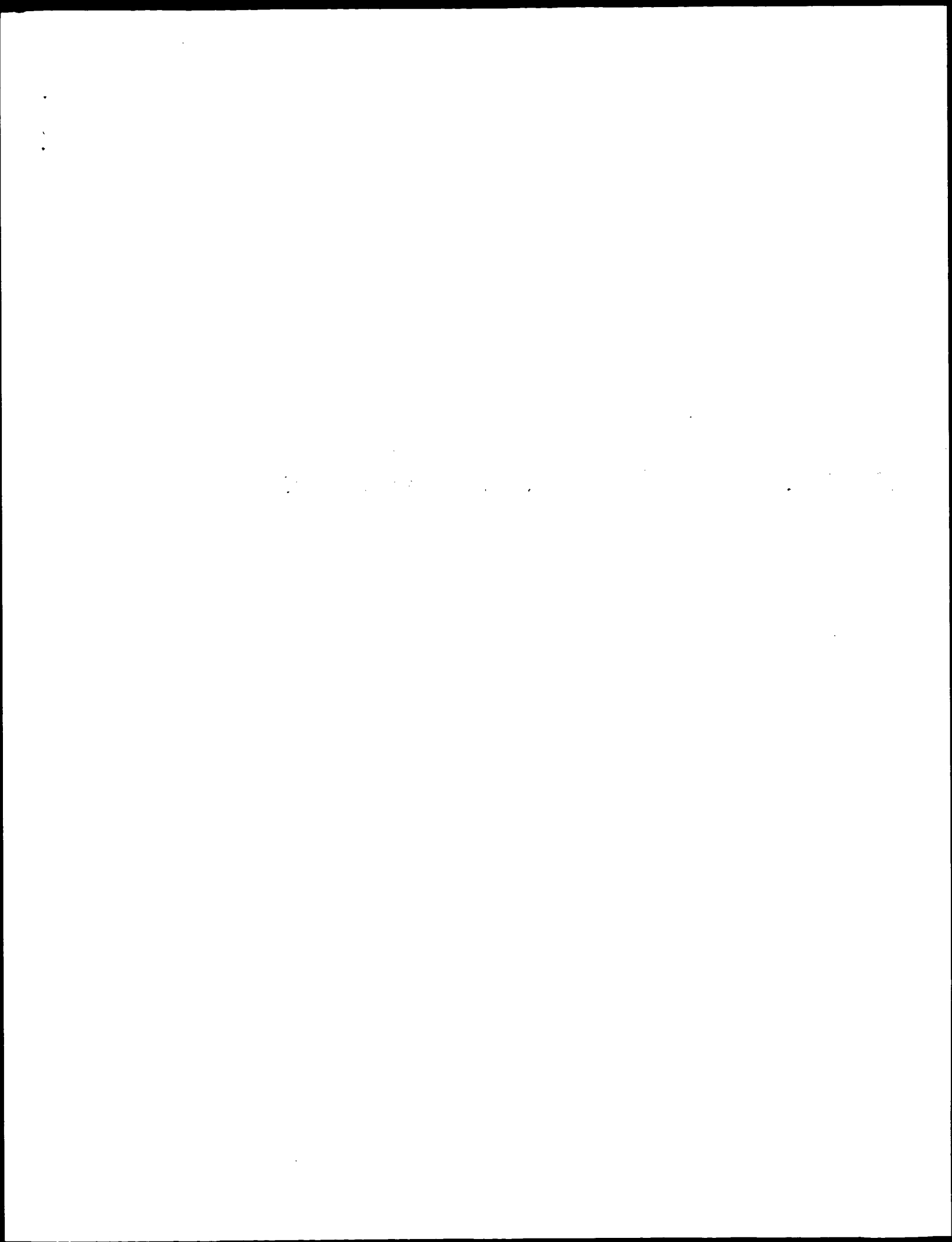
CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 579 AA;

Query Match 100.0%; Score 156; DB 22; Length 579;
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKRGIAQLQYRDRLVWGSSDNTIRLW 29
 |||
 Db 437 NGHKRGIAQLQYRDRLVWGSSDNTIRLW 465

Search completed: April 11, 2003, 11:48:16
 Job time : 8.93666 secs



GenCore version 5.1.4_P5_A578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.00244 Seconds
(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168B-2_COPY_427_455
Perfect score: 156
Sequence: 1 NGHKGICLQYRDRLVYSGSSDNTIRLM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574 ;

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/5A.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	100.0	517	1	US-08-190-802A-30
2	156	100.0	517	4	US-08-477-346-30
3	156	100.0	517	4	US-08-473-089-30
4	156	100.0	517	4	US-08-477-072A-30
5	150	96.2	29	1	US-08-190-802A-87
6	150	96.2	29	4	US-08-477-346-87
7	150	96.2	29	4	US-08-473-089-87
8	150	96.2	29	4	US-08-487-072A-87
9	87	55.8	34	1	US-08-190-802A-83
10	87	55.8	34	4	US-08-477-346-83
11	87	55.8	34	4	US-08-473-089-83
12	87	55.8	34	4	US-08-487-072A-83
13	82.5	52.9	28	1	US-08-190-802A-84
14	82.5	52.9	28	4	US-08-477-346-84
15	82.5	52.9	28	4	US-08-473-089-84
16	82.5	52.9	28	4	US-08-487-072A-84
17	78	50.0	640	4	US-09-177-165A-30
18	74.5	47.8	209	3	US-08-899-578-6
19	74.5	47.8	587	3	US-08-899-578-2
20	70	44.9	31	1	US-08-190-802A-93
21	70	44.9	31	1	US-08-190-802A-230
22	70	44.9	31	4	US-08-477-346-93
23	70	44.9	31	4	US-08-477-346-230
24	70	44.9	31	4	US-08-473-089-93
25	70	44.9	31	4	US-08-473-089-230
26	70	44.9	31	4	US-08-487-072A-93
27	70	44.9	31	4	US-08-487-072A-230

28	70	44.9	704	1	US-08-190-802A-62	Sequence 62, Appl
29	70	44.9	704	1	US-08-188-582-5	Sequence 5, Appl
30	70	44.9	704	1	US-08-646-715-5	Sequence 5, Appl
31	70	44.9	704	2	US-08-308-818-3	Sequence 3, Appl
32	70	44.9	704	4	US-08-477-346-62	Sequence 62, Appl
33	70	44.9	704	4	US-08-473-089-62	Sequence 62, Appl
34	70	44.9	704	4	US-08-487-072A-62	Sequence 31, Appl
35	70	44.9	906	1	US-08-190-802A-31	Sequence 31, Appl
36	70	44.9	906	4	US-08-473-089-31	Sequence 31, Appl
37	70	44.9	906	4	US-08-487-072A-31	Sequence 23, Appl
38	70	44.9	906	4	US-08-988-856B-23	Sequence 7, Appl
39	69.5	44.6	41	3	US-08-899-578-7	Sequence 32, Appl
40	69.5	44.6	212	3	US-08-190-802A-32	Sequence 32, Appl
41	69.5	44.6	779	1	US-08-477-346-32	Sequence 32, Appl
42	69.5	44.6	779	4	US-08-473-089-32	Sequence 32, Appl
43	69.5	44.6	779	4	US-08-487-072A-32	Sequence 29, Appl
44	69.5	44.6	779	4	US-09-177-165A-29	
45	69.5	44.6	779	4		

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Kon, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Delinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 517 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

US-08-190-802A-30

Query Match 100.0% ; Score 156; DB 1; Length 517;
Best Local Similarity 100.0% ; Pred. No. 1.3e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NGHKGICLQYRDRLVYSGSSDNTIRLM 29

Db 391 NGHKGRIACLOYRDRLVYSGSSDNTIRLM 419

RESULT 2

US-08-477-346-30
 ; Sequence 30, Application US/08477346
 ; Patent No. 6262023
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,346
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/487,072
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2550-0025.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 517 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 ; US-08-477-346-30

Query Match 100.0%; Score 156; DB 4; Length 517;
 Best local Similarity 100.0%; Pred. No. 1.3e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGRIACLOYRDRLVYSGSSDNTIRLM 29
 Db 391 NGHKGRIACLOYRDRLVYSGSSDNTIRLM 419

RESULT 3

US-08-473-089-30
 ; Sequence 30, Application US/08473089
 ; Patent No. 6342368
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,089
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 517 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 US-08-473-089-30

Query Match 100.0%; Score 156; DB 4; Length 517;
 Best local Similarity 100.0%; Pred. No. 1.3e-16;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHKGRIACLOYRDRLVYSGSSDNTIRLM 29
 Db 391 NGHKGRIACLOYRDRLVYSGSSDNTIRLM 419

RESULT 4

US-08-487-072A-30
 ; Sequence 30, Application US/08487072A
 ; Patent No. 6423684
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,072A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2550-0025.20
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 100.0%; Score 156; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 29
DB 391 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 419

RESULT 5
US-08-190-802A-87
Sequence 87, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190.802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-190-802A-87

Query Match 96.2%; Score 150; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 29

DB 1 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 28

RESULT 6
US-08-477-346-87
Sequence 87, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morlison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-477-346-87

Query Match 96.2%; Score 150; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 29
DB 1 GHKRGIAQLQYRDRLVYSGSSDNTIRLM 28

RESULT 7
US-08-473-089-87
Sequence 87, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morlison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/473.089
APPLICATION NUMBER: US/08/473.089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-473-089-87

Query Match 96.2%; Score 150; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GHKRGIACTGYRDLRYVSGSSDNTIRLM 29
DB 1 GHKRGIACTGYRDLRYVSGSSDNTIRLM 28

RESULT 8
US-08-487-072A-87
Sequence 87, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/487.072A
APPLICATION NUMBER: US/08/487.072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-487-072A-87

Query Match 96.2%; Score 150; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GHKRGIACTGYRDLRYVSGSSDNTIRLM 29
DB 1 GHKRGIACTGYRDLRYVSGSSDNTIRLM 28

RESULT 9
US-08-190-802A-83
Sequence 83, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/190.802A
APPLICATION NUMBER: US/08/190.802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP IV, Fig. 13
US-08-190-802A-83

Query Match 55.8%; Score 87; DB 1; Length 34;
Best Local Similarity 56.0%; Pred. No. 4.4e-07;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 5 RGIACTGYRDLRYVSGSSDNTIRLM 29

Db 9 KGVYCLQYDDQKIVSGLRDNTIKIW 33

RESULT 10

US-08-477-346-83
Sequence 83, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-477-346-83

Query Match 55.8%; Score 87; DB 4; Length 34;
Best Local Similarity 56.0%; Pred. No. 4.4e-07;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 5 RGIAQLQYRDLRVVSGSSDNTIRLM 29
Db 9 KGVYCLQYDDQKIVSGLRDNTIKIW 33

RESULT 11

US-08-473-089-83
Sequence 83, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rI, Fig. 13
US-08-473-089-83

Query Match 55.8%; Score 87; DB 4; Length 34;
Best Local Similarity 56.0%; Pred. No. 4.4e-07;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 5 RGIAQLQYRDLRVVSGSSDNTIRLM 29
Db 9 KGVYCLQYDDQKIVSGLRDNTIKIW 33

RESULT 12

US-08-487-072A-83
Sequence 83, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-487-072A-83

Query Match 52.8%; Score 87; DB 4; Length 34;
Best Local Similarity 56.0%; Pred. No. 4.4e-07;
Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 5 GKIACIQYRDLVYSGSSDNTIRLM 29
DB 9 KGVYCLQYDDQKIVSGLRDNTIKIW 33

RESULT 13
US-08-190-802A-84
Sequence 84, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33, 875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-190-802A-84

Query Match 52.9%; Score 82.5; DB 1; Length 28;
Best Local Similarity 46.4%; Pred. No. 1.8e-06;
Matches 13; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

OY 2 GKKRIACIQYRDLVYSGSSDNTIRLM 29

DB 1 GHTGSVLCIQYDERVITIG-SDSTVRW 27

RESULT 14
US-08-477-346-84
Sequence 84, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/487, 072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-477-346-84

Query Match 52.9%; Score 82.5; DB 4; Length 28;
Best Local Similarity 46.4%; Pred. No. 1.8e-06;
Matches 13; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

OY 2 GHTGSVLCIQYDERVITIG-SDSTVRW 27
DB 1 GHTGSVLCIQYDERVITIG-SDSTVRW 27

RESULT 15
US-08-473-089-84
Sequence 84, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF INVENTION: Theof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

```

: STREET: 2000 Pennsylvania Avenue, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,089
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 2550-0025.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 84:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: BETA TRCP r11, Fig. 13
: US-08-473-089-84

Query Match 52.9%; Score 82.5; DB 4; Length 28;
Best Local Similarity 46.4%; Pred. No. 1.8e-06;
Matches 13; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

Oy 2 GHKRGICLOYRDRLVVGSSDNTIRLM 29
| | : | | | : | | | | : | | : |
Db 1 GHTGSVLCLOYDERVITIG-SDSTVRVW 27

```

Search completed: April 10, 2003, 12:51:19
 Job time : 3.00244 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 2.96711 Seconds
(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_427_455

Perfect score: 156

Sequence: 1 NGHKRGACLOQRDLRVVSGSSDNTIRLM 29

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	156	100.0	569	12	US-10-042-417-2
3	91	58.3	678	10	US-09-801-368-314
4	79	50.6	540	9	US-09-213-888-7
5	79	50.6	540	9	US-09-213-888-10
6	79	50.6	540	9	US-09-328-877A-7
7	79	50.6	540	9	US-09-328-877A-10
8	79	50.6	545	9	US-09-213-888-6
9	79	50.6	545	9	US-09-328-877A-6
10	79	50.6	553	9	US-09-213-888-5
11	79	50.6	553	9	US-09-328-877A-5
12	79	50.6	559	9	US-09-213-888-9
13	79	50.6	559	9	US-09-328-877A-9
14	79	50.6	589	9	US-09-213-888-8
15	79	50.6	589	9	US-09-328-877A-8
16	79	50.6	592	9	US-09-213-888-4
17	79	50.6	626	9	US-09-328-877A-4
18	79	50.6	626	9	US-09-213-888-21
19	79	50.6	626	9	US-09-328-877A-21

20	79	50.6	627	9	US-09-213-888-3	Sequence 3, Appli
21	79	50.6	627	9	US-09-328-877A-3	Sequence 3, Appli
22	79	50.6	666	9	US-09-213-888-27	Sequence 27, Appli
23	79	50.6	666	9	US-09-328-877A-27	Sequence 27, Appli
24	79	50.6	669	9	US-09-213-888-25	Sequence 25, Appli
25	79	50.6	669	9	US-09-328-877A-25	Sequence 25, Appli
26	78	50.0	640	9	US-09-213-888-25	Sequence 25, Appli
27	70	44.9	744	10	US-10-060-019-30	Sequence 30, Appli
28	69.5	44.6	744	10	US-09-925-300-1347	Sequence 1347, Ap
29	69.5	44.6	779	9	US-09-843-845-23	Sequence 23, Appli
30	68.5	43.9	779	9	US-10-060-019-29	Sequence 29, Appli
31	68	43.6	732	9	US-09-832-357-897	Sequence 897, App
32	68	43.6	732	9	US-09-832-292-12	Sequence 12, Appli
33	67	42.9	1146	9	US-09-994-485-8	Sequence 8, Appli
34	67	42.9	1146	9	US-09-832-292-10	Sequence 10, Appli
35	65.5	42.0	484	9	US-09-843-845-6	Sequence 6, Appli
36	65.5	42.0	484	9	US-10-132-744A-2	Sequence 2, Appli
37	65.5	42.0	485	9	US-10-132-744A-6	Sequence 6, Appli
38	65	41.7	44	10	US-09-843-845-26	Sequence 26, Appli
39	65	41.7	296	9	US-10-083-357-1300	Sequence 1300, Ap
40	65	41.7	713	10	US-09-801-368-408	Sequence 408, App
41	63.5	40.4	64	10	US-09-843-845-20	Sequence 20, Appli
42	63	40.4	422	12	US-09-864-761-36159	Sequence 36159, A
43	63	40.4	422	12	US-10-042-417-4	Sequence 4, Appli
44	62	39.7	114	9	US-09-796-692-1445	Sequence 1445, Ap
45	62	39.7	114	9	US-09-796-692-1541	Sequence 1541, Ap

ALIGNMENTS

RESULT 1
US-10-038-010-8 Application US/10038010
Sequence 8, Appli
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT FILING DATE: 2002-07-23
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/10/038,010
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta-TrCP1
LOCATION: (1)..(569)
OTHER INFORMATION:
US-10-038-010-8

Query Match 100.0% Score 156; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 2,4e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGHKRGACLOQRDLRVVSGSSDNTIRLM 29
Db 427 NGHKRGACLOQRDLRVVSGSSDNTIRLM 455

RESULT 2
US-10-042-417-2
Sequence 2, Appli Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pagano, M
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042.417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 156; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRGACLOYRDRLVSSSDNTIRLW 29
Db 427 NGRGACLOYRDRLVSSSDNTIRLW 455

RESULT 3
US-09-801-368-314
Sequence 314, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 314
LENGTH: 678
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-801-368-314

Query Match 58.3%; Score 91; DB 10; Length 678;
Best Local Similarity 53.6%; Pred. No. 4.7e-06;
Matches 15; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHRGACLOYRDRLVSSSDNTIRLW 29
Db 387 GHRGACLOYRDRLVSSSDNTIRLW 414

RESULT 4
US-09-213-888-7
Sequence 7, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 50.6%; Score 79; DB 9; Length 540;
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHRGACLOYRDRLVSSSDNTIRLW 29
Db 252 GHRGACLOYRDRLVSSSDNTIRLW 279

RESULT 5
US-09-213-888-10
Sequence 10, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-10

Query Match 50.6%; Score 79; DB 9; Length 540;
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHRGACLOYRDRLVSSSDNTIRLW 29
Db 252 GHRGACLOYRDRLVSSSDNTIRLW 279

RESULT 6
US-09-328-877A-7
Sequence 7, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT

ORGANISM: Homo sapiens
US-09-328-877A-7

Query Match
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHKRGACLOYRDLRVSGSSDNTIRLW 29
Db 252 GHTGCVSSQMRDNIISGSTDRTLKW 279

RESULT 7

US-09-328-877A-10
Sequence 10, Application US/09328877A
Patent No. US2002017187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-10

Query Match
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHKRGACLOYRDLRVSGSSDNTIRLW 29
Db 252 GHTGCVSSQMRDNIISGSTDRTLKW 279

RESULT 8

US-09-213-888-6
Sequence 6, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-6

Query Match
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHKRGACLOYRDLRVSGSSDNTIRLW 29
Db 257 GHTGCVSSQMRDNIISGSTDRTLKW 284

RESULT 9
US-09-328-877A-6

Sequence 6, Application US/09328877A
Patent No. US2002017187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-6

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Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHKRGACLOYRDLRVSGSSDNTIRLW 29
Db 257 GHTGCVSSQMRDNIISGSTDRTLKW 284

RESULT 10

US-09-213-888-5
Sequence 5, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-5

Query Match
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHKRGACLOYRDLRVSGSSDNTIRLW 29
Db 265 GHTGCVSSQMRDNIISGSTDRTLKW 292

RESULT 11

US-09-328-877A-5
Sequence 5, Application US/09328877A
Patent No. US2002017187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

FILE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match 50.6%; Score 79; DB 9; Length 553;
Best Local Similarity 42.9%; Pred. No. 0.00028;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSGSSDNTIRLM 29
DB 265 GHTGGVSSQMRDNIISGSTDRILKYM 292

RESULT 12
US-09-213-888-9
Sequence 9, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-9

Query Match 50.6%; Score 79; DB 9; Length 559;
Best Local Similarity 42.9%; Pred. No. 0.00029;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSGSSDNTIRLM 29
DB 271 GHTGGVSSQMRDNIISGSTDRILKYM 298

RESULT 13
US-09-328-877A-9
Sequence 9, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-9

Query Match 50.6%; Score 79; DB 9; Length 559;
Best Local Similarity 42.9%; Pred. No. 0.00029;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSGSSDNTIRLM 29
DB 271 GHTGGVSSQMRDNIISGSTDRILKYM 298

RESULT 14
US-09-213-888-8
Sequence 8, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 589
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-8

Query Match 50.6%; Score 79; DB 9; Length 589;
Best Local Similarity 42.9%; Pred. No. 0.00031;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSGSSDNTIRLM 29
DB 301 GHTGGVSSQMRDNIISGSTDRILKYM 328

RESULT 15
US-09-328-877A-8
Sequence 8, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 589
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-8

Query Match 50.6%; Score 79; DB 9; Length 589;
Best Local Similarity 42.9%; Pred. No. 0.00031;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSGSSDNTIRLM 29
DB 301 GHTGGVSSQMRDNIISGSTDRILKYM 328

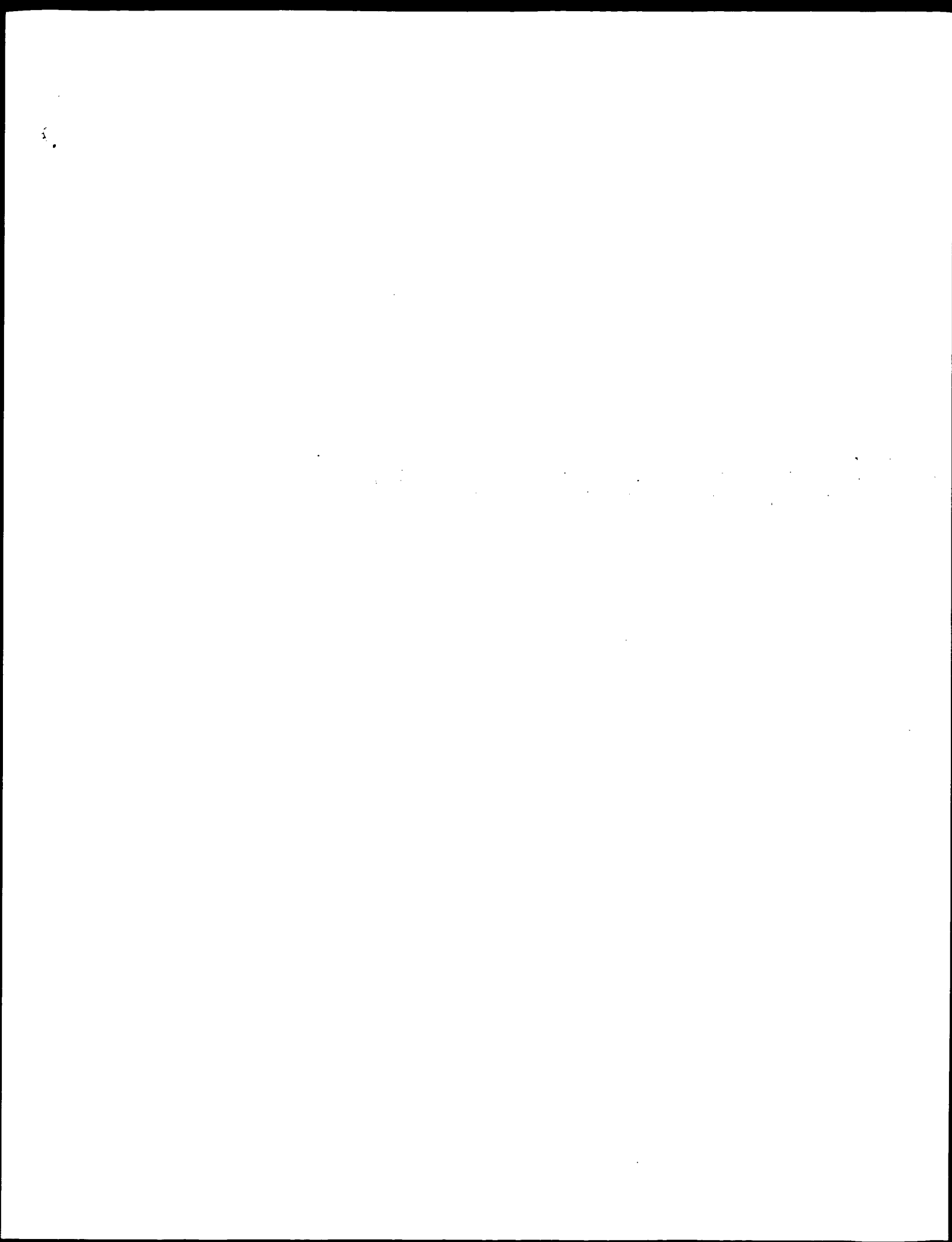
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Fri Apr 11 13:31:12 2003

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Page 5

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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.35566 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_427_455
Perfect score: 156
Sequence: 1 NGHKRGIAQLQYRDRLVYSGSSDNTIRLM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	95	60.9	506	2	T50211
5	87	55.8	650	2	T46660
6	86	55.1	605	2	T38932
7	79	50.6	415	2	T00642
8	79	50.6	438	2	T45823
9	78.5	50.3	558	2	T40651
10	78	50.0	640	2	T49952
11	77	49.4	651	2	T50289
12	76	48.7	465	2	T00982
13	75	48.1	1893	2	T22661
14	75	48.1	703	2	T43557
15	74.5	47.8	579	2	T22703
16	73	46.8	659	2	S38108
17	73	46.8	1747	2	AC1842
18	72.5	46.5	760	2	T41644
19	72	46.2	532	2	T18432
20	72	46.2	1201	1	ERBYA
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22	70	44.9	265	2	AP1890
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25	70	44.9	715	2	S38051
26	70	44.9	906	2	S35342
27	70	44.9	906	2	S35312
28	70	44.9	961	2	E86245
29	70	44.9	1184	2	A96638

30	69.5	44.6	779	2	S56245	cell division cont
31	69	44.2	333	2	G85034	probable WD-repeat
32	69	44.2	777	2	T41075	hypothetical WD-re
33	68.5	43.9	473	2	T33805	hypothetical prote
34	68.5	43.9	601	2	T38258	coronin-like prote
35	68	43.6	495	2	T04784	hypothetical prote
36	68	43.6	614	2	S58306	WD-40 repeat regul
37	68	43.6	755	2	T00066	hypothetical prote
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ALIGNMENTS

RESULT 1
B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trop
C:Species: Xenopus laevis (African clawed frog)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; MUID:93330289; PMID:8393141
A:Accession: B48088
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SP>
A:Cross-references: GB:98268; NID:9295542; PIDN:AAA02810.1; PID:9295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <WD1>

Query Match 100.0%; Score 156; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NGHKRGIAQLQYRDRLVYSGSSDNTIRLM 29
DB 392 NGHKRGIAQLQYRDRLVYSGSSDNTIRLM 420

RESULT 2

T16607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
R:Miller, N.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: Z18545
A:Accession: T16607
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-701 <ML>
A:Cross-references: EMBL:028730; NID:9860694; PID:9860695; PIDN:AAA68258.1; CESP:K10B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.1
A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
Query Match 89.7%; Score 140; DB 2; Length 701;
Best Local Similarity 92.9%; Pred. No. 1.4e-13;
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVVGSSDNTIRLM 29
 ||:||||||| |||||||||||||
 Db 419 GHKRGIAQLQYRDRLVVGSSDNTIRLM 446

RESULT 3

S62507
 hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
 C:Accession: T38502; S62507
 R:Jones, L.; Murphy, L.; McNeill, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandream,
 submitted to the EMBL Data Library, October 1995
 A:Reference number: Z21798
 A:Accession: T38502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1267 <02>
 A:Cross-references: EMBL:266525; NID:g1044926; PIDN:CAA91423.1; PID:g1044927; GSPDB:GN00
 C:Genetics:
 A:Map position: 1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:18-51/Domain: WD repeat homology <WD1>
 F:104-137/Domain: WD repeat homology <WD2>

Query Match 60.9%; Score 95; DB 2; Length 267;
 Best Local Similarity 58.6%; Pred. No. 5.5e-07;
 Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GHKRGIAQLQYRDRLVVGSSDNTIRLM 29
 ||:||||||| |||||||||||||
 Db 147 GHKRGIAQLQYRDRLVVGSSDNTIRLM 175

RESULT 4

T50211
 WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
 C:Accession: T50211
 R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; Mc
 submitted to the EMBL Data Library, January 2000
 A:Reference number: Z25046
 A:Accession: T50211
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1506 <MCD>
 A:Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05
 A:Experimental source: strain 972h(-); cosmid G30
 C:Genetics:
 A:Gene: SPAC29E6.01; SPDB:SPAC30.05
 A:Map position: 1
 A:Introns: 43/1; 74/3
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 60.9%; Score 95; DB 2; Length 506;
 Best Local Similarity 58.6%; Pred. No. 1.1e-06;
 Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GHKRGIAQLQYRDRLVVGSSDNTIRLM 29
 ||:||||||| |||||||||||||
 Db 386 GHKRGIAQLQYRDRLVVGSSDNTIRLM 414

RESULT 5

T46660
 sulfur controller-2 protein [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
 C:Accession: T46660
 R:Kumar, A.; Paietta, J.V.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995

A:Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encode
 A:Reference number: Z23121; MUID:95241499; PMID:7724564
 A:Accession: T46660
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1650 <KUM>
 A:Cross-references: EMBL:U17251; NID:g806757; PIDN:AAA68968.1; PID:g806758
 C:Genetics:
 A:Gene: scon-2
 A:Map position: 3
 A:Introns: 75/3; 319/1; 354/1
 C:Function:
 A:Description: negatively regulates sulfur structural gene expression
 A:Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to t
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 55.8%; Score 87; DB 2; Length 650;
 Best Local Similarity 46.4%; Pred. No. 2.5e-05;
 Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVVGSSDNTIRLM 29
 ||:||||||| |||||||||||||
 Db 292 GHKRGIAQLQYRDRLVVGSSDNTIRLM 319

RESULT 6

T38932
 probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
 C:Accession: T38932
 R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, April 1997
 A:Reference number: Z21818
 A:Accession: T38932
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1605 <BAD>
 A:Cross-references: EMBL:Z94864; PIDN:CAB08168.1; GSPDB:GN00066; SPDB:SPAC57A10.05C
 A:Experimental source: strain 972h(-); cosmid c57A10
 C:Genetics:
 A:Gene: SPDB:SPAC57A10.05C
 A:Map position: 1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 55.1%; Score 86; DB 2; Length 605;
 Best Local Similarity 50.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVVGSSDNTIRLM 29
 ||:||||||| |||||||||||||
 Db 311 GHKRGIAQLQYRDRLVVGSSDNTIRLM 338

RESULT 7

T00642
 hypothetical protein F316.5 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 22-Oct-1999
 C:Accession: T00642
 R:Federpiet, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Arau
 submitted to the EMBL Data Library, February 1998
 A:Reference number: Z14197
 A:Accession: T00642
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1415 <RED>
 A:Cross-references: EMBL:AC002396; NID:g2749918; PID:g2829890; GSPDB:GN00059; ATSP:F3
 C:Genetics:
 A:Gene: ATSP:F316.5
 A:Map position: 1

Query Match 50.6%; Score 79; DB 2; Length 415;
 Best Local Similarity 46.4%; Pred. No. 0.00028;
 Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 2 GHRKGACLOVRRLVSSGSDNTIRLW 29
 DB 326 GHRKATMCLAVASDLVSLVSGSDKSLRW 353

RESULT 8

hypothetical protein F2K15.40 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45823
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
 A:Reference number: 223015
 A:Accession: T45823
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-438 <RIE>
 A:Cross-references: EMBL:AL132956
 A:Experimental source: cultivar Columbia; BAC clone F2K15

C:Genetics:
 A:Map position: 3
 A:Introns: 68/3; 151/2; 200/3; 263/2; 306/1; 389/3
 A:Note: F2K15.40

Query Match 50.6%; Score 79; DB 2; Length 438;
 Best Local Similarity 48.4%; Pred. No. 0.0003;
 Matches 15; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

OY 1 NGHRGIACLOVR--DRLVSSGSDNTIRLW 29
 DB 117 NGHRYVTCLVFSGDDSLVSGSDGIRW 147

RESULT 9

T40651
 pre-mrna splicing factor, WD repeat protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T40651
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hamlin, N.; Churcher, C.M. submitted to the EMBL Data Library, February 1998
 A:Reference number: Z21943
 A:Accession: T40651
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-558 <WOO>

A:Cross-references: EMBL:AL021838; PIDN:CA117053.1; GSPDB:GNO0067; SPDB:SPBC6B1.10
 A:Experimental source: strain 972h-; cosmid c6B1
 C:Genetics:
 A:Gene: SPDB:SPBC6B1.10
 A:Map position: 2
 A:Introns: 37/3; 292/3; 498/1; 514/1

Query Match 50.3%; Score 78.5; DB 2; Length 558;
 Best Local Similarity 45.2%; Pred. No. 0.00046;
 Matches 14; Conservative 8; Mismatches 6; Indels 3; Gaps 1;

OY 2 GHRGIACLOVR--RDRLVSSGSDNTIRLW 29
 DB 264 GHRKIGISCLRFPPISGILLSSGMDNOKIW 294

RESULT 10

S49932

MET30 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein Y19905.02; protein YIL046W
 C:Species: Saccharomyces cerevisiae
 C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 26-May-2000

C:Accession: S49932; S43750
 R:Odell, C.; Bowman, S. submitted to the EMBL Data Library, December 1994
 A:Reference number: S49931
 A:Accession: S49932
 A:Molecule type: DNA
 A:Residues: 1-640 <ODE>

A:Cross-references: GB:Z47047; EMBL:Z46861; NID:9603997; PID:9763300; MIPS:YIL046W
 R:Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y. submitted to the EMBL Data Library, December 1993
 A:Reference number: S43750
 A:Accession: S43750
 A:Molecule type: DNA
 A:Residues: 1-60; '1', 62-640 <THO>

A:Cross-references: EMBL:126505; NID:g432493; PID:g432494
 C:Genetics:
 A:Gene: SGD:MET30
 A:Cross-references: SGD:S0001308; MIPS:YIL046W
 A:Map position: 9L
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:298-329/Domain: WD repeat homology <WD1>
 F:338-369/Domain: WD repeat homology <WD2>
 F:374-409/Domain: WD repeat homology <WD3>
 F:417-450/Domain: WD repeat homology <WD4>

Query Match 50.0%; Score 78; DB 2; Length 640;
 Best Local Similarity 44.8%; Pred. No. 0.00064;
 Matches 13; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 NGHRGIACLOVRRLVSSGSDNTIRLW 29
 DB 339 SGHSDGVKTLVFDKRLTGSIDKTIW 367

RESULT 11

T50289
 WD repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T50289
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25054
 A:Accession: T50289
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-651 <WOO>

A:Cross-references: EMBL:AL157993; PIDN:CA876232.1; GSPDB:GNO0066; SPDB:SPACUNK12.01
 A:Experimental source: strain 972h(-); cosmid c25D11
 C:Genetics:
 A:Gene: SPDB:SPACUNK12.01
 A:Map position: 1

Query Match 49.4%; Score 77; DB 2; Length 651;
 Best Local Similarity 42.9%; Pred. No. 0.00093;
 Matches 12; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 2 GHRGIACLOVRRLVSSGSDNTIRLW 29
 DB 372 GHSDVYCLAIODSFLATGSMOTVRLW 399

RESULT 12

T00982

En/Spm-like transposon protein [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T9J22.16
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T00982; B84661
 R:Hounsley, S.D.; Jin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, April 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
 A:Reference number: Z14161

A:Accession: T00982
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-465 <R0U>
 A:Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739374
 A:Experimental source: cultivar Columbia
 R:Rill, X.; Kaul, S.; Rounsley, S.D.; Shee, T.F.; Bentto, M.L.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84661
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <STO>
 A:Cross-references: GB:AE002093; NID:g2739374; PIDN:AAC14498.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT2g26490; T9J22.16
 A:Map position: 2

Query Match 48.7%; Score 76; DB 2; Length 465;
 Best Local Similarity 50.0%; Pred. No. 0.00093;
 Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 2 GHRGACIACLODRRLVSSGSSDNTIRLW 29
 ||| : ||: ||||| : ||: ||
 Db 336 GHKLAVLCLEAVAGSIVFGSADKTCICW 363

RESULT 13

T22661

hypothetical protein T01G1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T22661; T24305

R:White, S.; Mortimore, B.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19594

A:Accession: T22661

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1893 <WIL>

A:Cross-references: EMBL:Z82271; PIDN:CAB05214.1; GSPDB:GN00022; CESP:T01G1.1

A:Experimental source: clone F54E12

R:Kershaw, J.

Submitted to the EMBL Data Library, March 1997

A:Reference number: Z19872

A:Accession: T24305

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1893 <W12>

A:Cross-references: EMBL:Z92811; PIDN:CAB07273.1; GSPDB:GN00022; CESP:T01G1.1

A:Experimental source: clone T01G1

C:Genetics:

A:Gene: CESP:T01G1.1

A:Map position: 4

A:introns: 65/3; 101/3; 194/3; 269/3; 299/2; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1;

Query Match

Best Local Similarity 48.7%; Score 76; DB 2; Length 1893;

Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 2 GHRGACIACLODRRLVSSGSSDNTIRLW 29

||| : ||: ||||| : ||: ||

Db 1570 GHARGVLSVDVNEKLVTSKDRITAKLW 1597

RESULT 14

T43557

F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: proteolysis factor stud1

C:Species: Schizosaccharomyces pombe

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T43557; T38794; T43798
 R:Wolff, D.A.; Jackson, P.K.

Submitted to the EMBL Data Library, December 1997

A:Description: fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in

A:Reference number: Z22576

A:Accession: T43557

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-703 <MOL>

A:Cross-references: EMBL:AF038867; PIDN:AA95480.1

A:Experimental source: strain h-972

R:Gentles, S.; Churcher, C.M.; Bartell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z21812

A:Accession: T38794

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-703 <GEN>

A:Cross-references: EMBL:Z98602; PIDN:CAB11275.1; GSPDB:GN00066; SPDB:SPAC4D7.03

A:Experimental source: strain 972h; cosmid c4D7

R:Jalilepalli, P.V.; Tien, D.; Kelly, T.J.

Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998

A:Title: Stud1 targets cyclin-dependent kinase-phosphorylated Cdc18 and Rnm1 proteins

A:Reference number: Z22686; MUID:98318628; PMID:9653157

A:Accession: T43798

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-703 <JAL>

A:Cross-references: EMBL:AF064515; NID:g3293382; PIDN:AAC39496.1; PID:g3293383

C:Genetics:

A:Gene: pop2; stud1; SPAC4D7.03

A:Map position: 1

C:Function: required to prevent spontaneous re-replication

Query Match 48.1%; Score 75; DB 2; Length 703;
 Best Local Similarity 42.9%; Pred. No. 0.0021;
 Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 2 GHRGACIACLODRRLVSSGSSDNTIRLW 29
 ||| : ||: ||||| : ||: ||
 Db 389 GHKEGVAVKIHEMLVSGSIDKTVRW 416

RESULT 15

T22703

hypothetical protein F55B12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22703

R:Sim, M.

submitted to the EMBL Data Library, September 1996

A:Reference number: Z19602

A:Accession: T22703

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-579 <WIL>

A:Cross-references: EMBL:Z79757; PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3

A:Experimental source: clone F55B12

C:Genetics:

A:Gene: CESP:F55B12.3

A:Map position: 5

A:introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1

Query Match 47.8%; Score 74.5; DB 2; Length 579;
 Best Local Similarity 44.8%; Pred. No. 0.002;
 Matches 13; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

OY 2 GHR-RTIACLODRRLVSSGSSDNTIRLW 29
 ||| : ||: ||||| : ||: ||
 Db 245 GHEDHVTICMGIHDDVLTGSDNTLRKW 273

Fri Apr 11 13:31:12 2003

us-09-601-168b-2_copy_427_455.rpr

Page 5

Search completed: April 10, 2003, 13:23:04
Job time : 4.35566 secs

8

1

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 2.08404 Seconds
(without alignments)

577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_427_455

Sequence: 1 NGHKRGICLQYRDLVSGSSDNTIRLM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	100.0	518	TRCB_XENLA	Q91854 xenopus lae
2	156	100.0	542	FW1B_HUMAN	Q9ukb1 homo sapien
3	156	100.0	605	FW1A_HUMAN	Q9y297 homo sapien
4	140	89.7	665	LI23_CAEEL	Q09990 caenorhabdi
5	95	60.9	506	POB2_SCHPO	Q09855 schizosacch
6	91	58.3	678	SCOB_MENMI	Q00659 emericella
7	87	55.8	650	SC02_NEUCR	Q01277 neurospora
8	86	55.1	640	POB1_SCHPO	P87053 schizosacch
9	78	50.0	640	MT30_YEAST	P39014 saccharomyc
10	77	49.4	651	Y1X1_SCHPO	Q9P713 schizosacch
11	76	48.7	684	CC4_CANAL	P53699 candida alb
12	75	48.1	703	POB2_SCHPO	Q14170 schizosacch
13	74.5	47.8	579	SE10_CAEEL	Q93794 caenorhabdi
14	73	46.8	659	YK16_YEAST	P36130 saccharomyc
15	72	46.2	473	PRP5_SCHPO	Q13615 schizosacch
16	72	46.2	1201	COPA_YEAST	P53622 saccharomyc
17	71	45.5	361	WDS_DROME	Q9Y318 drosophila
18	70.5	45.2	446	CRH3_SCHPO	Q10272 schizosacch
19	70	44.9	704	T2D4_DROME	P49846 drosophila
20	70	44.9	715	DOA1_YEAST	P36037 saccharomyc
21	70	44.9	905	COPB_BOVIN	P36605 bos taurus
22	70	44.9	905	COPB_HUMAN	P055029 homo sapien
23	70	44.9	905	COPB_MOUSE	O55029 mus musculu
24	69.5	44.6	779	CC4_YEAST	P07834 saccharomyc
25	69	44.2	604	RCO1_NEUCR	P78706 neurospora
26	69	44.2	904	COPB_RAT	O35142 rattus norv
27	68.5	43.9	601	COPB_SCHPO	O13923 schizosacch
28	68	43.6	317	GBLP_HYDAT	Q25189 hydra atten
29	68	43.6	614	TU11_SCHPO	Q09715 schizosacch
30	68	43.6	732	KMBB_DICDI	P90648 dictyosteli
31	67	42.9	1146	KMRA_BOVIN	P42527 dictyosteli
32	67	42.9	1224	COPA_BOVIN	O27954 bos taurus
33	67	42.9	1224	COPA_HUMAN	P53621 homo sapien

34	66.5	42.6	515	1	YCW2_YEAST	P25382 saccharomyc
35	66	42.3	1000	1	COPB_CAEEL	Q20168 caenorhabdi
36	65	41.7	432	1	WDPI_HUMAN	Q9bv38 homo sapien
37	65	41.7	713	1	TUPL_YEAST	P16649 saccharomyc
38	65	41.7	800	1	T2D4_HUMAN	Q15542 homo sapien
39	64.5	41.3	578	1	YDEM_CAEEL	Q19124 caenorhabdi
40	64	41.0	334	1	WDR5_HUMAN	Q9ugp9 homo sapien
41	64	41.0	376	1	YKY4_CAEEL	Q17963 caenorhabdi
42	64	41.0	535	1	SIF2_YEAST	P38262 saccharomyc
43	64	41.0	714	1	YUJ2_YEAST	P47025 saccharomyc
44	64	41.0	910	1	PWP2_CAEEL	P91341 caenorhabdi
45	64	41.0	1258	1	YS00_ANASP	O8ytc2 anabaena sp

ALIGNMENTS

```

RESULT 1
ID      TRCB_XENLA      STANDARD:      PRT;      518 AA.
AC      Q91854: P70037; P70038;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Beta-TTCP (Beta-transducin repeat-containing protein).
GN      FBXW1 OR BTCP.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipodae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8335;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93330289; PubMed=8393141;
RA      Spevak W., Keiper B.D., Stratowa C., Castanon M.J.;
RT      "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
RT      anaphase are rescued by Xenopus CDNs encoding N-ras or a protein
RT      with beta-transducin repeats."
RL      Mol. Cell. Biol. 13:4953-4966(1993).
RN      [2]
RP      SEQUENCE OF 302-518 FROM N.A.
RX      MEDLINE=97109804; PubMed=8952061;
RA      Hudson J.W., Alarcon V.B., Ellinson R.P.;
RT      "Identification of new localized RNAs in the Xenopus oocyte by
RT      differential display PCR."
RL      Dev. Genet. 19:190-198(1996).
CC      -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC      proteins and promotes their ubiquitination and degradation.
CC      -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
CC      (BY SIMILARITY).
CC      -1- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
CC      MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
CC      GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
CC      NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
CC      TADPOLE EMBRYO.
CC      -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC      -1- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: M98268: AAA02810.1; -
DR      EMBL: U63921: AAB49671.1; -
DR      EMBL: U63922: AAB49672.1; -
DR      InterPro: IPR001810; F-box.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00400; WD40; 7.

```

FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=99075339; PubMed=9859996;
RX

RA Yaron A., Hatzubal A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase.";
 RL Nature 396:590-594(1998).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE-Lymphoid;
 RC MEDLINE=98325370; PubMed=9660940;
 RA Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebelt K., Benarous R.;
 RT "A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif.";
 RL Mol. Cell 11:565-574(1998).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RN CHARACTERIZATION.
 RP MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
 RA Harper J.W.;
 RT "The SCF(beta-Trcp)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and
 RT beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
 RL Genes Dev. 13:270-283(1999).
 CC -1- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA
 CC (UBIQUITINATION AND DEGRADATION).
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: AF101784; AAD08702.1; -
 CC EMBL: Y14153; CAAT4572.1; -
 CC EMBL: AF129530; AAF04464.1; -
 CC Genew: HGNC:1144; BTRC.
 CC MIM: 603482; -
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF004400; WD40; 7.
 CC Pfam: PF00646; F-box; 1.
 CC PRINTS: PR00320; GPROTEINRPT.
 CC PRODOM: PD000018; WD40; 4.
 CC SMART: SM00256; FBOX; 1.
 CC SMART: SM00320; WD40; 7.
 CC PROSITE: PS00181; FBOX; 1.
 CC PROSITE: PS00678; WD_REPEATS_1; 6.
 CC PROSITE: PS00082; WD_REPEATS_2; 7.
 CC PROSITE: PS0294; WD_REPEATS_REGION; 1.
 CC Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 KW DOMAIN 190 228 F-BOX.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.

FT REPEAT 553 590 WD 7.
 FT VARSPIC 17 52 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 605 AA: 68866 MW: 4C67FB7E400FD37 CRC64;
 Query Match 100.0%; Score 156; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 7.9e-17;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NGHKGIGACIQYRDRLVYSGSSDNTIRLM 29
 Db 463 NGHKGIGACIQYRDRLVYSGSSDNTIRLM 491
 RESULT 4
 ID LI23_CAEEL STANDARD; PRT; 665 AA.
 AC Q09990; Q09990; 36, Created)
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein lin-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderiinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RA MEDLINE=20515608; PubMed=11060233;
 RA Kipreos E.T., Gehl S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein lin-23 functions
 RT to limit cell division during development.";
 RL Development 127:5071-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterson R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 CC cycle progression. Required to restrain cell proliferation in
 CC response to developmental cues. Probably recognizes and binds to
 CC some proteins and promotes their ubiquitination and degradation
 CC (by similarity).
 CC -1- SUBUNIT: Part of a SCF (SKP1-Cullin-F-box) protein ligase complex
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 CC levels in larvae. Maternal expression results in high zygotic
 CC levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
 CC -----
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 CC -----
 CC EMBL: AF275253; AAG28037.1; -
 CC EMBL: U28730; AAA68258.2; -
 CC Wormpep: K10B2.1; CE28600.
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF004400; WD40; 7.
 CC Pfam: PF00646; F-box; 1.
 CC PRINTS: PR00320; GPROTEINRPT.

DR PRODOM; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Developmental protein; Cell cycle; Cell division;
 KW Ub1 conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 81 127
 FT REPEAT 220 257
 FT REPEAT 260 299
 FT REPEAT 301 337
 FT REPEAT 343 380
 FT REPEAT 383 420
 FT REPEAT 423 460
 FT REPEAT 472 509
 FT DOMAIN 525 582
 FT MUTAGEN 441 441
 SQ SEQUENCE 665 AA; 75916 MW; BF3P9AF51P12EC64; C64;
 G->R: IN LIN-32(RH293).
 Query Match 89.7%; Score 140; DB 1; Length 665;
 Best Local Similarity 92.9%; Pred. No. 3e-14; Mismatches 1; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GHRGIACTQYRRLVYSSSDNTIRLW 29
 DB 383 GHRGIACTQYRRLVYSSSDNTIRLW 410
 ID POFB_SCHPO STANDARD; PRT; 506 AA.
 AC 009855; 09P7V1;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein profilin.
 GN Profilin or SPAC295F.01 OR SPAC30.05.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harrison C.L., Toda T.;
 RT "Systematic genome-wide analysis of F-box protein-encoding genes in
 RL fission yeast."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peal N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Wellens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert A.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Beyer P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J.,
 RA Shipkavski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
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 CC -----
 DR EMBL; AB061694; BAB5543.1; -;
 DR EMBL; AL136538; CAB66464.1; -;
 DR EMBL; Z66525; CAA91423.1; -;
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00440; WD40; 7.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PRO0320; GPROTEINRPT.
 DR PRODOM; PD000018; WD40; 3.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 8.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT DOMAIN 70 116
 FT REPEAT 219 256
 FT REPEAT 259 298
 FT REPEAT 301 338
 FT REPEAT 345 386
 FT REPEAT 388 426
 FT REPEAT 427 464
 FT REPEAT 468 505
 SQ SEQUENCE 506 AA; 58257 MW; CEE34DAEFFEC2E10 C64;
 Query Match 60.9%; Score 95; DB 1; Length 506;
 Best Local Similarity 58.6%; Pred. No. 2.9e-07;
 Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 OY 1 NGHRGIACTQYRRLVYSSSDNTIRLW 29
 DB 386 HAHORGIACTQYRRLVYSSSDNTIRLW 414
 ID SCOB_EMENI STANDARD; PRT; 678 AA.
 AC 000659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sulfur metabolite repression control protein.
 GN SCOB OR MAPB1.
 OS Emricella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiaceae; Trichocomaceae; Emerticella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Natorff R.;
 RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
 CC REPRESSION.
 CC -1- SIMILARITY: CONTAINS 8 WD_REPEATS (TRP-ASP DOMAINS).
 CC -----

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CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
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CC -----
DR EMBL; U21220; AAC15905.1; .
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF004400; WD40; 7.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR Transcription regulation; Repeat; WD repeat.
KW DOMAIN
FT REPEAT 178 224 F-BOX.
FT REPEAT 347 375 WD 1.
FT REPEAT 387 415 WD 2.
FT REPEAT 427 455 WD 3.
FT REPEAT 466 496 WD 4.
FT REPEAT 508 543 WD 5.
FT REPEAT 553 595 WD 6.
FT REPEAT 607 635 WD 7.
FT REPEAT 647 675 WD 8.
SQ SEQUENCE 678 AA; 76070 MW; D840D452E37B4C53 CRC64;

Query Match
Best Local Similarity 58.3%; Score 91; DB 1; Length 678;
Matches 15; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSSGSSDNTIRLW 29
DB 387 GHESGIRCLQFDFTKLSSMDRTIKW 414

RESULT 7
SC02_NEUCR STANDARD; PRT; 650 AA.
AC 001277;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfur controller-2 (SCON2).
GN SCON-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=95241499; PubMed=7724564;
RA Kumar A., Paletta J.V.;
RT "The sulfur controller-2 negative regulatory gene of Neurospora
RT crassa encodes a protein with beta-transducin repeats.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
CC -1- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.

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CC -----
DR EMBL; U17251; AAA68968.1; .
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF004400; WD40; 7.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 6.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR Transcription regulation; Repeat; WD repeat.
KW DOMAIN
FT REPEAT 124 170 F-BOX.
FT REPEAT 292 320 WD 1.
FT REPEAT 332 360 WD 2.
FT REPEAT 372 400 WD 3.
FT REPEAT 411 441 WD 4.
FT REPEAT 453 488 WD 5.
FT REPEAT 528 564 WD 6.
FT REPEAT 576 604 WD 7.
FT REPEAT 616 644 WD 8.
SQ SEQUENCE 650 AA; 72189 MW; 7473859C99F1B028 CRC64;

Query Match
Best Local Similarity 55.8%; Score 87; DB 1; Length 650;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRDRLVSSGSSDNTIRLW 29
DB 292 GHENGVTCQLQDDNLLATSGSYDTIKIW 319

RESULT 8
POF1_SCHPO STANDARD; PRT; 605 AA.
AC P87053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof1 (Skp1-binding protein 1).
GN POF1 OR SBP1 OR SPAC57A10.05C.
OS Schizosaccharomyces pombe (fission yeast).
OC Schizosaccharomycetes; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Katayama S., Kilamuna K., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RT fission yeast.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

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RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Moorey P., Mole S., Mingall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gynopreux B.,
 RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Filiz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
 RT "the genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB032410; BAA84528.1; -
 DR EMBL: Z94864; CAB08168.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 5.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS00682; WD_REPEATS_2; 7.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Uni conjugation; Repeat; WD repeat.
 KW F-BOX.
 FT DOMAIN 107 153
 FT REPEAT 271 299 WD 1.
 FT REPEAT 311 339 WD 2.
 FT REPEAT 350 379 WD 3.
 FT REPEAT 390 420 WD 4.
 FT REPEAT 432 460 WD 5.
 FT REPEAT 472 500 WD 6.
 FT REPEAT 510 538 WD 7.
 SO SEQUENCE 605 AA; 67110 MW; 711809379BEC5C1F0 CRC64;

Query Match 55.18; Score 86; DB 1; Length 605;
 Best Local Similarity 50.0%; Pred. No. 9.4e-06;
 Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 GHKRGIAQLQYRRLVWGSSDNTIRLM 29
 DB 311 GHSSGVTCIAPDQCKLLSGSMKTRIM 338

RESULT 9
 MT30_YEAST STANDARD; PRT; 640 AA.
 ID MT30_YEAST

AC P39014;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MEM30 protein.
 GN MEM30 OR Y11046W.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180-1A;
 RC MEDLINE=96069360; PubMed=8524217;
 RA Thomas D., Kuras L., Barbey R., Charest H., Blaiseau P.L.,
 RA Surdin-Kerjan Y.,
 RT "Met30p, a yeast transcriptional inhibitor that responds to S-
 RT adenosylmethionine, is an essential protein with WD40 repeats";
 RL Mol. Cell. Biol. 15:6526-6534(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Barrett B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentles S., Hamlyn N., Hornsby T.S., Hunt S., Jagels K., Jones M.,
 RA Louis E., Lye G., Mole S., Mouton T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BIOSYNTHESIS
 CC GENES EXPRESSION.
 CC -1- SUBUNIT: SEEMS TO INTERACT WITH MET4.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE MET30/SCOF/SCON-2 FAMILY OF WD-REPEAT
 CC PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z46861; CAA86905.1; -
 DR EMBL: L26505; AAA96717.1; -
 DR SGD: S0001308; MET30.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transcription regulation; Methionine biosynthesis;
 KW Cysteine biosynthesis; Repeat; WD repeat.
 FT DOMAIN 181 227
 FT REPEAT 300 328 WD 1.
 FT REPEAT 340 368 WD 2.
 FT REPEAT 380 408 WD 3.
 FT REPEAT 419 449 WD 4.
 FT REPEAT 461 499 WD 5.
 FT REPEAT 509 538 WD 6.
 FT REPEAT 550 578 WD 7.
 FT REPEAT 607 635 WD 8 (POTENTIAL).
 FT CONFLICT 61 61 M -> I (IN REF. 1).
 SO SEQUENCE 640 AA; 72835 MW; 5135DABCA2E1B97 CRC64;

FT	REPEAT	478	506	WD 5.
FT	REPEAT	519	549	WD 6.
FT	REPEAT	561	589	WD 7.
SO	SEQUENCE	684 AA:	76090 MW:	3DD65DB31293b107 CRC64:
Query Match				
Best Local Similarity		48.7%:	Score 76:	DB 1; length 684;
Matches 12:		Conservative	8:	Mismatches 8; Indels 0; Gaps 0;
O7	2	GKKRRIACIQYRDRLVSSSSDNTIRLW 29		
Db	363	GHEGVMALKITGNTLVTSIDRTYKRV 390		
RESULT 12				
POP2_SCHPO				
ID	POP2_SCHPO	STANDARD:	PRT:	703 AA.
AC	014170:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUN-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	WD-repeat protein pop2 (Proteolysis factor sud1).			
GN	POP2 OR SUDI OR SPAC4D7.03.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OX	Schizosaccharomyces.			
OX	NCBI_TaxID=4896;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=99227353; PubMed=10209119;			
RA	Wolf D.A., McKeon F., Jackson P.K.;			
RT	"F-box/MD-repeat proteins pop1 and sud1/pop2 form complexes that			
RT	bind and direct the proteolysis of cdc18p.";			
RL	Curr. Biol. 9:373-376(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=98318628; PubMed=9653157;			
RA	Jaelllell P.V., Tien D., Kelly T.J.;			
RT	"sud1 targets cyclin-dependent kinase-phosphorylated Cdc18 and Runt			
RT	proteins for degradation and stops unwanted diploidization in fission			
RL	yeast.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:8159-8164(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Squires J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,			
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,			
RA	Rutherford K., Ritter S., Saunders D., Seeger K., Sharp S.,			
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Voiclaert G., Aert R., Robben J., Grymoprez B.,			
RA	Wetlens J., Vantrelts E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzym K., Langer I., Beck A., Lehnert H., Reinhardt R., Pohl T.M.,			
RA	Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Motter S.,			
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Roohet M., Galliard C., Tallada V.A., Garzon A., Thode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,			
RA	Cerrutti L., Lowe T., Mccombie W.R., Paulsen I., Potashkin J.,			
RA	Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;			
RT	"The genome sequence of Schizosaccharomyces pombe.";			

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RL Nucleotide 415:871-880(2002).
RM [4]
RP FUNCTION, AND SUBUNIT.
RC STRAIN=972;
RX MEDLINE=99144318; PubMed=9990507;
RA Komihama K.-I., Ochotorena I., Toda T.;
RT "Two F-box/WD-repeat proteins Popl and Pop2 form hetero- and homo-
RT complexes together with cullin-1 in fission yeast SCP (Skip-cullin-1-
RT F-box) ubiquitin ligase."
RL Genes Cells 3:721-735(1998).
CC -i- FUNCTION: Involved in maintenance of ploidy through proteasome
CC dependent degradation of CDK inhibitor run1 and 5-phase initiator
CC cdc18. Functions as a recognition factor for run1 and cdc18, which
CC are subsequently ubiquitinated and targeted to the 26S proteasome
CC for degradation.
CC -i- SUBUNIT: Homodimer and heterodimer with popl. Binds to pop1 and
CC cdc18.
CC -i- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -i- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF038667; AAC95480.1; -.
DR EMBL: AF064515; AAB9496.1; -.
DR EMBL: Z98602; CAB11275.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 3.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 6.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 3.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT DOMAIN 236 .. 283 F-BOX.
FT REPEAT 389 .. 417 WD 1.
FT REPEAT 429 .. 473 WD 2.
FT REPEAT 505 .. 533 WD 3.
FT REPEAT 545 .. 575 WD 4.
FT REPEAT 587 .. 615 WD 5.
FT REPEAT 625 .. 654 WD 6.
SO SEQUENCE 703 AA; 79605 MW; 0336A0568C152396 CRC64;

Query Match 48.1%; Score 75; DB 1; Length 703;
Best Local Similarity 42.9%; Pred. No. 0.00061;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 2 GHKRGIAQLQYRDRLVYSGSSDNTIRLW 29
||| | : : : |||| | | : |
Db 389 GHKEGVMAVKIHEHTLVSGSIDKTVRW 416

RESULT 13
SE10_CAEEL
ID SE10_CAEEL STANDARD; PRT; 579 AA.
AC Q93794;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sel-10 protein.
GN SEL-10 OR F55B12.3.
GC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
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CC Rhabditiidae; Peloderinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Sims M.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RA Jones S.J.M.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 CC EMBL: Z79757; CAB02129.1;
 CC WormPep: F55B12.3; CE16120.
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF00400; WD40; 7.
 CC Pfam: PF00646; F-box; 1.
 CC PRINTS: PR00320; GPROTEINBRPT.
 CC ProDom: PD000018; WD40; 5.
 CC SMART: SM00320; WD40; 7.
 CC SMART: SM00320; WD40; 7.
 CC PROSITE: PS50181; FBOX; 1.
 CC PROSITE: PS00678; WD_REPEATS; 1; 5.
 CC PROSITE: PS50082; WD_REPEATS; 2; 7.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 CC Repeat: WD repeat.
 CC DOMAIN 113 159 F-BOX.
 CC FT REPEAT 245 274 WD 1.
 CC FT REPEAT 286 316 WD 2.
 CC FT REPEAT 328 356 WD 3.
 CC FT REPEAT 368 396 WD 4.
 CC FT REPEAT 408 438 WD 5.
 CC FT REPEAT 453 481 WD 6.
 CC FT REPEAT 493 522 WD 7.
 CC FT REPEAT 522 552 WD 7.
 CC FT REPEAT 552 582 WD 6.
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 CC FT REPEAT 5290 5320 WD 6.
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Yeast 16:71-80(2000).

[3]
SEQUENCE FROM N.A.

RC STRAIN=972;

RA MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgueros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,

RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer T., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Spapakowski G.V., Ussey D., Barrell B.G., Nurse P.,

RA "The genome sequence of Schizosaccharomyces pombe."

RT Nature 415:871-880(2002).

CC -!- FUNCTION: Required for both cell cycle progression at G2/M

CC and pre-mRNA splicing.

CC -!- SUBUNIT: INTERACTS WITH CDC5.

CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -!- SIMILARITY: CONTACTS 7 WD REPEATS (TRP-ASP DOMAINS).

CC -!- SIMILARITY: BELONGS TO THE PRL1/PRL2 FAMILY OF WD-REPEAT PROTEINS.

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CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF251148; AAC01399.1; -

DR EMBL; AB004535; BAA21403.1; -

DR EMBL; AL590883; CAC37375.1; -

DR InterPro: IPR001680; WD40.

DR Pfam: PF004400; WD40; 7.

DR PRINTS; PR00320; GPROTEINBRPT.

DR PRODom; PD000018; WD40; 4.

DR SMART; SM00320; WD40; 7.

DR PROSITE; PS00678; WD_REPEATS_1; 2.

DR PROSITE; PS00082; WD_REPEATS_2; 5.

DR PROSITE; PS0294; WD_REPEAT_REGION; 1.

KW Cell cycle; Repeat; WD repeat; mRNA processing; mRNA splicing;

KW Nuclear protein.

FT REPEAT 161 191 WD 1.

FT REPEAT 203 233 WD 2.

FT REPEAT 245 275 WD 3.

FT REPEAT 287 317 WD 4.

FT REPEAT 329 358 WD 5.

FT REPEAT 370 399 WD 6.

FT REPEAT 419 449 WD 7.

SO SEQUENCE 473 AA; 52418 MW; 941F3B31A8C19799 CRC64;

Query Match 46.2%; Score 72; DB 1; Length 473;

Best Local Similarity 54.8%; Pred. No. 0.0012;

Matches 17; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Db 286 SGHKTASLAVOEFDPQVVTGSMDSIRLM 316

Search completed: April 10, 2003, 13:19:37
Job time : 3.08404 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 6.85262 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_427_455
Perfect score: 156
Sequence: 1 NGHRRGIACLOXRDLRVVSGSSDNTIRLM 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	252	11	0922C7 mus musculus
2	156	100.0	563	11	0923H0 mus musculus
3	156	100.0	569	11	0921G7 mus musculus
4	156	100.0	569	11	092159 mus musculus
5	156	100.0	569	11	092159 mus musculus
6	152	97.4	510	5	044382 drosophila
7	152	97.4	510	5	09VDE3 drosophila
8	143	91.7	430	5	09B554 drosophila
9	136	87.2	122	13	08U0N3 xenopus lae
10	83	53.2	1326	5	09VZP4 drosophila
11	81	51.9	280	5	08S7Z5 encephalito
12	81	51.9	730	5	08S7O2 dictyosteli
13	80	51.3	196	13	08OGU0 melanocthr
14	80	51.3	196	13	08OGT9 astatocthr
15	80	51.3	196	13	08OGT8 labidochrom
16	80	51.3	196	13	08OGT7 tropheus du

17	80	51.3	196	13	08OGT6
18	80	51.3	196	13	08OGT5
19	80	51.3	196	13	08OGT3
20	80	51.3	196	13	08OGT2
21	80	51.3	196	13	08OGT1
22	80	51.3	196	13	08OGT0
23	80	51.3	196	13	08OGS9
24	80	51.3	196	13	08OGS8
25	80	51.3	423	5	08SSJ1
26	80	51.3	808	4	09GA78
27	79	50.6	196	13	08OGT4
28	79	50.6	415	10	048679
29	79	50.6	438	10	09M3B4
30	79	50.6	553	4	09NUX6
31	79	50.6	561	4	09NUR2
32	79	50.6	589	4	0961E0
33	79	50.6	627	4	096A16
34	79	50.6	629	11	08VHP4
35	79	50.6	629	11	08VBP4
36	79	50.6	707	4	0969H0
37	78.5	50.3	558	3	043071
38	77	49.4	38	13	08U0N4
39	76	48.7	465	10	048716
40	76	48.7	1609	5	09GRC3
41	76	48.7	1893	5	017887
42	74.5	47.8	585	5	0952T0
43	74.5	47.8	587	5	044083
44	74	47.4	47	13	08U0N5
45	73	46.8	296	5	09VXJ1

ALIGNMENTS

Result 1
ID 0922C7 PRELIMINARY: PRT: 252 AA.

AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to f-box and WD-40 domain protein 1B (Fragment).
GN FBXN1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: BC008552; AA08552.1; -.
DR MGI: 2144023; Fbxn1b.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRT.
DR PRODOM: PD000018; WD40; 3.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN-5.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
SQ SEQUENCE 252 AA; 28424 MW; F71737C8D7A9F75F CRC64;

Query Match 100.0%; Score 156; DB 11; Length 252;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHRRGIACLOXRDLRVVSGSSDNTIRLM 29
DB 110 NGHRRGIACLOXRDLRVVSGSSDNTIRLM 138

RESULT 2	0923H0	PRELIMINARY;	PRT;	563 AA.
ID	0923H0			
AC	0923H0;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	F-box/WD40 repeat-containing protein HOS.			
GN	FBXW1B.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N.			
RA	Bhalla N., Hertler J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;			
RT	"Mouse homolog of HOS (mHOS) is overexpressed in skin tumors and implicated in constitutive activation of NF-kappa."			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
DR	EMBL: AY038079; AAK72095.1; .			
DR	MGI: MGI:2144023; Fbxw1b.			
DR	InterPro: IPR001810; F-box.			
DR	InterPro: IPR001680; WD40.			
DR	Pfam: PF00646; F-box; 1.			
DR	Pfam: PF00400; WD40; 7.			
DR	ProDom: PD000018; WD40; 4.			
DR	PROSITE: PS00181; FBOX; 1.			
DR	PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.			
DR	PROSITE: PS50082; WD_REPEATS_2; 7.			
DR	PROSITE: PS50294; WD_REPEATS_REGION; 1.			
KW	Repeat; WD repeat.			
SQ	SEQUENCE 563 AA; 64741 MW; 9AB562F3FF5E3496 CRC64;			
Query Match	100.0%; Score 156; DB 11;			
Best Local Similarity	100.0%; Pred. No. 9,6e-16;			
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1 NGHKGITACIQYRDRLVSGSSDNTIRLW 29			
Db	421 NGHKGITACIQYRDRLVSGSSDNTIRLW 449			
RESULT 3				
09R1G7				
ID	09R1G7	PRELIMINARY;	PRT;	569 AA.
AC	09R1G7;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Beta-transducin repeat-containing protein.			
GN	BTRC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Winston J., Ellledge S.J., Harper J.W.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
DR	EMBL: A1110396; AADA1025.1; .			
DR	MGI: MGI:1338871; Btrc.			
DR	InterPro: IPR001810; F-box.			
DR	InterPro: IPR001680; WD40.			
DR	Pfam: PF00400; WD40; 7.			
DR	PROSITE: PS00320; GPROTEINRPT.			
DR	ProDom: PD000018; WD40; 4.			
DR	SMART; SM00326; FBOX; 1.			
DR	SMART; SM00320; WD40; 7.			

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9119275; PubMed=10097128;
 RA Hatakeyama S., Kitagawa M., Nakayama K., Shitane M., Matsumoto M.,
 RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
 RA Nakayama K.-I.;
 RT "ubiquitin-dependent degradation of IkappaBalpha is mediated by a
 RT ubiquitin ligase Skp1/Cul1/F-box protein FMDL";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99075339; PubMed=9859996;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase";
 RL Nature 396:590-594(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBD databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/SV;
 RC MEDLINE=21601157; PubMed=11735228;
 RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
 RA Nakayama K.-I.;
 RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
 RT Caenorhabditis elegans SEL-10";
 RL Genomics 78:214-222(2001).
 CC -1 SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF081887; AAD17755.1; -;
 DR EMBL: AF099932; AAD08701.1; -;
 DR EMBL: BC003989; AAH03989.1; -;
 DR EMBL: AF391190; AAL40929.1; JOINED.
 DR EMBL: AF391178; AAL40929.1; JOINED.
 DR EMBL: AF391179; AAL40929.1; JOINED.
 DR EMBL: AF391180; AAL40929.1; JOINED.
 DR EMBL: AF391181; AAL40929.1; JOINED.
 DR EMBL: AF391182; AAL40929.1; JOINED.
 DR EMBL: AF391183; AAL40929.1; JOINED.
 DR EMBL: AF391184; AAL40929.1; JOINED.
 DR EMBL: AF391185; AAL40929.1; JOINED.
 DR EMBL: AF391186; AAL40929.1; JOINED.
 DR EMBL: AF391187; AAL40929.1; JOINED.
 DR EMBL: AF391188; AAL40929.1; JOINED.
 DR EMBL: AF391189; AAL40929.1; JOINED.
 DR MGI: MGI:1338871; BtG.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW ligase; Repeat; WD repeat.
 SQ SEQUENCE 369 AA; 65105 MW; BC7D6544815H296 CRC64;

Query Match 100.0%; Score 156; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 9, 7e-16;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NGHKGIACTQYRDLRVVSGSSDNTIRLM 29
 |||

DB 427 NGHKGIACTQYRDLRVVSGSSDNTIRLM 455
 RESULT 6
 ID 044382 PRELIMINARY; PRT; 510 AA.
 AC 044382;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SLMB.
 GN SLMB OR SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121115; PubMed=9461217;
 RA Jiang J., Struhl G.;
 RT "Regulation of the Hedgehog and Wingless signalling pathways by the F-
 RT box/WD40-repeat protein Slmb";
 RL Nature 391:493-496(1998).
 CC -1 SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF032878; AAC38852.1; -;
 DR FLYBASE: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;

Query Match 97.4%; Score 152; DB 5; Length 510;
 Best Local Similarity 96.6%; Pred. No. 3, 6e-15;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 NGHKGIACTQYRDLRVVSGSSDNTIRLM 29
 |||

DB 370 NGHKGIACTQYRDLRVVSGSSDNTIRLM 398

RESULT 7
 ID 09VDE3 PRELIMINARY; PRT; 510 AA.
 AC 09VDE3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SLMB protein (SLMB).
 GN SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek J.R.G., Champe M., Pfeiffer B.D.,

RA Abn K.J., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wanl J.F., Abayavani A., An H.-J., Andrews-Plankoch C., Ballowin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Butts J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry K.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Doudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslcr C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Krift C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky T.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mishina N.V., Mobery C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Slden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Welstock G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [21]
RN SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND IMAGINAL DISC;
RX MEDLINE=20245299; PubMed=10781936;
RT Miletich I., Limbourg-Bouchon B.;
RT "Drosophila null limb clones transiently deregulate Hedgehog-
RT independent transcription of wingless in all limb discs, and induce
RT decapentaplegic transcription linked to imaginal disc regeneration.";
RL Mech. Dev. 93:15-26(2000).
CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AE003733; AAF55853.1; -
DR EMBL; AE222924; AAF63214.1; -
DR EMBL; AF222923; AAF63213.1; -
DR FLYBase; FBgn0023423; slmb.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PSS0181; FBOX; 1.
DR PROSITE; PSS0678; WD_REPEATS_1; 5.
DR PROSITE; PSS0082; WD_REPEATS_2; 7.
DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; FAD5DF126F58A012 CRC64;

Query Match	97.4%	Score 152	DB 5	Length 510
Best Local Similarity	96.6%	Pred. No. 3.6e-15		
Matches 22	Conservative 1	Mismatches 0	Indels 0	Gaps 0
Qy	1	NGHRRGIACIQYDRILRVSSGSDNTRIM	29	
Db	370	NGHRRGIACIQYDRILRVSSGSDNTRIM	398	

RESULT 8
Q9BJ54

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ID      09BJ54      PRELIMINARY;      PRT;      430 AA.
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DS      Beta-transducin repeat-containing protein (Fragment).
OS      Heterodera glycines (soybean cyst nematode).
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchinae;
OC      Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX      NCBI_TaxID=51029;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kovaleva E.S., Yakovlev A.G., Masler E.P.;
RT      "Plant parasitic nematode b-TrCP.";
RC      Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
CC      -1. SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR      EMBL: AF391901; AAC6376.1; -.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00400; WD40; 7.
DR      PRINTS: PR00320; GPROTEINRPT.
DR      ProDom: PD000018; WD40; 4.
DR      SMART: SM00320; WD40; 7.
DR      PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
DR      PROSITE: PSS0082; WD_REPEATS_2; 6.
DR      PROSITE: PSS0294; WD_REPEATS_REGION; 1.
KW      Repeat; WD repeat.
FT      NON_TER
SQ      SEQUENCE      430 AA;      47916 MW;      4ABC3F2DFE3A50B CRC64;

Query Match      91.7%; Score 143; DB 5; Length 430;
Best Local Similarity      89.7%; Pred. No. 7.6e-14;
Matches      26; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

OY      1 NGHRRGIACLDYRDLRVSGSSDNTIRLM 29
          |||||||:|||||:|||||:|||||
Db      251 NGHRRGIACLDYRDLRVSGSSDYSIRLM 279

RESULT 9
OBUN3      PRELIMINARY;      PRT;      122 AA.
ID      08UN3;
AC      08UN3;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Beta-Trcp protein (Fragment).
GN      BETA-TRCP.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Carnevali F.;
RT      Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RC      [2]
DR      SEQUENCE FROM N.A.
RP      "Analisi strutturale e funzionale del gene beta-Trcp in Xenopus
RT      laevis.";
RT      Thesis (2001),
RT      Department of Genetics and Molecular Biology "Charles Darwin",
RT      University of Rome La Sapienza, Rome, Italy.
DR      EMBL: AF428938; CAD21935.1; -.
DR      InterPro: IPR001680; WD40.
DR      Pfam: PF00400; WD40; 3.
DR      PRINTS: PR00320; GPROTEINRPT.
DR      ProDom: PD000018; WD40; 2.
DR      SMART: SM00320; WD40; 3.
DR      PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
DR      PROSITE: PSS0082; WD_REPEATS_2; 3.
DR      PROSITE: PSS0294; WD_REPEATS_REGION; 1.

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FT NON_TER 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA: 13682 MW: 36BB6B39AC8F5387 CRC64:

Query Match 87.2% Score 136; DB 13; Length 122;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NGHRRGIACIQYRDLRVSSGSSDNTI 26
 Db 97 NGHRRGIACIQYRDLRVSSGSSDNTI 122

RESULT 10
 09VZF4 PRELIMINARY; PRT; 1326 AA.
 AC 09VZF4
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE CG15010 protein (LD21322p) (LD30271p).
 OS AGO OR CG15010.
 GN Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherter S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova K.Y., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavalier S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Krat C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Long Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RP SEQUENCE FROM N.A.
 RP STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno C., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celiker S.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RP STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno C., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celiker S.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF003480; AAG22246.1; -;
 DR EMBL: AY061300; AAL28848.1; -;
 DR EMBL: AY075401; AAL68231.1; -;
 DR FlyBase: FBgn0041171; ago.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 2.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 1326 AA: 141360 MW: 3F42C873CFA3027F CRC64;

Query Match 53.2% Score 83; DB 5; Length 1326;
 Best Local Similarity 44.8%; Pred. NO. 0.00059;
 Matches 13; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY 1 NGHRRGIACIQYRDLRVSSGSSDNTIRLM 29
 Db 1235 NGHRRGIACIQYRDLRVSSGSSDNTIRLM 1263

RESULT 11
 08STZ5 PRELIMINARY; PRT; 280 AA.
 AC 08STZ5
 DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Hypothetical protein ECUI1_1970.
 GN ECUI1_1970.
 OS Encephalitozoon cuniculi.
 CC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 ON NCBI_TaxID=6035;
 RX SEQUENCE FROM N.A.
 RX STRAIN-GB-M1;
 RC Genoscope;
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RP STRAIN-GB-M1;
 RC MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretallade E., Brotlier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.,
 RT "Genome sequence and gene compaction of the eukaryote parasite
 Encephalitozoon cuniculi."
 RL Nature 414:450-453(2001).
 RM EMBL: AL590450; CAD26107.1; -;

Fri, Apr 11 13:31:12 2003

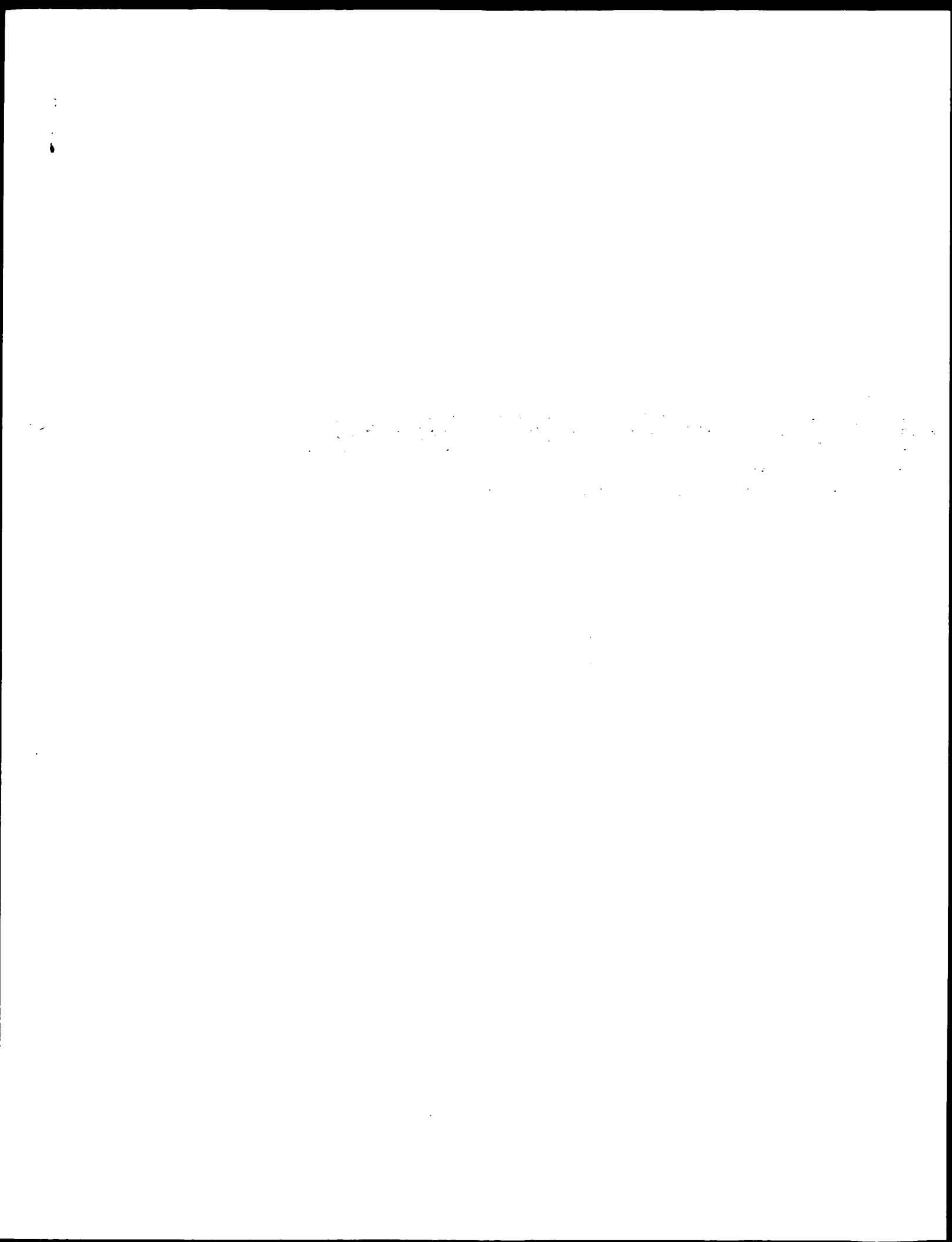
us-09-601-168b-2_copy_427_455.rspt

Page 7

Query Match	51.3%	Score 80;	DB 13;	Length 196;
Best Local Similarity	41.4%	Pred. No. 0.00021;		
Matches 12; Conservative	8;	Mismatches 9;	Indels 0;	Gaps 0;

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QY      1  NGHKRGIAcLOYRDLVYSGSSDNTIRLW  29
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Db      34  SGHNQEVNCVDAKDGLISGRDRTARIW  62
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Search completed: April 11, 2003, 11:51:52
Job time : 14.8526 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 : Search time 8.01218 Seconds
(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492
Perfect score: 138
Sequence: 1 EGHETLVRCIFEDNKRIVSGAYDGKI 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : A-Geneseq.101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	517	AA85852	WD-40 domain-contg
2	138	100.0	542	AA96696	Human E3 ubiquitin
3	138	100.0	542	AA79127	Human protein SEQ
4	138	100.0	542	AA40208	Human polypeptide
5	138	100.0	550	AA41994	Human polypeptide
6	138	100.0	569	AA24054	A human beta-trans
7	138	100.0	569	AA12812	Mouse ubiquitin 11
8	138	100.0	569	AA12813	Human beta-transdu
9	138	100.0	569	AA96697	Human beta-TrCP
10	138	100.0	569	AA783041	F-box protein FBP-

11	138	100.0	569	AA83250	F-box protein hbet
12	138	100.0	569	AA83254	F-box protein FWD1
13	138	100.0	569	AA74249	Human cell signal1
14	138	100.0	569	AA84828	Human F2F1 protein
15	138	100.0	579	AA78583	Human protein SEQ
16	138	100.0	590	AA00847	Human bone marrow
17	138	100.0	605	AA78582	Human protein SEQ
18	138	100.0	608	AA00960	Human bone marrow
19	138	100.0	632	AA78584	Human protein SEQ
20	138	100.0	654	AA79567	Human protein SEQ
21	138	100.0	654	AA79568	Human protein SEQ
22	138	100.0	654	AA79569	Human protein SEQ
23	133	96.4	29	AA84940	Peptide rvt from a
24	132	95.7	510	AB59857	Drosophila melanog
25	82	59.4	540	AA72465	Human mammary sel-
26	82	59.4	540	AA72466	Human mammary sel-
27	82	59.4	540	AA72467	Human mammary sel-
28	82	59.4	545	AA72468	Human mammary sel-
29	82	59.4	545	AA72469	Human mammary sel-
30	82	59.4	545	AA72470	Human mammary sel-
31	82	59.4	553	AA72471	Human mammary sel-
32	82	59.4	553	AA72472	Human mammary sel-
33	82	59.4	553	AA72473	Human mammary sel-
34	82	59.4	559	AA72474	Human mammary sel-
35	82	59.4	559	AA72475	Human mammary sel-
36	82	59.4	589	AA72476	Human mammary sel-
37	82	59.4	589	AA72477	Human mammary sel-
38	82	59.4	589	AA72478	Human mammary sel-
39	82	59.4	592	AA72479	Human mammary sel-
40	82	59.4	592	AA72480	Human mammary sel-
41	82	59.4	626	AA72481	Human mammary sel-
42	82	59.4	626	AA72482	Human mammary sel-
43	82	59.4	627	AA72483	Human mammary sel-
44	82	59.4	627	AA72484	Human mammary sel-
45	82	59.4	666	AA72485	Human C-term mychi

ALIGNMENTS

RESULT 1
AA85852 standard; peptide: 517 AA.
ID AA85852 standard; peptide: 517 AA.
XX
AC AA85852:
XX
XX 13-SEP-1996 (first entry)
XX
DE WD-40 domain-contg. beta-TRCP protein.
XX
XX
KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signalling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme; activity; isozyme; human.
XX
OS Synthetic.
XX
XX WO9521252-A2.
XX
XX 10-AUG-1995.
XX
XX 31-JAN-1995; 95WO-US01210.
XX
XX PF 01-FEB-1994; 94US-0190802.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Mochly-Rosen D. Ron D;
XX
XX WPI; 1995-283772/37.
XX
XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
XX activity of a protein, eg. protein kinase C, which interacts with a
XX protein contg. a WD-40 region.
PT

XX Example 5: Page 80-82; 351pp; English.

PS
CC Proteins AAR8581-92 are protein which contain at least one WD-40 (also
CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signaling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR8585). Proteins AAR8581-82 were isolated based
CC on homology with beta-transducin, whereas proteins AAR8582-92 were
CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
CC The proteins were used to construct the peptides AAR84928-R85063 and
CC AAR85786-R85842. The peptides can be used to identify target proteins
CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC proteins involved in protein-protein interaction and to screen for drugs
CC that will affect protein-protein interaction involving WD-40 domains.

SO Sequence 517 AA;

Query Match 100.0%; Score 138; DB 16; Length 517;
Best Local Similarity 100.0%; Pred. No. 8.4e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26
DB 431 EGHELVRCIRFDNKRIVSGAYDGKI 456
|||||

RESULT 2
ID AAY96696 standard; Protein: 542 AA.
XX
AC AAY96696;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human E3 ubiquitin ligase.
XX
DE Human E3 ubiquitin ligase.
XX
KM E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KM nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KM anti-inflammatory; immunosuppressive; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200034447-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US29371.
XX
PR 10-DEC-1998; 98US-0210060.
XX
PA (SIGN-) SIGNAL PHARM INC.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
PI Lavon I, Yaron A;
XX
DR WPI: 2000-431294/37.
DR N-PSDB; AAK51228.
XX
PT Polypeptide enhancing phosphorylated IkkappaB ubiquitination useful for
PT treating disorder associated with NF-kappaB activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
XX variant
XX
PS Claim 1: Page 70-72; 77pp; English.
XX
CC This is human E3 ubiquitin ligase (E3), which is homologous to human
CC beta-TrCP, an F-box/WD protein family member. E3 enhances ubiquitination
CC of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor
CC kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the
CC ubiquitin pathway is useful for identifying modulators of this process

CC for use in treating diseases associated with activation of NF-kappa-B. In
CC vitro analysis suggests that deletion of the F-box results in a protein
CC that functions as a dominant negative molecule in vivo. Transient
CC over-expression of delta-beta-TrCP (a deletion mutant) inhibited the
CC degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells,
CC resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be
CC used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP
CC can be used to modulate NF-kappa-B to treat inflammatory diseases,
CC autoimmune diseases, cancer and viral infections.

SO Sequence 542 AA;

Query Match 100.0%; Score 138; DB 21; Length 542;
Best Local Similarity 100.0%; Pred. No. 8.9e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26
DB 440 EGHELVRCIRFDNKRIVSGAYDGKI 465
|||||

RESULT 3
ID AAM79127 standard; Protein: 542 AA.
XX
AC AAM79127;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1789.
XX
DE Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AD, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAK52260.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20: Page 4147-4148; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM60020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 542 AA;

Query Match 100.0%; Score 138; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 8.9e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 |||||
 Db 440 EGHEELVRCIRFDNKRIVSGAYDGKI 465

RESULT 4
 AAM40208
 ID AAM40208 standard; Protein: 542 AA.

XX
 AC AAM40208;

XX
 DT 22-OCT-2001 (first entry)

XX
 DE Human polypeptide SEQ ID NO 3353.

XX
 DE Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.

XX
 OS Homo sapiens.

XX
 PN WO200153312-A1.

XX
 PD 26-JUL-2001.

XX
 PF 26-DEC-2000; 2000WO-US34263.

XX
 PR 21-JAN-2000; 2000US-0488725.

XX
 PR 25-APR-2000; 2000US-0552317.

XX
 PR 09-JUL-2000; 2000US-0598042.

XX
 PR 19-JUL-2000; 2000US-0620312.

XX
 PR 03-AUG-2000; 2000US-0653450.

XX
 PR 14-SEP-2000; 2000US-0662191.

XX
 PR 19-OCT-2000; 2000US-0693036.

XX
 PR 29-NOV-2000; 2000US-0727344.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX
 PI WPI: 2001-442253/47.

XX
 DR N-PSDB: AAI59364.

XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX
 PS Example 5; SEQ ID NO 3353; 10078bp; English.

XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX
 SQ Sequence 542 AA;

Query Match 100.0%; Score 138; DB 22; Length 542;
 Best Local Similarity 100.0%; Pred. No. 8.9e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 |||||
 Db 440 EGHEELVRCIRFDNKRIVSGAYDGKI 465

RESULT 5
 AAM41994
 ID AAM41994 standard; Protein: 550 AA.

XX
 AC AAM41994;

XX
 DT 22-OCT-2001 (first entry)

XX
 DE Human polypeptide SEQ ID NO 6925.

XX
 DE Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.

XX
 OS Homo sapiens.

XX
 PN WO200153312-A1.

XX
 PD 26-JUL-2001.

XX
 PF 26-DEC-2000; 2000WO-US34263.

XX
 PR 21-JAN-2000; 2000US-0488725.

XX
 PR 25-APR-2000; 2000US-0552317.

XX
 PR 09-JUL-2000; 2000US-0598042.

XX
 PR 19-JUL-2000; 2000US-0620312.

XX
 PR 03-AUG-2000; 2000US-0653450.

XX
 PR 14-SEP-2000; 2000US-0662191.

XX
 PR 19-OCT-2000; 2000US-0693036.

XX
 PR 29-NOV-2000; 2000US-0727344.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX
 PI WPI: 2001-442253/47.

XX
 DR N-PSDB: AAI61150.

XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX
 PS Example 2; SEQ ID NO 6925; 10078bp; English.

XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

CC Sequence 550 AA;

Query Match 100.0%; Score 138; DB 22; Length 550;
 Best Local Similarity 100.0%; Pred. No. 9e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26
 DB 448 EGHELVRCIRFDNKRIVSGAYDGKI 473

RESULT 6

ID AAY24054 standard; Protein; 569 AA.

XX AAY24054;

DT 30-SEP-1999 (first entry)

XX A human beta-transducin repeat containing protein.

XX Beta-transducin repeat containing protein; beta-Trcp; Skp1p;

KW proteosome degradation pathway; Vpu protein; beta-catenin;

KW human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;

KW ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;

KW antiviral; antitumour; cell cycle regulation; protein degradation;

KW and anti-inflammatory; osteo-articular inflammation; acute inflammation;

XX tumour necrosis factor.

XX Homo sapiens.

XX Location/Qualifiers

FT Region 147..191

FT Region /note= "F box sequence"

FT Region 259..292

FT Region /note= "WD motif"

FT Region 304..332

FT Region /note= "WD motif"

FT Region 343..372

FT Region /note= "WD motif"

FT Region 387..415

FT Region /note= "WD motif"

FT Region 427..455

FT Region /note= "WD motif"

FT Region 467..492

FT Region /note= "WD motif"

FT Region 516..544

FT Region /note= "WD motif"

XX MO938969-A1.

XX 05-AUG-1999.

XX 29-JAN-1999;

XX 99WO-FR00196.

XX 09-DEC-1998;

XX 98FR-0015545.

XX 30-JAN-1998;

XX 98FR-0001100.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR.

XX Arenzana Seisdedos F, Benarous R, Concordet J, Durand H;

XX Kroll M, Margottin F;

XX WPI; 1999-469329/39.

XX N-PSDB; AAX86501.

XX New human beta-transducin repeat containing protein and its

XX fragments useful as, or to screen for, antiviral, antitumour,

XX anti-inflammatory and anti-Alzheimer's agents

XX Claim 1; Page 60-61; 71pp; French.

The present sequence represents a human beta-transducin repeat containing
 protein (beta-Trcp). The protein directs proteins to the proteosome
 degradation pathways. The protein is able to interact with the Vpu
 protein of human immune deficiency virus-1 (HIV-1), cellular proteins
 Ikappab or beta-catenin (bc) and/or protein Skp1p. The protein controls
 ubiquitinylation of phosphorylated proteins and thus their targeting to
 proteosomes for degradation. Depending on whether the process is
 inhibited or promoted, the result may be delayed breakdown of CD4 (in
 cases of HIV-1 infection); increased activity of IxB (and thus reduced
 activity of NFkappab) and increased degradation of mutant bc in tumour
 cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
 patients. The beta-Trcp protein, and its active peptide fragments, or its
 nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
 CC antitumour agents that disrupt cell cycle regulation or protein
 CC degradation in human tumour cells, and anti-inflammatory agents that
 CC disrupt activation by NFkappab. Fragments of the protein are also
 CC useful for treating osteo-articular inflammation or acute inflammation
 CC associated with release of tumour necrosis factor.

XX Sequence 569 AA;

Query Match 100.0%; Score 138; DB 20; Length 569;
 Best Local Similarity 100.0%; Pred. No. 9.4e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26
 DB 467 EGHELVRCIRFDNKRIVSGAYDGKI 492

RESULT 7

AAAB12812

ID AAB12812 standard; Protein; 569 AA.

XX AAB12812;

DT 27-NOV-2000 (first entry)

XX Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

XX ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;

KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;

KW gene therapy; colon cancer; beta-transducin repeat containing protein;

XX beta-Trcp.

XX Mus musculus.

XX JP2000166542-A.

XX 20-JUN-2000.

XX 02-DEC-1998;

XX 98JP-0343437.

XX 02-DEC-1998;

XX 98JP-0343437.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2000-485550/43.

DR	N-PSDB; AAA73131.
XX	F-box protein of ubiquitin ligase SCF complex which promotes the
PT	ubiquitination of Ikappab or beta-catenin
XX	
PS	Claim 2; Page 9-10; 19pp; Japanese.
XX	
CC	The present invention describes an F-box motif protein of ubiquitin
CC	ligase SCF complex which promotes the ubiquitination of Ikappab or
CC	beta-catenin and is constituted by Skp1 protein, Cull protein and a
CC	complex (SCF complex) of F-box protein containing F-box motif and Wd40
CC	repeat motif and has the amino acid sequence of 45 residues (AAB12811)
CC	or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
CC	ligase FMO1 protein) and (AAB12813, which is human beta-transducin
CC	repeat containing protein (beta-Trcp)). The F-box protein can be used for
CC	the gene therapy of colon cancer by being recombined to a virus vector.
XX	
SQ	Sequence 569 AA;
Query Match	100.0%; Score 138; DB 21; Length 569;
Best Local Similarity	100.0%; Pred. No. 9,4e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 EGHLELVRCIRPDNKRIVSGAYDGI 26
DB	467 EGHLELVRCIRPDNKRIVSGAYDGI 492
RESULT 8	
ID	AAB12813 standard; protein; 569 AA.
XX	
AC	AAB12813;
XX	
DT	27-NOV-2000 (first entry)
DE	
XX	Human beta-transducin repeat containing protein (beta-Trcp) SEQ ID NO:3.
KW	ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
KM	beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FMO1;
KW	gene therapy; colon cancer; beta-transducin repeat containing protein;
XX	beta-Trcp.
OS	Homo sapiens.
XX	
PN	JP2000165542-A.
XX	
PD	20-JUN-2000.
PF	02-DEC-1998; 98JP-0343437.
XX	
PR	02-DEC-1998; 98JP-0343437.
PA	(KAGA-) KAGAKU GIJUTSU SHINKO JIGODAN.
XX	
DR	WPI: 2000-485550/43.
XX	N-PSDB; AAA73132.
PT	
XX	F-box protein of ubiquitin ligase SCF complex which promotes the
PT	ubiquitination of Ikappab or beta-catenin
XX	
PS	Claim 3; Page 10-12; 19pp; Japanese.
XX	
CC	The present invention describes an F-box motif protein of ubiquitin
CC	ligase SCF complex which promotes the ubiquitination of Ikappab or
CC	beta-catenin and is constituted by Skp1 protein, Cull protein and a
CC	complex (SCF complex) of F-box protein containing F-box motif and Wd40
CC	repeat motif and has the amino acid sequence of 45 residues (AAB12811)
CC	or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
CC	ligase FMO1 protein) and (AAB12813, which is human beta-transducin
CC	repeat containing protein (beta-Trcp)). The F-box protein can be used for
CC	the gene therapy of colon cancer by being recombined to a virus vector.
XX	

QY	Sequence	569 AA:	Score 138:	DB 21:	Length 569:
QY	Query Match	100.0%;	Pred. No. 9,4e-15;		
QY	Best Local Similarity	100.0%;	Pred. No. 9,4e-15;		
QY	Matches 26; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
DB	1 EGHLELVLCIRFDNKRIVSGAYDGKI 26				
DB	467 EGHLELVLCIRFDNKRIVSGAYDGKI 492				
RESULT 9					
AA96697					
AA96697	standard; Protein: 569 AA.				
AC	AA96697;				
DT	26-SEP-2000 (first entry)				
DE	Human beta-TrCP.				
XX	E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;				
KW	nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;				
KW	anti-inflammatory; immunosuppressive; cyostatic.				
XX	Homo sapiens.				
PN	WO200034447-A2.				
PD	15-JUN-2000.				
PF	10-DEC-1999; 99WO-US29371.				
PR	10-DEC-1998; 98US-0210060.				
XX	(SIGN-) SIGNAL PHARM INC.				
PA	(YISS) YISSUM RES & DEV CO.				
PI	Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;				
PI	Lavon I, Yaron A;				
XX	WPI: 2000-431294/37.				
DR	N-PSDB; AAA51229.				
XX	Polypeptide enhancing phosphorylated I-kappa-B ubiquitination useful for				
PT	treating disorder associated with NF-kappa-B activation e.g. cancer,				
PT	comprising amino acid sequence of human E3 ubiquitin ligase or its				
PT	variant				
PS	Claim 21: Page 72-74; 77pp; English.				
XX	Human beta-TrCP, an F-box/WD protein family member, has been shown to				
CC	have homology to human E3 ubiquitin ligase (E3). E3 enhances				
CC	ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of				
CC	nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B				
CC	degradation via the ubiquitin pathway is useful for identifying				
CC	modulators of this process for use in treating diseases associated with				
CC	activation of NF-kappa-B. In vitro analysis suggests that deletion of				
CC	the F-box results in a protein that functions as a dominant negative				
CC	molecule in vivo. Transient over-expression of delta-beta-TrCP (a				
CC	deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha				
CC	in stimulated Jurkat cells, resulting in accumulation of phosphorylated				
CC	I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B				
CC	activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat				
CC	inflammatory diseases, autoimmune diseases, cancer and viral infections.				
XX	Sequence 569 AA:				
QY	Query Match	100.0%;	Score 138:	DB 21:	Length 569:
QY	Best Local Similarity	100.0%;	Pred. No. 9,4e-15;		
QY	Matches 26; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 EGHLELVLCIRFDNKRIVSGAYDGKI 26				

Db 467 EGHELVRCIRFDNKRIVSGAYDCKI 492

RESULT 10

AAV83041

16-AUG-2000 (first entry)

F-box protein FBP-1.

F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer; small cell lung carcinoma; immune disorder; cardiovascular disorder; inflammatory disorder; human.

Homo sapiens.

WO200012679-A1.

09-MAR-2000.

27-AUG-1999; 99WO-US19560.

28-AUG-1998; 98US-0098355.

03-FEB-1999; 99US-0118568.

15-MAR-1999; 99US-0124449.

(UYNT) UNITV NEW YORK STATE.

Chiaur DS, Pagano M, Latres E;

WPI: 2000-256635/22.

N-PSDB: AA293350.

Novel nucleic acid for screening compounds useful for treating

proliferative and differentiative disorders such as cancer and immune

disorders comprises sequences encoding ubiquitin ligases

Disclosure; Figure 3a; 245pp; English.

Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases with F-box motifs (F-box proteins) are useful for diagnosis of proliferative and differentiated related disorders by measuring FBP gene expression. Cells expressing such proteins or their fragments are useful for screening compounds. The compounds are agonists or antagonists, which are useful for treating a proliferative or differentiative disorder in a mammal such as breast, ovarian and prostate cancer and small cell lung carcinoma and also major opportunistic infections, immune disorders, cardiovascular diseases and inflammatory disorders. FBP protein, analogs, derivatives and their subsequences, anti-FBP antibodies are also useful in diagnosis of the disorders.

Sequence 569 AA;

Query Match 100.0%; Score 138; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDCKI 26
|||||

Db 467 EGHELVRCIRFDNKRIVSGAYDCKI 492

RESULT 11
AAV83250
ID AAV83250 standard; Protein; 569 AA.
XX

AAV83250;

16-AUG-2000 (first entry)

F-box protein hBetatrcp.

Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems; human.

Homo sapiens.

WO200022110-A2.

20-APR-2000.

08-OCT-1999; 99WO-US23705.

09-OCT-1998; 98US-0103787.

(HARD) HARVARD COLLEGE.

Zhou P, Howley P;

WPI: 2000-317970/27.

N-PSDB: AA293710.

Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic compound

Claim 9; Page 171; 185pp; English.

The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targeted degradation of a target polypeptide in vivo. Targeted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of oncoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the mature animal.

Sequence 569 AA;

Query Match 100.0%; Score 138; DB 21; Length 569;
Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDCKI 26
|||||

Db 467 EGHELVRCIRFDNKRIVSGAYDCKI 492

RESULT 12
AAV83254
ID AAV83254 standard; Protein; 569 AA.
XX
AC AAV83254;
XX
DT 16-AUG-2000 (first entry)
XX

F-box protein FWDip.

PT Human cell signaling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders -
 PS Claim 1; Page 77-78; 90pp; English.
 CC The present sequence is cell signalling protein-12 (CSIGP-12) encoded
 CC by cDNA obtained from Inocyte clone 3239149 of COLAUCT01 library. It is
 CC expressed in musculoskeletal, gastrointestinal and nervous tissues and is
 CC found to be homologous to beta-transducin repeats containing
 CC protein. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC them with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 SQ Sequence 569 AA;
 Query Match 100.0%; Score 138; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 9,4e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 467 EGHEELVRCIRFDNKRIVSGAYDGKI 492
 RESULT 14
 AAB48298
 ID AAB48298 standard; protein; 569 AA.
 AC AAB48298;
 XX
 DT 02-APR-2001 (first entry)
 DE Human ZF11 protein.
 XX
 XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KM CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KM Bad; Bcl-2; tumour; cytostatic.
 XX
 OS Homo sapiens.
 PN WO200075184-A1.
 PD 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000WO-US15449.
 XX
 PR 04-JUN-1999; 9905-0137494.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Zhang H, Tsvetkov LM, Kondo T;
 DR WPI; 2001-061703/07.
 DR N-PSDB; AAC84610.
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 PS Claim 3; Page 130-132; 162pp; English.
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for

CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between Skp and target proteins are useful for
 CC treating tumours.
 SQ Sequence 569 AA;
 Query Match 100.0%; Score 138; DB 22; Length 569;
 Best Local Similarity 100.0%; Pred. No. 9,4e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 467 EGHEELVRCIRFDNKRIVSGAYDGKI 492
 RESULT 15
 AAM78583
 ID AAM78583 standard; protein; 579 AA.
 AC AAM78583;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 1245.
 XX
 KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PF 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0653561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK51716.
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 PS Claim 20; Page 3504-3505; 6221pp; English.
 CC The invention relates to polynucleotides (AAK51456-AAK51435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 579 AA;

Query Match 100.0%; Score 138; DB 22; Length 579;
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGI 26
 |||
 Db 477 EGHELVRCIRFDNKRIVSGAYDGI 502

Search completed: April 11, 2003, 11:48:17
 Job time : 9.01218 secs

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 2.69184 Seconds

(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492

Perfect score: 138

Sequence: 1 EGHELVRCIRFDNKRIVSGAYDGKI 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	138	100.0	517	1	US-08-190-802A-30	Sequence 30, Appl
2	138	100.0	517	4	US-08-477-346-30	Sequence 30, Appl
3	138	100.0	517	4	US-08-473-089-30	Sequence 30, Appl
4	138	100.0	517	4	US-08-487-072A-30	Sequence 30, Appl
5	133	96.4	29	1	US-08-190-802A-88	Sequence 88, Appl
6	133	96.4	29	4	US-08-477-346-88	Sequence 88, Appl
7	133	96.4	29	4	US-08-473-089-88	Sequence 88, Appl
8	133	96.4	29	4	US-08-487-072A-88	Sequence 88, Appl
9	76	55.1	269	3	US-08-899-578-6	Sequence 6, Appl
10	74	53.6	387	3	US-08-899-578-2	Sequence 2, Appl
11	63	45.7	318	1	US-08-190-802A-33	Sequence 33, Appl
12	63	45.7	318	4	US-08-477-346-33	Sequence 33, Appl
13	63	45.7	318	4	US-08-473-089-33	Sequence 33, Appl
14	63	45.7	318	4	US-08-487-072A-33	Sequence 33, Appl
15	62	44.9	640	1	US-08-177-165A-30	Sequence 30, Appl
16	58	42.0	33	1	US-08-190-802A-103	Sequence 103, App
17	58	42.0	33	4	US-08-477-346-103	Sequence 103, App
18	58	42.0	33	4	US-08-473-089-103	Sequence 103, App
19	58	42.0	33	4	US-08-487-072A-103	Sequence 103, App
20	57	41.3	212	3	US-08-899-578-7	Sequence 7, Appl
21	57	41.3	779	1	US-08-190-802A-32	Sequence 32, Appl
22	57	41.3	779	4	US-08-477-346-32	Sequence 32, Appl
23	57	41.3	779	4	US-08-473-089-32	Sequence 32, Appl
24	57	41.3	779	4	US-08-487-072A-32	Sequence 32, Appl
25	57	41.3	779	4	US-09-177-165A-29	Sequence 29, Appl
26	56	40.6	210	4	US-09-291-170A-11	Sequence 11, Appl
27	56	40.6	210	4	US-09-724-884-11	Sequence 11, Appl

28	56	40.6	395	3	US-09-032-372-1	Sequence 1, Appl
29	55	39.9	29	1	US-08-190-802A-99	Sequence 99, Appl
30	55	39.9	29	4	US-08-477-346-99	Sequence 99, Appl
31	55	39.9	29	4	US-08-473-089-99	Sequence 99, Appl
32	55	39.9	29	4	US-08-487-072A-99	Sequence 99, Appl
33	55	39.9	1146	4	US-08-914-999-6	Sequence 6, Appl
34	52	37.7	29	1	US-08-190-802A-87	Sequence 87, Appl
35	52	37.7	29	4	US-08-477-346-87	Sequence 87, Appl
36	52	37.7	29	4	US-08-473-089-87	Sequence 87, Appl
37	52	37.7	29	4	US-08-487-072A-87	Sequence 87, Appl
38	52	37.7	606	2	US-08-883-534-3	Sequence 3, Appl
39	52	37.7	606	3	US-09-204-764-3	Sequence 3, Appl
40	52	37.7	906	1	US-08-190-802A-31	Sequence 31, Appl
41	52	37.7	906	4	US-08-477-346-31	Sequence 31, Appl
42	52	37.7	906	4	US-08-473-089-31	Sequence 31, Appl
43	52	37.7	906	4	US-08-487-072A-31	Sequence 31, Appl
44	51	37.0	34	1	US-08-190-802A-83	Sequence 83, Appl
45	51	37.0	34	4	US-08-477-346-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1

US-08-190-802A-30

Sequence 30, Application US/08190802A

Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OR INVENTION: Theoret

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Delinger & Associates

STREET: P.O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33, 875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 517 amino acids

TYPE: amino acid

MOLECULE TYPE: unknown

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

US-08-190-802A-30

Query Match

Best Local Similarity 100.0%; Score 138; DB 1; Length 517;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 431 EGHELVRCIRFDNKRIVSGAYDGKI 456

RESULT 2

US-08-477-346-30
; Sequence 30, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
; US-08-477-346-30

Query Match 100.0%; Score 138; DB 4; Length 517;

Best Local Similarity 100.0%; Pred. No. 8.7e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26

Db 431 EGHELVRCIRFDNKRIVSGAYDGKI 456

RESULT 3

US-08-473-089-30
; Sequence 30, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 517 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

US-08-473-089-30

OY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26

Db 431 EGHELVRCIRFDNKRIVSGAYDGKI 456

RESULT 4

US-08-487-072A-30
; Sequence 30, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:


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TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match          100.0%; Score 138; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 8.7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELYRCIRFDNKRIVSGAYDGKI 26
|||||
Db 431 EGHELYRCIRFDNKRIVSGAYDGKI 456

RESULT 5
US-08-190-802A-88
Sequence 88, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190.802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-190-802A-88

Query Match          96.4%; Score 133; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYDGKI 26
|||||
Db 2 GHEELVRCIRFDNKRIVSGAYDGKI 26

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|||||
Db 1 GHEELVRCIRFDNKRIVSGAYDGKI 25

RESULT 6
US-08-477-346-88
Sequence 88, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-477-346-88

Query Match          96.4%; Score 133; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYDGKI 26
|||||
Db 1 GHEELVRCIRFDNKRIVSGAYDGKI 25

RESULT 7
US-08-473-089-88
Sequence 88, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

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STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-473-089-88

Query Match 96.4%; Score 133; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1,9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYDGKI 26
Db 1 GHEELVRCIRFDNKRIVSGAYDGKI 25

RESULT 8
US-08-487-072A-88
Sequence 88, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVI, Fig. 13
US-08-487-072A-88

Query Match 96.4%; Score 133; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1,9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYDGKI 26
Db 1 GHEELVRCIRFDNKRIVSGAYDGKI 25

RESULT 9
US-08-899-578-6
Sequence 6, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-899-578-6

Query Match 55.1%; Score 76; DB 3; Length 209;
Best Local Similarity 52.2%; Pred. No. 0.00018;
Matches 12; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYD 23
Db 90 DGHAAVRCVQFDGTIVSGGYD 112

```

1      FILING DATE: 01-FEB-1994
2      CLASSIFICATION: 530
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Fabian, Gary R.
5      REGISTRATION NUMBER: 33, 875
6      REFERENCE/DOCKET NUMBER: 8600-0139
7      TELECOMMUNICATION INFORMATION:
8      TELEPHONE: (415) 324-0880
9      TELEFAX: (415) 324-0960
10     INFORMATION FOR SEQ ID NO: 33:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 318 amino acids
13     TYPE: amino acid
14     TOPOLOGY: unknown
15     MOLECULE TYPE: protein
16     HYPOTHETICAL: NO
17     ANTI-SENSE: NO
18     ORIGINAL SOURCE:
19     INDIVIDUAL ISOLATE: GBLP -CHLAMYDOMONAS HOMOLOG, Fig. 16
20     US-08-190-802A-33
21
22     Query Match
23     Best Local Similarity 45.7%; Score 63; DB 1; Length 318;
24     Matches 14; Conservative 51.9%; Pred. No. 0.032;
25     Mismatches 2; Indels 7; Gaps 1.
26
27     OY 1 EGHEELVRCIRFD---NKRIVSGAYD 23
28     ||| | | | | | | | | | | | | |
29     Db 147 EGHEEWSCVRFSPMTNPILVSGWMD 173
30
31     RESULT 12
32     US-08-477-346-33
33     / Sequence 33, Application US/08477346
34     / Patent No. 6262023
35     / GENERAL INFORMATION:
36     / APPLICANT: Mochly-Rosen, Darla
37     / APPLICANT: Ron, Dorit
38     / TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
39     / TITLE OF INVENTION: Theroef
40     / NUMBER OF SEQUENCES: 265
41     / CORRESPONDENCE ADDRESS:
42     / ADDRESSEE: Morrison & Foerster
43     / STREET: 2000 Pennsylvania Avenue, NW
44     / CITY: Washington
45     / STATE: DC
46     / COUNTRY: USA
47     / ZIP: 20006-1812
48
49     / COMPUTER READABLE FORM:
50     / MEDIUM TYPE: Floppy disk
51     / COMPUTER: IBM PC compatible
52     / OPERATING SYSTEM: PC-DOS/MS-DOS
53     / SOFTWARE: PatentIn Release #1.0, Version #1.25
54     / CURRENT APPLICATION DATA:
55     / APPLICATION NUMBER: US/08/477,346
56     / FILING DATE: 07-JUN-1995
57     / CLASSIFICATION: 514
58     / PRIOR APPLICATION DATA:
59     / APPLICATION NUMBER: 08/487,072
60     / FILING DATE: 07-JUN-1995
61     / ATTORNEY/AGENT INFORMATION:
62     / NAME: MURASHIGE, KATE H.
63     / REGISTRATION NUMBER: 29,959
64     / REFERENCE/DOCKET NUMBER: 2550-0025.20
65     / TELECOMMUNICATION INFORMATION:
66     / TELEPHONE: (202) 887-1500
67     / TELEFAX: (202) 887-0763
68     / INFORMATION FOR SEQ ID NO: 33:
69     / SEQUENCE CHARACTERISTICS:
70     / LENGTH: 318 amino acids
71     / TYPE: amino acid
72     / TOPOLOGY: unknown
73     / MOLECULE TYPE: protein
74     / HYPOTHETICAL: NO
75

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ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBLP -CHLAMYDOMONAS HOMOLOG, Fig. 16
US-08-477-346-33

Query Match 45.7%; Score 63; DB 4; Length 318;
Best Local Similarity 51.9%; Pred. No. 0.032;
Matches 14; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 1 EGHEELVRCIRFD---NKRIVSGAYD 23
DB 147 EGHEWVSCVRFSPMTNPIIVSGWMD 173

RESULT 13
US-08-473-089-33
Sequence 33, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morlison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBLP -CHLAMYDOMONAS HOMOLOG, Fig. 16
US-08-473-089-33

Query Match 45.7%; Score 63; DB 4; Length 318;
Best Local Similarity 51.9%; Pred. No. 0.032;
Matches 14; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 1 EGHEELVRCIRFD---NKRIVSGAYD 23
DB 147 EGHEWVSCVRFSPMTNPIIVSGWMD 173

RESULT 14
US-08-487-072A-33
Sequence 33, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morlison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBLP -CHLAMYDOMONAS HOMOLOG, Fig. 16
US-08-487-072A-33

Query Match 45.7%; Score 63; DB 4; Length 318;
Best Local Similarity 51.9%; Pred. No. 0.032;
Matches 14; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 1 EGHEELVRCIRFD---NKRIVSGAYD 23
DB 147 EGHEWVSCVRFSPMTNPIIVSGWMD 173

RESULT 15
US-09-177-165A-30
Sequence 30, Application US/09177165A
Patent No. 6426205
GENERAL INFORMATION:
APPLICANT: Tyters, Mike
APPLICANT: Williams, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.10USU1
CURRENT APPLICATION NUMBER: US/09/177,165A
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

Query Match 44.98; Score 62; DB 4; Length 640;
 Best Local Similarity 56.08; Pred. No. 0.1;
 Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
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 Db 550 GHVGVWDIAADNFRITSSHDGSI 574

Search completed: April 10, 2003, 12:51:19
 Job time : 2.69184 secs

1. The first part of the report is a general introduction to the subject of the study. It discusses the importance of the study and the objectives of the research. It also provides a brief overview of the methodology used in the study.

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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 : Search time 2.66017 Seconds

(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492

Sequence: 1 ECHHELVCIRFDNKRIVSGAYDGI 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Published Applications-AA:*

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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	569	9 US-10-038-010-8	Sequence 8, Appl1
2	138	100.0	569	12 US-10-042-417-2	Sequence 2, Appl1
3	82	59.4	540	9 US-09-213-888-7	Sequence 7, Appl1
4	82	59.4	540	9 US-09-213-888-10	Sequence 10, Appl1
5	82	59.4	540	9 US-09-328-877A-7	Sequence 7, Appl1
6	82	59.4	540	9 US-09-328-877A-10	Sequence 10, Appl1
7	82	59.4	545	9 US-09-213-888-6	Sequence 6, Appl1
8	82	59.4	545	9 US-09-328-877A-6	Sequence 6, Appl1
9	82	59.4	553	9 US-09-213-888-5	Sequence 5, Appl1
10	82	59.4	553	9 US-09-328-877A-5	Sequence 5, Appl1
11	82	59.4	559	9 US-09-213-888-9	Sequence 9, Appl1
12	82	59.4	559	9 US-09-328-877A-9	Sequence 9, Appl1
13	82	59.4	589	9 US-09-213-888-8	Sequence 8, Appl1
14	82	59.4	589	9 US-09-328-877A-8	Sequence 8, Appl1
15	82	59.4	592	9 US-09-213-888-4	Sequence 4, Appl1
16	82	59.4	592	9 US-09-328-877A-4	Sequence 4, Appl1
17	82	59.4	626	9 US-09-213-888-21	Sequence 21, Appl1
18	82	59.4	626	9 US-09-328-877A-21	Sequence 21, Appl1
19	82	59.4	627	9 US-09-213-888-3	Sequence 3, Appl1

20	82	59.4	627	9 US-09-328-877A-3	Sequence 3, Appl1
21	82	59.4	666	9 US-09-213-888-27	Sequence 27, Appl1
22	82	59.4	666	9 US-09-328-877A-27	Sequence 27, Appl1
23	82	59.4	669	9 US-09-213-888-25	Sequence 25, Appl1
24	82	59.4	669	9 US-09-328-877A-25	Sequence 25, Appl1
25	71	51.4	678	10 US-09-801-368-314	Sequence 314, App
26	62	44.9	640	9 US-10-060-019-30	Sequence 30, Appl1
27	57	41.3	779	9 US-10-060-019-29	Sequence 29, Appl1
28	56	40.6	353	10 US-09-326-248B-6	Sequence 6, Appl1
29	56	40.6	371	10 US-09-925-297-699	Sequence 699, App
30	55	39.9	1146	9 US-09-832-292-10	Sequence 10, Appl1
31	55	39.9	1146	10 US-09-994-485-6	Sequence 6, Appl1
32	54	39.1	1198	10 US-09-866-582-36	Sequence 36, Appl1
33	54	39.1	1241	12 US-10-001-215-5	Sequence 5, Appl1
34	54	39.1	1356	9 US-10-077-111-10	Sequence 10, Appl1
35	53.5	38.8	392	10 US-09-925-300-1085	Sequence 1085, Ap
36	53	38.4	464	10 US-09-925-302-775	Sequence 775, App
37	52	37.7	744	10 US-09-925-300-1347	Sequence 1347, Ap
38	50.5	36.6	1194	10 US-09-876-667-2	Sequence 2, Appl1
39	50.5	36.6	1205	10 US-09-876-667-16	Sequence 16, Appl1
40	50	36.2	114	9 US-09-796-692-1541	Sequence 1541, Ap
41	49	35.5	44	10 US-09-843-845-26	Sequence 26, Appl1
42	49	35.5	70	9 US-09-796-692-1822	Sequence 1822, Ap
43	49	35.5	70	9 US-09-796-692-2077	Sequence 2077, Ap
44	49	35.5	114	9 US-09-796-692-1445	Sequence 1445, Ap
45	49	35.5	114	9 US-09-796-692-1895	Sequence 1895, Ap

ALIGNMENTS

RESULT 1
US-10-038-010-8
Sequence 8, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: Hybrigenics
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/10/038,010
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: beta-TCP1
LOCATION: (1)..(569)
OTHER INFORMATION:
US-10-038-010-8
Query Match 100.0%; Score 138; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0;
Qy 1 ECHHELVCIRFDNKRIVSGAYDGI 26
Db 467 ECHHELVCIRFDNKRIVSGAYDGI 492
RESULT 2
US-10-042-417-2
Sequence 2, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 138; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 2,6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGI 26
DB 467 EGHELVRCIRFDNKRIVSGAYDGI 492

RESULT 3

US-09-213-888-7
Sequence 7, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 59.4%; Score 82; DB 9; Length 540;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
DB 332 GHVAAVRCVQYDGRVVSAYD 353

RESULT 4

US-09-213-888-10
Sequence 10, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens

US-09-213-888-10

Query Match 59.4%; Score 82; DB 9; Length 540;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
DB 332 GHVAAVRCVQYDGRVVSAYD 353

RESULT 5

US-09-328-877A-7
Sequence 7, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-7

Query Match 59.4%; Score 82; DB 9; Length 540;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
DB 332 GHVAAVRCVQYDGRVVSAYD 353

RESULT 6

US-09-328-877A-10
Sequence 10, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-10

Query Match 59.4%; Score 82; DB 9; Length 540;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
DB 332 GHVAAVRCVQYDGRVVSAYD 353


```
RESULT 7
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6

Query Match          59.4%; Score 82; DB 9; Length 545;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
  |||:::|:|:|||||
Db 337 GHVAAVRCVQYDGRRVSGAYD 358

RESULT 8
US-09-328-877A-6
; Sequence 6, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-6

Query Match          59.4%; Score 82; DB 9; Length 545;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
  |||:::|:|:|||||
Db 337 GHVAAVRCVQYDGRRVSGAYD 358

RESULT 9
US-09-213-888-5
; Sequence 5, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-5

Query Match          59.4%; Score 82; DB 9; Length 553;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-5

Query Match          59.4%; Score 82; DB 9; Length 553;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
  |||:::|:|:|||||
Db 345 GHVAAVRCVQYDGRRVSGAYD 366

RESULT 10
US-09-328-877A-5
; Sequence 5, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match          59.4%; Score 82; DB 9; Length 553;
Best Local Similarity 59.1%; Pred. No. 0.0001;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
  |||:::~|:~|:|||||
Db 345 GHVAAVRCVQYDGRRVSGAYD 366

RESULT 11
US-09-213-888-9
; Sequence 9, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-9
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Query Match	59.48;	Score 82;	DB 9;	Length 559;
Best Local Similarity	59.18;	Pred. No. 0.00011;		
Matches 13; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      2 GHEELVRCIRFDNKRIVSGAYD 23
          || |||:::| :|:|||||
Db     351 GHVAAVRCVQYDGRRVVSGAYD 372
```

```

RESULT 12
US-09-328-877A-9
: Sequence 9, Application US/09328877A
: Patent No. US20020177187A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: FILE REFERENCE: 6142 Encode Them
: CURRENT APPLICATION NUMBER: US/09/328.877A
: CURRENT FILING DATE: 1999-06-09
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 559
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-328-877A-9

```

Query Match	59.4%	Score 82;	DB 9;	Length 559;
Best Local Similarity	59.1%;	Pred. No. 0.00011;		
Matches 13; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      2 GHEELVRCIREDNKRIVSGAYD 23
      || |||:::| :|:|||||
Db     351 GHVAAVRCVQYDGRRVSGAYD 372
```

```

RESULT 13
US-09-213-888-8
: Sequence 8, Application US/09213888A
: Patent NO. US20020164683A1
:
GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: TITLE OF INVENTION: Encode them
: FILE REFERENCE: 6142
: CURRENT APPLICATION NUMBER: US/09/213, 888A
: CURRENT FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 8
: LENGTH: 589
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
:
: US-09-213-888-8

```

Query Match	59.4%;	Score 82;	DB 9;	Length 589;
Best Local Similarity	59.1%;	Pred. No. 0.00011;		
Matches 13; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      2 GHEELVRCIRFDNKRIVSGAYD 23
      11 111::1 :1:111111
Db     381 GHVAAVRCVQYDGRRVSGAYD 402
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RESULT 14
US-09-328-877A-8

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: Sequence 8 Application US/09328877A
: Patent No. US20020177187A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: FILE REFERENCE: 6142
: CURRENT APPLICATION NUMBER: US/09/328,877A
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 589
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-328-877A-8

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Query Match	59.4%;	Score 82;	DB 9;	Length 589;
Best Local Similarity	59.1%;	Pred. No. 0.00011;		
Matches 13;	Conservative 5;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      2 GHEELVRCIRFDNKRIVSGAYD 23
      || |||:::| :|:|||||
Db     381 GHVAAVRCVQYDGRRVSGAYD 402
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RESULT 15
US-09-213-888-4
: Sequence 4, Application US/09213888A
: Patent No. US20020164683A1
: GENERAL INFORMATION:
: APPLICANT: gurney, Mark E.
: APPLICANT: Li, Jinne
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: TITLE OF INVENTION: Encode Them
: FILE REFERENCE: 6142
: CURRENT APPLICATION NUMBER: US/09/213,888A
: CURRENT FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-213-888-4

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Query Match	59.48;	Score 82;	DB 9;	Length 592;
Best Local Similarity	59.18;	Pred. No. 0.00011;		
Matches 13; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

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QY      2 GHEELVRCIRFDNKRIVSGAYD 23
          || ||::| :|:|||||
Db     384 GHVAAVRCVQYDGRRVSGAYD 405
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Search completed: April 10, 2003, 13:16:47
Job time : 3.66017 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.00853 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492
Perfect score: 138
Sequence: 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	518	2	B48088
2	132	95.7	701	2	T16607
3	92	66.7	267	2	S62507
4	92	66.7	506	2	T50211
5	74	53.6	579	2	T22703
6	68	49.3	1101	2	T26919
7	63	45.7	318	2	S11904
8	63	45.7	605	2	T38932
9	62	44.9	601	2	JF0238
10	62	44.9	640	2	S49932
11	61	44.2	615	2	S54468
12	59	42.8	650	2	T46660
13	59	42.8	659	2	S38108
14	59	42.8	1888	2	T14273
15	58	42.0	357	2	AT2099
16	57.5	41.7	386	2	T26805
17	57	41.3	440	2	T01768
18	57	41.3	522	2	D96764
19	57	41.3	580	2	G72202
20	57	41.3	582	2	S56245
21	56.5	40.9	494	2	T40471
22	56.5	40.9	586	2	T39769
23	56	40.6	283	2	T17256
24	56	40.6	325	2	G87344
25	56	40.6	353	2	A54969
26	55	39.9	714	2	S56893
27	55	39.9	1146	2	A55532
28	54	39.1	334	2	T03764
29	54	39.1	586	2	T38992

30	54	39.1	651	2	T50289	WD repeat protein
31	54	39.1	1198	2	T43484	hypothetical prote
32	54	39.1	1356	2	T18521	beta transducin-11
33	53	38.4	304	2	A61837	WD-40 repeat prote
34	53	38.4	314	2	T43299	probable GTP-bind
35	53	38.4	316	2	S57839	CPC2 protein - Neu
36	53	38.4	438	2	T45823	hypothetical prote
37	53	38.4	510	2	T20276	hypothetical prote
38	53	38.4	745	2	S74281	hypothetical prote
39	52.5	38.0	1043	2	T23875	hypothetical prote
40	52	37.7	370	2	A66741	hypothetical wd-40
41	52	37.7	399	2	T38388	WDRI protein - hum
42	52	37.7	606	2	T13152	Colg1-associated p
43	52	37.7	906	2	S35342	coatomer complex b
44	52	37.7	906	2	S35312	hypothetical prote
45	51	37.0	395	2	T23317	hypothetical prote

ALIGNMENTS

RESULT 1

B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trop
C:Species: Xenopus laevis (African clawed frog)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; M0ID:93330289; PMID:8393141
A:Accession: B48088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SPC>
A:Cross-References: GB:98268; NID:q295542; PIDN:AAA02810.1; PID:q295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <WD1>

Query Match 100.0%; Score 138; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
DB 432 EGHLELVRCIRFDNKRIVSGAYDGKI 457

RESULT 2

T16607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16607
R:Miller, N.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: 218545
A:Accession: T16607
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-701 <MIT>
A:Cross-References: EMBL:U28730; NID:9860694; PID:9860695; PIDN:AAA68258.1; CESP:K10B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.1
A:introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3

Query Match 95.7%; Score 132; DB 2; Length 701;
Best Local Similarity 96.2%; Pred. No. 6.8e-12;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
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 Db 458 EGHLELVRCIRFDNKRIVSGAYDGKI 483

RESULT 3

S62507
 hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
 C:Accession: T38502, S62507
 R:Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandream, A.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: T21798
 A:Accession: T38502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <J02>
 A:Cross-references: EMBL:Z66525; NID:g1044926; PIDN:CA91423.1; PID:g1044927; GSPDB:GNOC
 C:Genetics:
 A:Map position: 1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:18-51/Domain: WD repeat homology <WD1>
 F:104-137/Domain: WD repeat homology <WD2>

Query Match 66.7%; Score 92; DB 2; Length 267;
 Best Local Similarity 53.8%; Pred. No. 2.9e-06;
 Matches 14; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
 |||||
 Db 187 QGHEDLIRTVRFNDEKIVSGYDGTIV 212

RESULT 4

T50211
 WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
 C:Accession: T50211
 R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; Mc
 submitted to the EMBL Data Library, January 2000
 A:Reference number: Z25046
 A:Accession: T50211
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-506 <MCD>
 A:Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05
 A:Experimental source: strain 972h(-); cosmid c30
 C:Genetics:
 A:Gene: SPAC29E6.01; SPDB:SPAC30.05
 A:Map position: 1
 A:Introns: 43/1; 74/3
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 66.7%; Score 92; DB 2; Length 506;
 Best Local Similarity 53.8%; Pred. No. 5.7e-06;
 Matches 14; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
 |||||
 Db 426 QGHEDLIRTVRFNDEKIVSGYDGTIV 451

RESULT 5
 T22703
 hypothetical protein F55B12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22703
 R:Sims, M.
 submitted to the EMBL Data Library, September 1996

A:Reference number: Z19602
 A:Accession: T22703
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-579 <WTL>
 A:Cross-references: EMBL:Z79757; PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3
 A:Experimental source: clone F55B12
 C:Genetics:
 A:Gene: CESP:F55B12.3
 A:Map position: 5
 A:Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1

Query Match 53.6%; Score 74; DB 2; Length 579;
 Best Local Similarity 54.5%; Pred. No. 0.0036;
 Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
 |||||
 Db 368 GHAAVRCVQFDGTVVSSGID 389

RESULT 6

T26919
 hypothetical protein Y45F10B.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26919
 R:McMurray, A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20286
 A:Accession: T26919
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1101 <WTL>
 A:Cross-references: EMBL:AL021487; PIDN:CA16357.1; GSPDB:GN00022; CESP:Y45F10B.10
 A:Experimental source: clone Y45F10B
 C:Genetics:
 A:Gene: CESP:Y45F10B.10
 A:Map position: 4
 A:Introns: 217/3; 292/1; 451/3; 556/2; 637/3; 755/3; 823/2; 946/1; 1078/3

Query Match 49.3%; Score 68; DB 2; Length 1101;
 Best Local Similarity 55.6%; Pred. No. 0.058;
 Matches 15; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 GHEELVRCIRFDNKRIVSGAYDGKI 26
 |||||
 Db 885 GHENVTCCCTSFDERIVVSGARDEKI 911

RESULT 7

S11904
 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S11904
 R:Schloss, J.A.
 Mol. Gen. Genet. 221, 443-452, 1990
 A:Title: A Chlamydomonas gene encodes a G protein beta subunit-like polypeptide.
 A:Reference number: S11904; MUID:90340296; PMID:2116589
 A:Accession: S11904
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-318 <MOL>
 A:Cross-references: EMBL:X53574; NID:g18144; PIDN:CA37638.1; PID:g18145
 C:Genetics:
 A:Introns: 37/2; 120/3; 177/3; 265/2
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 F:11-46/Domain: WD repeat homology <WD1>
 F:60-93/Domain: WD repeat homology <WD2>
 F:102-135/Domain: WD repeat homology <WD3>
 F:146-181/Domain: WD repeat homology <WD4>
 F:190-223/Domain: WD repeat homology <WD5>

A:Reference number: 223121; MUID:95241499, PMID:7724564
A:Accession: T46660
A>Status: preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-650 <KDM>
A:Cross-references: EMBL:U17251; NID:g806757; PIDN:AAA68968.1; PID:g806758
C:Genetics:
A:Gene: scon-2
A:Map position: 3
A:Introns: 75/3; 319/1; 354/1
C:Function:
A:Description: negatively regulates sulfur structural gene expression
A>Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to the C::Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 42.8%; Score 59; DB 2; Length 650;
Best Local Similarity 38.5%; Pred. No. 0.76;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVGAYDGKI 26
 ||| | : : : : : : : :
Db 291 KGHNGVCTCIQDDNNIATGSTDTTT 316

RESULT 13
S38108
hypothetical protein YKR036c - yeast (*Saccharomyces cerevisiae*)
C:Species: *Saccharomyces cerevisiae*
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: S38108
R:Urrestarazu, L.A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38097
A:Accession: S38108
A:Molecule type: DNA
A:Residues: 1-659 <0RR>
A:Cross-references: EMBL:Z28261; NID:9486472; PIDD:CAA82110.1; PIDD:9486473; MIPS:YKR036c
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:CAF4
A:Cross-references: SGD:S0001744; MIPS:YKR036c
A:Map position: 11R
C:Superfamily: yeast hypothetical protein YKR036c; WD repeat homology
F:374-408/domain: WD repeat homology <WD2>
F:436-467/domain: WD repeat homology <WD3>
F:541-572/domain: WD repeat homology <WD5>

Query Match	42.8%	Score 59	DB 2	Length 659
Best Local Similarity	30.8%	Pred. No. 0.78		
Matches	8	Conservative 11	Mismatches 7	Indels 0
Gaps				0

QY	1	EGHELVRCIRFDNKNRIVSGAIDGKI	26
		::: ::: :	
Db	542	EGHVDGTLTKLPSEKLVGTGMDNSV	567

RESULT 14
T14273 zinc finger protein 106 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14273
R:Zuberi, A.R.; Christianson, G.J.; Mendoza, L.M.; Shastri, N.; Roopentlan, D.C.
Immunity 9, 687-698, 1998
A:Title: Positional cloning and molecular characterization of an immunodominant cytotoxic
A:Reference number: Z17953; MUID:99060924; PMID:9846490
A:Accession: T14273
A:Status: preliminary; translated from GB/EMBL/DBDUT
A:Molecule type: mRNA
A:Residues: 1-1888 <ZUB>
C:Cross-references: EMBL:AF060246; NID:g3372656; PID:g3372657; PIDN:AAD04329.1
C:Genetics:
A:Note: Z1P106

	Query Match	42.8%	Score 59	DB 2:	Length 1888;
	Best Local Similarity	36.0%	Pred. No. 2.4'		
Matches	9; Conservative	6; Mismatches	10; Indels	0; Gaps	0.
Cy	2 GHELVRCIRPDKNRIVSCATYNGKI	26			
	: : : : :				
Db	1783 GHKMDIMCMTIHKRSVITTCGDSGI	1807			

RESULT 15
AI2099
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AI2099
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyama, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata-Nakazaki, N.; Shimo, S., 2001
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Nostoc sp. strain PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2099
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <KUP>
A:Cross-references: GB:BA000019; PIDN:BAB74051.1; PID:917131444; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all12352

Query Match	42.0%	Score 58:	DB 2:	Length 357;
Best Local Similarity	44.4%:	Pred. No. 0.57;		
Matches 12;	Conservative	4:	Mismatches	9; Indels 2; Gaps 1
QY	2	GHEELVRCIRF--DNKRIVSGAYDGKI	26	
	: :	: :		
Db	319	GHSQWVAIAIEFSPDGKTLASGGFDGRI	345	

Search completed: April 10, 2003, 13:23:05
Job time : 4.00853 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:51:26 ; Search time 1.86845 seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492

Perfect score: 138

Sequence: 1 EGHEELVRCIRFDNKRIVSGAYDKRI 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	518	1	TRCB_XENLA
2	138	100.0	542	1	FWIB_HUMAN
3	138	100.0	605	1	FWIA_HUMAN
4	132	95.7	665	1	L123-CAEEL
5	92	66.7	506	1	POFB_SCHPO
6	74	53.6	579	1	SEIO-CAEEL
7	71	51.4	678	1	SCOB-EMENI
8	66	47.8	1261	1	APAF-BRARE
9	63	45.7	318	1	GRUP-CHURE
10	63	45.7	605	1	POFI-SCHPO
11	62	44.9	601	1	WD66-PHYRO
12	62	44.9	640	1	MT30-YEAST
13	61	44.2	615	1	ATP1-YEAST
14	59	42.8	650	1	SCO2-NEUCR
15	59	42.8	659	1	YK16-YEAST
16	57	41.3	779	1	CC4-TEAST
17	56	40.6	353	1	GBB5_HUMAN
18	56	40.6	353	1	GBB5_MOUSE
19	56	40.6	714	1	Y12L-YEAST
20	55	39.9	1146	1	KMHA-DICDI
21	54	39.1	317	1	GRUP-OREMI
22	54	39.1	334	1	GRUP-ORISA
23	54	39.1	586	1	T012-SCHPO
24	54	39.1	651	1	Y1X1-SCHPO
25	54	39.1	1242	1	WDRA_HUMAN
26	54	39.1	1356	1	HEFI-PODAN
27	53	38.4	314	1	GRUP-SCHPO
28	53	38.4	316	1	GRUP-NEUCR
29	53	38.4	608	1	W0R1-XENLA
30	53	38.4	682	1	Y124_HUMAN
31	53	38.4	759	1	YCD9-YEAST
32	52	37.7	318	1	GRUP-DROME
33	52	37.7	327	1	GRUP-ARATH

ALIGNMENTS

RESULT 1	ID	TRCB_XENLA	STANDARD:	PRT:	518 AA.
AC	091854	P70037; P70038;			
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Beta-TRCP (Beta-transducin repeat-containing protein).				
GN	FBXW1 OR BTCP.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9330289; PubMed=8393141;				
RA	Spevak W., Keiper B.D., Stratowa C., Gastanon M.J.;				
RT	"Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in				
RT	anaphase are rescued by Xenopus CDNAs encoding N-ras or a protein				
RT	with beta-transducin repeats.";				
RL	Mol. Cell. Biol. 13:4953-4966(1993).				
RN	[2]				
RP	SEQUENCE OF 302-518 FROM N.A.				
RX	MEDLINE=97109804; PubMed=8952061;				
RA	Hudson J.W., Alarcon V.B., Elinson R.P.;				
RT	"Identification of new localized RNAs in the Xenopus oocyte by				
RT	differential display PCR.";				
RL	Dev. Genet. 19:190-198(1996).				
CC	-1- FUNCTION: Probably recognizes and binds to some phosphorylated				
CC	proteins and promotes their ubiquitination and degradation.				
CC	-1- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX				
CC	(BY SIMILARITY).				
CC	-1- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-				
CC	MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC				
CC	GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO				
CC	NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR				
CC	TADPOLE EMBRYO.				
CC	-1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).				
CC	-1- SIMILARITY: STRONG. TO C.ELEGANS K10B2.1.				
CC	-----				
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CC	-----				
DR	EMBL; M98268; AAA02810.1; -				075083 homo sapien
DR	EMBL; U63921; AAB4671.1; -				088342 mus musculus
DR	EMBL; U63922; AAB4672.1; -				035142 ratus norv
DR	InterPro: IPR001810; F-box.				P35605 bos taurus
DR	InterPro: IPR001800; WD40.				P35606 homo sapien
DR	Pfam; PF00400; WD40; 7.				055029 mus musculus
					P46800 dictyostell
					093847 caenorhabdi
					P25362 saccharomyc
					093277 gallus gall
					062621 drosophila
					Q12024 saccharomyc

DR Pfam: PR00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat; WD repeat.
 KW DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.
 FT REPEAT 516 548 GEM -> EFR (IN REF. 2).
 FT CONFLICT 302 304 GEM -> AAH (IN REF. 2).
 FT CONFLICT 516 518
 SQ SEQUENCE 518 AA: 59507 MM: 2A52EC19028127F3 CRC64;

Query Match 100.0%; Score 138; DB 1; Length 518;
 Best local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 432 EGHEELVRCIRFDNKRIVSGAYDGKI 457

RESULT 2

FW1A_HUMAN STANDARD; PRT; 542 AA.

AC Q9YKBJ; Q9YAC6; Q9P2S8; Q9P2S9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-Trop2).
 GN FBXW1B OR FBW1B OR BTROP2 OR KIAA0696.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chlaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE-Petal lung;
 RX MEDLINE=20160456; PubMed=10694485;
 RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katoh M.;
 RT "Molecular cloning and genomic structure of the betaTRCP2 gene on
 RT chromosome 5q35.1";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishitaka K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kocani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A, B AND C (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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DR EMBL: AF176022; AAF04528.1; -
 DR EMBL: AB033279; BAA92329.1; -
 DR EMBL: AB033280; BAA92330.1; -
 DR EMBL: AB033281; BAA92331.1; -
 DR EMBL: AB014596; BAA1671.1; ALT_INIT.
 DR Genew; HGNC:13607; FBXW1B.
 DR MIM: 605651; -
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 KW DOMAIN 129 167 F-BOX.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT REPEAT 527 542 MISSING (IN ISOFORM A).
 FT VARSPLIC 16 49 CSVPRLSLGCAINVESKACLSQSPSVKCL -> NTSV
 FT VARSPLIC 16 48 MEDONEDSPKKNITL (IN ISOFORM B).
 SQ SEQUENCE 542 AA: 62090 MM: 7CD40087EFAA5C8A CRC64;

Query Match 100.0%; Score 138; DB 1; Length 542;
 Best local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 440 EGHEELVRCIRFDNKRIVSGAYDGKI 465

RESULT 3

FW1A_HUMAN STANDARD; PRT; 605 AA.

AC Q9Y297; Q9Y213;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-Trop2)
 DE (E3S1kappab) (pikappaBap1a-E3 receptor subunit).
 GN FBXW1A OR FBW1A OR BTROP OR BTROP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996;

RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the Ikapbalpha-
 RT ubiquitin ligase.";
 RL Nature 396:590-594(1998).
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940;
 RA Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.;
 RT "A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif.";
 RL Mol. Cell 1:565-574(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
 RA Harper J.W.;
 RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in I-kappa-B-alpha and
 RT beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
 RL Genes Dev. 13:270-283(1999).
 CC -1- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA
 CC (P/ARPA/BALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR
 CC UBIQUITINATION AND DEGRADATION.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 DR EMBL: AF101784; AAC08702.1; -;
 DR EMBL: Y14153; CAAT74572.1; -;
 DR EMBL: AF129530; AAF04464.1; -;
 DR Genew: HGNC:1144; BTRC.
 DR MIM: 603482; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS50678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 190 228 F-BOX.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.

FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 605 AA; 68866 MW; 4C673B7E400FD37 CRC64;
 Query Match 100.0%; Score 138; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 1,8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ECHELVRCIRFDNKRIVSGAVDGKI 26
 Db 503 ECHELVRCIRFDNKRIVSGAVDGKI 528
 RESULT 4
 L123_CAEEL STANDARD: PRT: 665 AA.
 AC Q09990; Q9GNM6;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein 1ln-23.
 GN 1ln-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RX MEDLINE=20515608; PubMed=11060233;
 RA Kipreos E.T., Gonel S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein 1ln-23 functions
 RT to limit cell division during development.";
 RL Development 127:5071-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 CC cycle progression. Required to restrain cell proliferation in
 CC response to developmental cues. Probably recognizes and binds to
 CC some proteins and promotes their ubiquitination and degradation
 CC (By similarity).
 CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 CC levels in larvae. Maternal expression results in high zygotic
 CC levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO X.LAEVIS PBXW1.
 CC -----
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 CC -----
 DR EMBL: AF75253; AAG28037.1; -;
 DR EMBL: U28730; AAA68258.2; -;
 DR WormPep: K10B2.1; CE28600.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.

ProDom: PD000018; WD40: 4.
 DR SMART: SM00256; FBOX: 1.
 DR SMART: SM00320; WD40: 7.
 DR PROSITE: PS00181; FBOX: 1.
 DR PROSITE: PS00678; WD_REPEATS_1: 5.
 DR PROSITE: PS00082; WD_REPEATS_2: 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION: 1.
 KW Developmental protein; Cell cycle; Cell division;
 KW Ubl conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 81
 FT REPEAT 127
 FT REPEAT 220
 FT REPEAT 257
 FT REPEAT 260
 FT REPEAT 299
 FT REPEAT 301
 FT REPEAT 337
 FT REPEAT 343
 FT REPEAT 380
 FT REPEAT 383
 FT REPEAT 420
 FT REPEAT 423
 FT REPEAT 460
 FT REPEAT 472
 FT REPEAT 509
 FT REPEAT 525
 FT REPEAT 582
 FT REPEAT 441
 FT MUTAGEN 441
 FT SEQUENCE 665 AA; 75916 MW; BF3E9AF51F12ECCC CRC64;

Query Match 95.7%; Score 132; DB 1; Length 665;
 Best Local Similarity 96.2%; Pred. No. 1.7e-12;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 422 EGHEELVRCIRFDNKRIVSGAYDGKI 447

RESULT 5
 ID POBRSCHPO STANDARD; PRT; 506 AA.
 AC 009855; Q9P7V1.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE F-box/WD-repeat protein pof1.
 GN POF1 OR SPAC29E6.01 OR SPAC30.05.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hartison C.L., Toda T.;
 RT "Systematic genome-wide analysis of F-box protein-encoding genes in
 RT fission yeast."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Mambrot R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaie V., Motlier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC - SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC - SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
 CC -----
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CC EMBL: AB061694; BAB5543.1; -
 CC EMBL: AL136538; CAB66464.1; -
 CC EMBL: Z66525; CA91423.1; -
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF00646; F-box; 1.
 CC Pfam: PF00646; F-box; 1.
 CC PRINTS: PR00320; GPROTEINRPT.
 CC PRODOM: PD000018; WD40: 3.
 CC SMART: SM00256; FBOX: 1.
 CC SMART: SM00320; WD40: 8.
 CC PROSITE: PS00181; FBOX: 1.
 CC PROSITE: PS00678; WD_REPEATS_1: 3.
 CC PROSITE: PS00082; WD_REPEATS_2: 6.
 CC PROSITE: PS50294; WD_REPEATS_REGION: 1.
 KW Repeat; WD repeat.
 FT DOMAIN 70
 FT REPEAT 116
 FT REPEAT 219
 FT REPEAT 256
 FT REPEAT 259
 FT REPEAT 298
 FT REPEAT 301
 FT REPEAT 338
 FT REPEAT 345
 FT REPEAT 386
 FT REPEAT 388
 FT REPEAT 426
 FT REPEAT 427
 FT REPEAT 464
 FT REPEAT 488
 FT REPEAT 505
 FT REPEAT 58257 MW; CEF34D4EFC2E10 CRC64;

Query Match 66.7%; Score 92; DB 1; Length 506;
 Best Local Similarity 53.8%; Pred. No. 1.7e-06;
 Matches 14; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 426 QGHEDLIRTVRFNDEKIVSGYDGTV 451

RESULT 6
 ID SE10_CAEEL STANDARD; PRT; 579 AA.
 AC Q93794;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Sel-10 protein
 GN SEL-10 OR F55B12.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 NX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Bristol N2;
 RA Sims M.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.

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CC -----
DR EMBL: U21220; AAC15905.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00440; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPOTREINERPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Transcription regulation; Repeat; WD repeat.
KW DOMAIN
FT 178 224 F-BOX.
FT REPEAT
FT 347 375 WD 1.
FT REPEAT
FT 387 415 WD 2.
FT REPEAT
FT 427 455 WD 3.
FT REPEAT
FT 466 496 WD 4.
FT REPEAT
FT 508 543 WD 5.
FT REPEAT
FT 553 595 WD 6.
FT REPEAT
FT 607 635 WD 7.
FT REPEAT
FT 647 675 WD 8.
SQ SEQUENCE 678 AA; 76070 MM; D840D452E37B4C53 CRC64;

OY 2 GHEELVRCIRFDNKRIVSGAYDGK1 26
Db 387 GHESGIRCLQFDDTKLISGMDRT1 411
| | | : | | : | | : | | : | |
| | | : | | : | | : | | : | |

RESULT 8
APAF_BRARE
ID APAF_BRARE STANDARD: PRT: 1261 AA.
DC Q919H8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptotic protease activating factor 1 (Apaf-1).
GN APAF1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CC NCBI_TaxID=7955;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=20373792; PubMed=10917738;
CC Inohara N., Nunez G.;
CC "Genes with homology to mammalian apoptosis regulators identified in
CC Zebrafish."
CC Cell Death Differ. 7:509-510(2000).
CC -!- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent
CC autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the
CC activation of caspase-3 and apoptosis. This activation requires
CC ATP (By similarity).
CC -!- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and
CC dATP (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -!- SIMILARITY: CONTAINS 13 WD_REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.
CC -----
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 CC -----
 CC EMBL: AF251502; AAF67189.1; -
 DR HSSP; 014727; 1C75.
 DR ZFIN; ZDB-GENE-000616-4; apa11.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002182; NB-ARC.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 12.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00320; GP00TEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00320; WD40; 11.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Apoptosis; ATP-binding; Repeat; WD repeat.
 FT DOMAIN 1 90
 FT NP_BIND 106 417 NB-ARC.
 FT REPEAT 154 161 ATP (POTENTIAL).
 FT REPEAT 615 654 WD 1.
 FT REPEAT 657 696 WD 2.
 FT REPEAT 700 743 WD 3.
 FT REPEAT 746 785 WD 4.
 FT REPEAT 798 836 WD 5.
 FT REPEAT 840 879 WD 6.
 FT REPEAT 882 921 WD 7.
 FT REPEAT 964 1003 WD 8.
 FT REPEAT 1006 1045 WD 9.
 FT REPEAT 1047 1088 WD 10.
 FT REPEAT 1091 1130 WD 11.
 FT REPEAT 1133 1172 WD 12.
 FT REPEAT 1184 1223 WD 13.
 SO SEQUENCE 1261 AA; 142933 MW; F80CC9CBA1764F1C CRC64;
 Query Match 47.8%; Score 66; DB 1; Length 1261;
 Best Local Similarity 50.0%; Pred. No. 0.042;
 Matches 14; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
 QY 1 EGHETLVRCIRF--DNKRIVSGATDGKI 26
 DB 1132 EGHKDCVRSRFSWMDKRIATGDDNGEI 1159
 RESULT 9
 GBLP_CHLRE STANDARD; PRT; 318 AA.
 AC P25387;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Guanine nucleotide-binding protein beta subunit-like protein.
 GN GBLP.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=219r;
 RX MEDLINE=90340296; PubMed=2116589;
 RA Schloss J.A.;
 RT "A Chlamydomonas gene encodes a G protein beta subunit-like
 RT polypeptide.";
 RL Mol. Genet. 221:443-452(1990).

-I- DEVELOPMENTAL STAGE: CONSTITUTIVELY EXPRESSED DURING THE CELL
 CC CYCLE AND FLAECILIA REGENERATION.
 CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC -----
 CC EMBL: X53574; CAA37638.1; -
 DR PIR; S11904; S11904.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GP00TEINBRPT.
 DR ProDom; PD000018; WD40; 5.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT REPEAT 13 45 WD 1.
 FT REPEAT 62 92 WD 2.
 FT REPEAT 104 134 WD 3.
 FT REPEAT 148 180 WD 4.
 FT REPEAT 192 222 WD 5.
 FT REPEAT 233 262 WD 6.
 FT REPEAT 283 313 WD 7.
 SO SEQUENCE 318 AA; 35145 MW; F545C3534D83B778 CRC64;
 Query Match 45.7%; Score 63; DB 1; Length 318;
 Best Local Similarity 51.9%; Pred. No. 0.028;
 Matches 14; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
 QY 1 EGHETLVRCIRFD---NKRIVSGAYD 23
 DB 147 EGHTEWVSCVRFSPMTNPLIVSGMD 173
 RESULT 10
 POFL_SCHPO STANDARD; PRT; 605 AA.
 AC P87053;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein poFl (Skp1-binding protein 1).
 GN POFL OR SBP1 OR SPAC57A10.05C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Katayama S., Kitamura K., Toda T.;
 RT "Systematic genome-wide analysis of F-box protein-encoding genes in
 RT fission yeast.";
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RX Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares K.,
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnietz B.,
 RA Weidjens I., Vanstreels E., Rieger M., Scheer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hiltner H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaive V., Motlier S.,
 RA Calbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Sprakowski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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 CC -----
 DR EMBL: AB032410; BAA84528.1; -
 DR EMBL: Z94864; CAB08168.1; -
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 5.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ub1 conjugation; Repeat; WD repeat.
 KW DOMAIN 107 153
 FT REPEAT 271 299 WD 1.
 FT REPEAT 311 339 WD 2.
 FT REPEAT 350 379 WD 3.
 FT REPEAT 390 420 WD 4.
 FT REPEAT 432 460 WD 5.
 FT REPEAT 472 500 WD 6.
 FT REPEAT 510 538 WD 7.
 SQ SEQUENCE 605 AA: 67110 MW: 7118C9379EC5C1F0 CRC64;

Query Match 45.7%; Score 63; DB 1; Length 605;
 Best Local Similarity 42.3%; Pred. No. 0.055;
 Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFD-NKRIYSGAYDGKI 26
 DB 310 EGHSGVGTCLPDKCKLTSGSMKRTI 335

RESULT 11
 ID WD66.PHYPO STANDARD: PRT: 601 AA.
 AC P90587;
 DT 15-JUL-1998 (rel. 36, Created)

DT 15-JUL-1998 (rel. 36, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE 66 kDa stress protein (p66).
 OS Physarum polycephalum (Slime mold).
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
 OC Physarum.
 OX NCBI_TaxID=5791;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98351989; PubMed=9685722;
 RA Matsumoto S., Ogawa M., Kasakura T., Shimada Y., Mitsui M., Maruya M.,
 RA Isobata M., Yahara I., Murakami-Murofushi K.,
 RT A novel 66-kDa stress protein, p66, associated with the process of
 RT cyst formation of *Physarum polycephalum* is a *Physarum* homologue of a
 RT yeast actin-interacting protein, Aip1."
 RL J. Biochem. 124:326-331(1998).
 CC -1- FUNCTION: ASSOCIATED WITH THE PROCESS OF CYST FORMATION.
 CC -1- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE AIP1 FAMILY OF WD-REPEAT PROTEINS.
 CC -----
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 CC -----
 DR EMBL: U86011; AAC26321.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 10.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR SMART: SM00320; WD40; 10.
 DR PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT REPEAT 56 95 WD 1.
 FT REPEAT 100 143 WD 2.
 FT REPEAT 145 184 WD 3.
 FT REPEAT 187 226 WD 4.
 FT REPEAT 233 272 WD 5.
 FT REPEAT 318 357 WD 6.
 FT REPEAT 357 395 WD 7.
 FT REPEAT 435 478 WD 8.
 FT REPEAT 483 522 WD 9.
 FT REPEAT 526 565 WD 9.
 FT REPEAT 569 600 WD 10.
 SQ SEQUENCE 601 AA: 64321 MW: F691217D838F747A CRC64;

Query Match 44.9%; Score 62; DB 1; Length 601;
 Best Local Similarity 46.4%; Pred. No. 0.078;
 Matches 13; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

QY 1 EGHELVRCIRFD-NKRIYSGAYDGKI 26
 DB 317 KGHNKLVTSIAFDTSKALYSIDGYI 344

RESULT 12
 ID MT30.YEAST STANDARD: PRT: 640 AA.
 AC P39014;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE MET30 protein.
 GN MET30 OR YIL046W.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*;
 OC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-X2180-1A;
MEDLINE=9069360; PubMed=8524217;
RA Thomas D., Kuras L., Barbery R., Cherest H., Blaiseau P.L.,
RA Surdin-Kerjan Y.,
RT "Wet30p, a yeast transcriptional inhibitor that responds to S-
adenosylmethionine, is an essential protein with WD40 repeats.",
RL Mol. Cell. Biol. 15:6526-6534(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Iye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.,
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BIOSYNTHESIS
CC GENES EXPRESSION.
CC -!- SUBUNIT: SEEMS TO INTERACT WITH MET4.
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: BELONGS TO THE MET30/SCOMB/SCON-2 FAMILY OF WD-REPEAT
CC PROTEINS.
CC -----
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CC -----
CC EMBL: 246861; CAA86905.1; -
CC EMBL: 126505; AAA96717.1; -
CC SGD: S0001308; MEM30.
CC DR InterPro: IPR001810; F-box.
CC DR InterPro: IPR001680; WD40.
CC DR Pfam: PF00400; WD40; 7.
CC DR Pfam: PF00646; F-box; 1.
CC DR PRINTS: PR00320; GPROTEINBRPT.
CC DR PRODOM: PD000018; WD40; 4.
CC DR SMART: SM00256; FBOX; 1.
CC DR SMART: SM00320; WD40; 6.
CC DR PROSITE: PS50181; FBOX; 1.
CC DR PROSITE: PS00678; WD_REPEATS_1; 4.
CC DR PROSITE: PS50082; WD_REPEATS_2; 6.
CC DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC KW Transcription regulation; Methionine biosynthesis;
CC Cysteine biosynthesis; Repeat; WD repeat.
CC FT DOMAIN 181 227
CC FT REPEAT 300 328 WD 1.
CC FT REPEAT 340 368 WD 2.
CC FT REPEAT 380 408 WD 3.
CC FT REPEAT 419 449 WD 4.
CC FT REPEAT 461 499 WD 5.
CC FT REPEAT 509 538 WD 6.
CC FT REPEAT 550 578 WD 7.
CC FT REPEAT 607 635 WD 8 (POTENTIAL).
CC FT CONFLICT 61 61 M -> I (IN REF. 1).
CC SO SEQUENCE 640 AA: 72835 MW: 513504BCA2E1E9B7 CRC64;
QY Query Match 44.9%; Score 62; DB 1; Length 640;
Best Local Similarity 56.0%; Pred. No. 0.083;
Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

RESULT 13
ATPL_YEAST

ID ATPL_YEAST STANDARD; PRT; 615 AA.
AC P46860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Actin interacting protein 1.
GN ATPL OR YMR092C OR YW9582.17C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Amberg D.C., Botstein D.,
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A.,
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP INTERACTION WITH COFILIN, AND FUNCTION.
RX PubMed=10366597;
RA Rodal A.A., Tetreault J.W., Lappalainen P., Drubin D.G., Amberg D.C.,
RT J. Cell Biol. 145:1251-1264(1999).
RL -!- FUNCTION: Involved in the depolymerization of actin filaments.
CC Enhances the filament disassembly activity of cofilin and
CC restricts cofilin localization to cortical actin patches.
CC -!- SUBUNIT: Interacts with actin and cofilin in a ternary complex.
CC -!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: BELONGS TO THE ATPL FAMILY OF WD-REPEAT PROTEINS.
CC -----
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CC -----
CC EMBL: U35666; AAA79141.1; -
CC EMBL: 249259; CAA89239.1; -
CC SGD: S0004698; ATPL.
CC DR InterPro: IPR001680; WD40.
CC DR Pfam: PF00400; WD40; 7.
CC DR PRINTS: PR00320; GPROTEINBRPT.
CC DR SMART: SM00320; WD40; 7.
CC DR PROSITE: PS00678; WD_REPEATS_1; FALSE_NEG.
CC DR PROSITE: PS50082; WD_REPEATS_2; 2.
CC DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
CC KW Actin-binding; Cytoskeleton; Repeat; WD repeat.
CC FT REPEAT 62 109 WD 1.
CC FT REPEAT 114 157 WD 2.
CC FT REPEAT 158 201 WD 3.
CC FT REPEAT 204 244 WD 4.
CC FT REPEAT 251 289 WD 5.
CC FT REPEAT 337 367 WD 6.
CC FT REPEAT 370 406 WD 7.
CC FT REPEAT 442 481 WD 8.
CC FT REPEAT 486 525 WD 9.
CC FT REPEAT 529 578 WD 10.
CC FT REPEAT 583 613 WD 11.
CC FT DOMAIN 363 366 POLY-SER.
CC SO SEQUENCE 615 AA: 67325 MW: B8340BF68DD08257 CRC64;
QY Query Match 44.2%; Score 61; DB 1; Length 615;
Best Local Similarity 39.4%; Pred. No. 0.11;
Matches 13; Conservative 7; Mismatches 5; Indels 8; Gaps 1;

QY 2 GHDELVRCIRFDNKR-----VSGAYDGKI 26
Db 327 GHDELVLCIRGNGKIGITALVNPISGSDGRI 359

RESULT 14
SC02_NEUCR STANDARD: PRT: 650 AA.
AC 001277: 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfur controller-2 (SCON2).
GN SCON-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=95241499; PubMed=7724564;
RA Kumar A., Palella J.V.;
RT "The sulfur controller-2 negative regulatory gene of Neurospora
crassa encodes a protein with beta-transducin repeats.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
CC -1- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
CC -1- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.
CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
PROTEINS.
CC -----
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CC -----
DR EMBL: U17251; AAA68968.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS00682; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Transcription regulation; Repeat; WD repeat.
KW DOMAIN 124 170 F-BOX.
FT REPEAT 292 320 WD 1.
FT REPEAT 332 360 WD 2.
FT REPEAT 372 400 WD 3.
FT REPEAT 411 441 WD 4.
FT REPEAT 453 488 WD 5.
FT REPEAT 528 564 WD 6.
FT REPEAT 576 604 WD 7.
FT REPEAT 616 644 WD 8.
SQ SEQUENCE 650 AA; 72189 MW; 7473859C99F1B028 CRC64;

Query Match 42.8%; Score 59; DB 1; Length 650;
Best Local Similarity 38.5%; Pred. No. 0.24;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

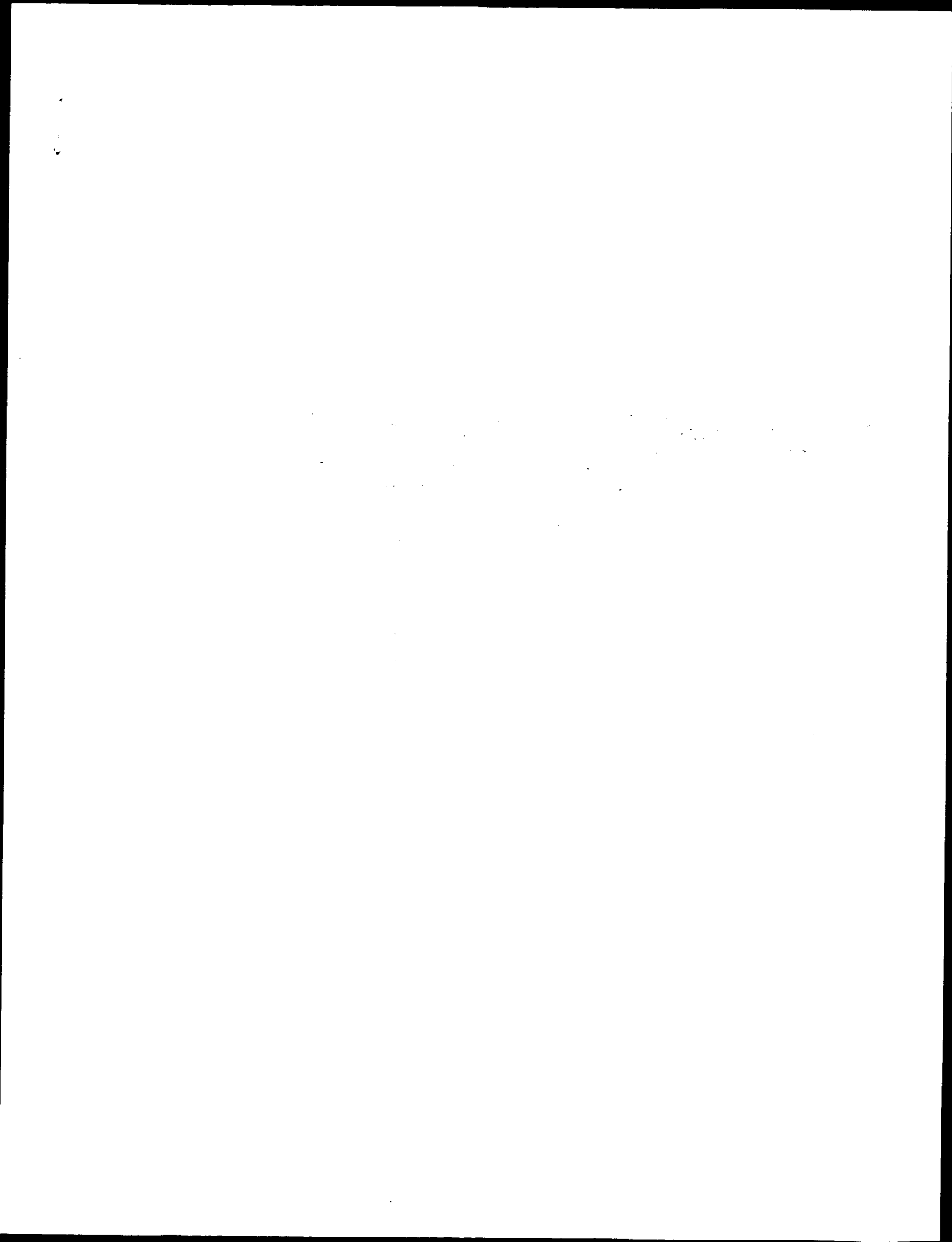
OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
DB 291 KGHNGVTCLODDNITLATGSYDTTI 316

RESULT 15

YK16_YEAST
ID YK16_YEAST STANDARD: PRT: 659 AA.
AC P36130: 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 74.7 kDa Trp-Asp repeats containing protein in DAL80-GAP1
intergenic region.
GN YK036C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Urrestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: Z28261; CA882110.1; -
DR PIR: S38108; S38108.
DR TRANSFAC: T04326; -
DR SGI: S0001744; YK036C.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 1.
DR SMART: SM00320; WD40; 5.
DR PROSITE: PS00678; WD_REPEATS_1; 4.
DR PROSITE: PS50082; WD_REPEATS_2; 5.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 333 364 WD 1.
FT REPEAT 376 407 WD 2.
FT REPEAT 438 466 WD 3.
FT REPEAT 503 531 WD 4.
FT REPEAT 543 571 WD 5.
FT REPEAT 582 610 WD 6.
SQ SEQUENCE 659 AA; 74709 MW; 139593554C56DD37 CRC64;

Query Match 42.8%; Score 59; DB 1; Length 659;
Best Local Similarity 30.8%; Pred. No. 0.25;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
DB 542 EGHITDGTSLKFDSEKLVGMSDNVS 567

Search completed: April 10, 2003, 13:19:38
Job time: 2.86845 secs



GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 6.14373 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_467_492

Perfect score: 138
Sequence: 1 EGHELVRCIRFDNKRIVSGAYDGKI 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	252	11	0922C7 mus musculu
2	138	100.0	563	11	0923H0 mus musculu
3	138	100.0	563	11	092159 mus musculu
4	138	100.0	563	11	090015 mus musculu
5	133	96.4	430	5	09B054 mus musculu
6	133	96.4	569	11	09R1G7 mus musculu
7	132	95.7	510	5	044382 drosophila
8	132	95.7	510	5	09VDE3 drosophila
9	82	59.4	553	4	09NUX6 homo sapien
10	82	59.4	561	4	096R12 homo sapien
11	82	59.4	589	4	096LE0 homo sapien
12	82	59.4	627	4	096A16 homo sapien
13	82	59.4	629	11	08VAP4 mus musculu
14	82	59.4	629	11	08VAP4 mus musculu
15	82	59.4	707	4	0969H0 homo sapien
16	78	56.5	1326	5	09VZF4 drosophila

17	74	53.6	585	5	095ZT0	095ZT0 caenorhabd
18	74	53.6	587	5	044083	044083 caenorhabd
19	68	49.3	1101	5	062471	062471 caenorhabd
20	65	47.1	329	5	08SSP4	08SSP4 dictyosteli
21	64	46.4	196	4	095611	095611 homo sapien
22	64	46.4	252	4	043848	043848 homo sapien
23	64	46.4	252	4	095170	095170 homo sapien
24	64	46.4	999	4	09H0F0	09H0F0 homo sapien
25	64	46.4	1061	4	08TC00	08TC00 homo sapien
26	63	45.7	423	5	08SSJ1	08SSJ1 encephalito
27	61	44.2	178	4	09H7B8	09H7B8 homo sapien
28	61	44.2	1883	4	09H2Y7	09H2Y7 homo sapien
29	59	42.8	176	11	09ESU3	09ESU3 mus musculu
30	59	42.8	339	11	088465	088465 mus musculu
31	59	42.8	562	10	09SC73	09SC73 oryza sativ
32	59	42.8	1888	11	088466	088466 mus musculu
33	58.5	42.4	589	5	096661	096661 trypanosoma
34	58	42.0	297	5	09VE10	09VE10 drosophila
35	58	42.0	357	16	08YUJ4	08YUJ4 anabaena sp
36	58	42.0	514	10	0941P9	0941P9 lycopersico
37	58	42.0	680	5	09V5W2	09V5W2 drosophila
38	57.5	41.7	386	5	09XWJ3	09XWJ3 caenorhabd
39	57	41.3	440	10	004634	004634 arabidopsis
40	57	41.3	511	10	08W117	08W117 arabidopsis
41	57	41.3	522	10	09C9T9	09C9T9 arabidopsis
42	57	41.3	580	16	09X2G1	09X2G1 thermotoga
43	56.5	40.9	494	3	094365	094365 schizosacch
44	56.5	40.9	586	3	060136	060136 schizosacch
45	56.5	40.9	774	5	09V767	09V767 drosophila

ALIGNMENTS

RESULT 1

ID 0922C7 PRELIMINARY: PRT: 252 AA.

AC 0922C7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to f-box and WD-40 domain protein 1B (Fragment).
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC008552; AAH08552.1; -
DR MGI; MGI:2144023; Fbxw1b.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINREP.
DR PRODOM; PD000018; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE; PS00082; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER
SQ
SD
252 AA: 28424 MW; F71737CBD7A9F75F CRC64;

Query Match 100.0%; Score 138; DB 11; Length 252;

Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHELVRCIRFDNKRIVSGAYDGKI 26
DB 150 EGHELVRCIRFDNKRIVSGAYDGKI 175

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RESULT 2
ID 0923HO PRELIMINARY; PRT; 563 AA.
AC 0923HO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE F-box/MD40 repeat-containing protein HOS.
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Bhalla N., Hetter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
RT "Mouse homolog of HOS (mHOS) is overexpressed in skin tumors and
RT implicated in constitutive activation of NF-kappaB."
CC Submitted (JUN-2001) to the EMBL/Genbank/DDBI databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY038079; AKK72095.1; -.
DR MGD: MGI:2144023; FBXW1B.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 7.
DR PROSITE: PS00678; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN. 5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 563 AA; 64741 MW; 9AB562E3FE5E3496 CRC64;

Query Match 100.0%; Score 138; DB 11; Length 563;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
DB 461 EGHLELVRCIRFDNKRIVSGAYDGKI 486

RESULT 3
ID 092159 PRELIMINARY; PRT; 569 AA.
AC 092159;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAY-2002 (TREMBLrel. 20, last annotation update)
DE Beta-transducin repeat containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99145465; PubMed=9990853;
RA Spencer E., Jiang J., Chen Z.J.;
RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
RT Slmb/beta-Trcp."
RL Genes Dev. 13:284-294(1999).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF112979; AAD04181.1; -.
DR MGD: MGI:1338871; BTRC.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.

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DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN. 6.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;

Query Match 100.0%; Score 138; DB 11; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHLELVRCIRFDNKRIVSGAYDGKI 26
DB 467 EGHLELVRCIRFDNKRIVSGAYDGKI 492

RESULT 4
ID 090U15 PRELIMINARY; PRT; 569 AA.
AC 090U15;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Ubiquitin ligase EMD1 (Beta-transducin repeat containing protein)
DE (F-box-WD40 repeat protein 1).
GN BTRC OR FBXW1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9919275; PubMed=10097128;
RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
RA Nakayama K.-I.;
RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a
RT ubiquitin ligase Skp1/Cul1/F-box protein FWD1."
RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9859996;
RA Varon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalpha-
RT ubiquitin ligase."
RL Nature 396:590-594(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DDBI databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA MEDLINE=21601157; PubMed=11735228;
RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA Nakayama K.-I.;
RT "Characterization of a Mouse Gene (FBXW6) That Encodes a Homologue of
RT Caenorhabditis elegans SEL-10."
RL Genomics 78:214-222(2001).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF081887; AAD17755.1; -.
DR EMBL: AF099932; AAD08701.1; -.
DR EMBL: BC003989; AAO03989.1; -.
DR EMBL: AF391190; AAL40929.1; -.
DR EMBL: AF391178; AAL40929.1; JOINED.
DR EMBL: AF391179; AAL40929.1; JOINED.
DR EMBL: AF391180; AAL40929.1; JOINED.
DR EMBL: AF391181; AAL40929.1; JOINED.
DR EMBL: AF391182; AAL40929.1; JOINED.

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DR EMBL: AF391183; AAL40929.1; JOINED.
 DR EMBL: AF391184; AAL40929.1; JOINED.
 DR EMBL: AF391185; AAL40929.1; JOINED.
 DR EMBL: AF391186; AAL40929.1; JOINED.
 DR EMBL: AF391187; AAL40929.1; JOINED.
 DR EMBL: AF391188; AAL40929.1; JOINED.
 DR EMBL: AF391189; AAL40929.1; JOINED.
 DR MGD: MGI:1338871; Btcr.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Ligase: Repeat; WD repeat.
 KW SEQUENCE 569 AA; 65105 MW; BCD6544815B2296 CRC64;

Query Match 100.0%; Score 138; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 4.9e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 467 EGHEELVRCIRFDNKRIVSGAYDGKI 492

RESULT 5
 Q9BJ54 PRELIMINARY: PRT: 430 AA.
 AC Q9BJ54
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Beta-transducin repeat-containing protein (fragment).
 OS Heterodera glycyines (Soybean cyst nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera;
 NCBI_TaxID=51029;

RA Kovalova E.S., Yakovlev A.G., Masler E.P.;
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF391101; AAK26376.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 6.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER 1
 SQ SEQUENCE 430 AA; 47916 MW; 4ABC3FE2DFE3A50B CRC64;

Query Match 96.4%; Score 133; DB 5; Length 430;
 Best Local Similarity 96.2%; Pred. No. 2.2e-12;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 291 EGHEELVRCIRFDNKRIVSGAYDGKI 316

RESULT 6

O9R1G7 PRELIMINARY: PRT: 569 AA.
 AC O9R1G7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Beta-transducin repeat-containing protein.
 GN BTRC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RA Winston J., Ellledge S.J., Harper J.W.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF110396; AAD41025.1; -
 DR MGD: MGI:1338871; Btcr.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D5519D CRC64;

Query Match 96.4%; Score 133; DB 11; Length 569;
 Best Local Similarity 96.2%; Pred. No. 3e-12;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 DB 467 EGHEELVRCIRFDNKRIVSGAYDGKI 492

RESULT 7
 O44382 PRELIMINARY: PRT: 510 AA.
 AC O44382
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE SLIMB.
 GN SLIMB OR SLIMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;

RA "Regulation of the Hedgehog and Wingless signalling pathways by the F-
 box/WD40-repeat protein Slmb.";
 RT Nature 391:493-496(1998).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF032878; AAC38852.1; -
 DR FlyBase: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.

DR SMART: SM00320; WD40: 1.
 DR SMART: SM00320; WD40: 7.
 DR PROSITE: PS00678; WD_REPEATS_1: UNKNOWN_5.
 DR PROSITE: PS00678; WD_REPEATS_2: 7.
 DR PROSITE: PS00678; WD_REPEATS_REGION: 1.
 KW Repeat: WD repeat.
 SQ SEQUENCE 510 AA: 58952 MW: DBB0243D3730A5E8 CRC64:

Query Match 95.7%; Score 132; DB 5; Length 510;
 Best Local Similarity 96.2%; Pred. No. 3.8e-12;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 Db 410 EGHEELVRCIRFDNKRIVSGAYDGKI 435

RESULT 8

AC Q9VDE3 PRELIMINARY; PRT; 510 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SLMB protein (SLMB).
 GN SLMB OR CG3412.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adell J.F., Agbayani A., An H.-J., Andrews-Plamkoc C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bokova D., Botchan M.R., Bouck J., Brostein P., Brothier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Glodok A., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jia H.M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kamell B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo K., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY; AND IMAGINAL DISC;
 RC MEDLINE=20245299; PubMed=10781936;
 RA Miletich I., Limbourg-Bouchon B.,
 RT "Drosophila null slmb clones transiently deregulate Hedgehog-
 RT independent transcription of wingless in all limb discs, and induce
 RT decapentaplegic transcription linked to imaginal disc regeneration."
 RL Mech. Dev. 93:15-26(2000).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC EMBL: AE003733; AAF5853.1;
 CC EMBL: AF222924; AAF63214.1;
 CC EMBL: AF222923; AAF63213.1;
 CC FLYBase: FBgn0023423; slmb.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00320; WD40: 1.
 DR SMART: SM00181; FBOX: 1.
 DR PROSITE: PS00181; FBOX: 1.
 DR PROSITE: PS00678; WD_REPEATS_1: 5.
 DR PROSITE: PS00678; WD_REPEATS_2: 7.
 DR PROSITE: PS0294; WD_REPEATS_REGION: 1.
 KW Repeat: WD repeat.
 SQ SEQUENCE 510 AA: 58952 MW: FAD5DF126F58A012 CRC64:

Query Match 95.7%; Score 132; DB 5; Length 510;
 Best Local Similarity 96.2%; Pred. No. 3.8e-12;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EGHEELVRCIRFDNKRIVSGAYDGKI 26
 Db 410 EGHEELVRCIRFDNKRIVSGAYDGKI 435

RESULT 9

AC Q9NUX6 PRELIMINARY; PRT; 553 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CDNA FLJ11071 fis, clone PLACE1004937, moderately similar to SFL-10
 DE protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Itoga T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
 RA Nakamura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Makumura Y., Nagahata K., Masuno Y., Sasaki N.,
 RT "NEO human cDNA sequencing project."
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC EMBL: AK001933; BAA91986.1;
 CC InterPro: IPR001810; F-box.
 CC InterPro: IPR001680; WD40.
 CC Pfam: PF00646; F-box; 1.
 CC Pfam: PF00400; WD40; 7.
 CC PRINTS: PR00320; GPROTEINBRPT.
 CC ProDom: PD000018; WD40; 2.
 DR SMART: SM00320; WD40: 1.
 DR SMART: SM00320; WD40: 7.
 DR PROSITE: PS00181; FBOX: 1.
 DR PROSITE: PS00678; WD_REPEATS_1: UNKNOWN_5.
 DR PROSITE: PS00678; WD_REPEATS_2: 7.

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DR PROSITE: PS50294; WD_REPEATS_REGION: 1.
KW Repeat; WD repeat.
SQ SEQUENCE 553 AA; 62280 MW; CA829C221986A3F2 CRC64;

Query Match
Best Local Similarity 59.4%; Score 82; DB 4; Length 553;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
II |||||:|:|:|
Db 345 GHVAAVRCVQYDGRRVSGAYD 366

RESULT 10
O96R12 PRELIMINARY; PRT; 561 AA.
AC O96R12;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE F-box protein FBX30 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DE EMBL: AF383178; AAK60269.1; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
SQ SEQUENCE 561 AA; 63165 MW; B81CC1E2206B0D88 CRC64;

Query Match
Best Local Similarity 59.4%; Score 82; DB 4; Length 561;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
II |||||:|:|:|
Db 353 GHVAAVRCVQYDGRRVSGAYD 374

RESULT 11
O96LE0 PRELIMINARY; PRT; 589 AA.
AC O96LE0;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE F-box protein SEL10.
GN SEL10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RA Li J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R.,
RA Buh A.E., Gunney M.E.;
RT "SEL-10 interacts with Presenilin 1, Facilitates Its Ubiquitination,
and Alters A-beta Production."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DE EMBL: AY008274; AAG16640.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 589 AA; 66120 MW; 2AFB6E8A36E6E8DE CRC64;

Query Match
Best Local Similarity 59.4%; Score 82; DB 4; Length 589;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 GHEELVRCIRFDNKRIVSGAYD 23
II |||||:|:|:|
Db 381 GHVAAVRCVQYDGRRVSGAYD 402

RESULT 12
O96A16 PRELIMINARY; PRT; 627 AA.
AC O96A16;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE F-box protein FBW7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2144947; PubMed=11565033;
RA Moberg K.H., Bell D.W., Wahrer D.C., Haber D.A., Hariharan I.K.;
RT "Archipelago regulates Cyclin E levels in Drosophila and is mutated in
human cancer cell lines."
RL Nature 413:311-316(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DE EMBL: AF411972; AAL06291.1; -.
DR EMBL: AY033553; AAK57547.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 627 AA; 70324 MW; 3D4107C053381BED CRC64;

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Query Match 59.4%; Score 82; DB 4; Length 627;
Best Local Similarity 59.1%; Pred. No. 0.00029;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GHEELVRCIRFDNKRIVSGAYD 23
Db 419 GHVAARVCYDGRRVVSGAYD 440

RESULT 13

Q8VHP4 PRELIMINARY; PRT; 629 AA.
AC Q8VHP4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F-box protein.
GN FBXW6
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Ilyin G.P.;
RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF427101; AAL50052.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PRO0320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 629 AA; 70562 MW; BE916405A3490A3E CRC64;

Query Match 59.4%; Score 82; DB 11; Length 629;
Best Local Similarity 59.1%; Pred. No. 0.00029;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GHEELVRCIRFDNKRIVSGAYD 23
Db 421 GHVAARVCYDGRRVVSGAYD 442

RESULT 14

Q8VHP4 PRELIMINARY; PRT; 629 AA.
AC Q8VHP4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F-box WD40 repeat protein 6.
GN FBXW6
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE=21601157; PubMed=11735228;
RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA Nakayama K.-I.;
RT "Characterization of a Mouse Gene (FBXW6) That Encodes a Homologue of
RT Caenorhabditis elegans SEL-10.";
RL Genomics 78:214-222(2001).
DR EMBL: AF391202; AAL40930.1; -

DR EMBL: AF391193; AAL40930.1; JOINED.
DR EMBL: AF391194; AAL40930.1; JOINED.
DR EMBL: AF391195; AAL40930.1; JOINED.
DR EMBL: AF391196; AAL40930.1; JOINED.
DR EMBL: AF391197; AAL40930.1; JOINED.
DR EMBL: AF391198; AAL40930.1; JOINED.
DR EMBL: AF391199; AAL40930.1; JOINED.
DR EMBL: AF391200; AAL40930.1; JOINED.
DR EMBL: AF391201; AAL40930.1; JOINED.
DR EMBL: AF391202; AAL40930.1; JOINED.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PRO0320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 629 AA; 70547 MW; 80483A7C2ED61FE7 CRC64;

Query Match 59.4%; Score 82; DB 11; Length 629;
Best Local Similarity 59.1%; Pred. No. 0.00029;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GHEELVRCIRFDNKRIVSGAYD 23
Db 421 GHVAARVCYDGRRVVSGAYD 442

RESULT 15

Q969H0 PRELIMINARY; PRT; 707 AA.
AC Q969H0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F-box protein CDC4 (Archipelago alpha form).
GN CDC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

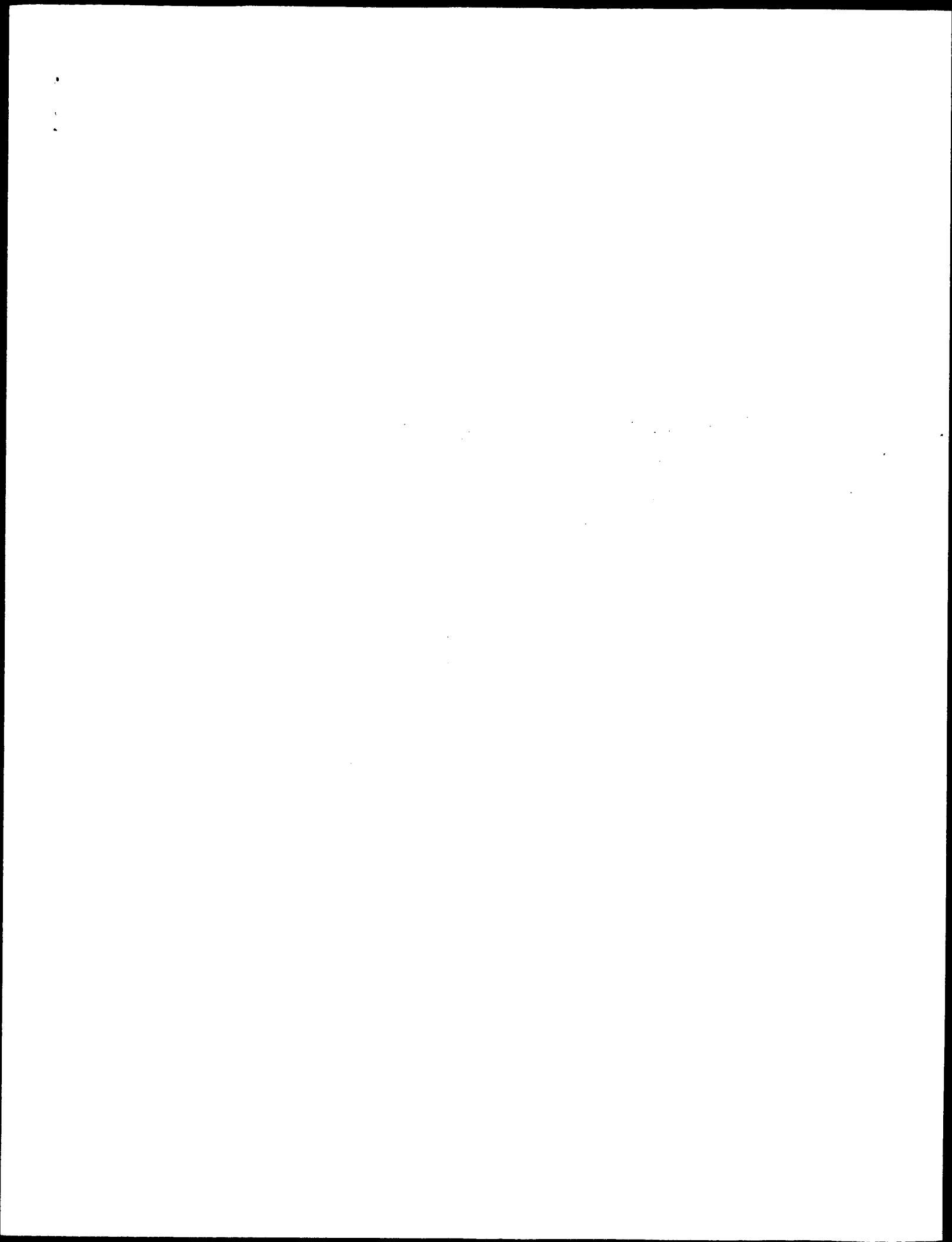
RA MEDLINE=21449048; PubMed=11565034;
RA Strohmaier H., Spruck C.H., Kaiser P., Won K.A., Sangfelt O.,
RA Reed S.L.;
RT "Human F-box protein hcdc4 targets cyclin E for proteolysis and is
RT mutated in a breast cancer cell line.";
RL Nature 413:316-322(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=21449047; PubMed=11565033;
RA Moberg K.H., Bell D.W., Wahner D.C., Haber D.A., Hariharan I.K.;
RT "Archipelago regulates cyclin E levels in Drosophila and is mutated in
RT human cancer cell lines.";
RL Nature 413:311-316(2001).
CC -!- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY049984; AAL07271.1; -
DR EMBL: AF411971; AAL06290.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRODOM: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

Repeat: WD repeat
SQ SEQUENCE 707 AA; 79663 MW; EAA357F76DFD8203 CRC64;

Query Match 59.4%; Score 82; DB 4; Length 707;
Best Local Similarity 59.1%; Pred. No. 0.00033;
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GHEELVRCIRFDNKRIVSGAYD 23
|||:::|:|:|
Db 499 GHVAARVCVOYDGRVVGAYD 520

Search completed: April 11, 2003, 11:51:54
Job time : 8.14373 secs



GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:20:44 ; Search time 8.93666 Seconds
(without alignments)
432.406 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544
Sequence: 1 VEHSGRVFRLQGFDEQIVSSHDDTLIN 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	100.0	517	16	AA85852
2	152	100.0	569	20	AA85852
3	152	100.0	569	21	AA85852
4	152	100.0	569	21	AA85852
5	152	100.0	569	21	AA85852
6	152	100.0	569	21	AA85852
7	152	100.0	569	21	AA85852
8	152	100.0	569	21	AA85852
9	152	100.0	569	21	AA85852
10	152	100.0	569	22	AA85852

11	152	100.0	579	22	AA85853	Human protein SEQ
12	152	100.0	590	22	AA85854	Human bone marrow
13	152	100.0	605	22	AA85852	Human protein SEQ
14	152	100.0	608	22	AA85852	Human bone marrow
15	152	100.0	632	22	AA85854	Human protein SEQ
16	152	100.0	654	22	AA85856	Human protein SEQ
17	152	100.0	654	22	AA85857	Human protein SEQ
18	152	100.0	654	22	AA85858	Human protein SEQ
19	151	99.3	542	21	AA85859	Human E3 ubiquitin
20	151	99.3	542	21	AA85860	Human polyubiquitin
21	151	99.3	542	22	AA85861	Human polyubiquitin
22	151	99.3	550	22	AA85862	Human polyubiquitin
23	149	98.0	510	16	AA85863	Drosophila melanog
24	148	97.4	29	16	AA85864	Peptide rvi1 from
25	73	48.0	540	20	AA85865	Human hippocampal
26	73	48.0	540	22	AA85866	Human mammary sel-
27	73	48.0	540	22	AA85867	Human hippocampal
28	73	48.0	540	22	AA85868	Human mammary sel-
29	73	48.0	545	20	AA85869	Human hippocampal
30	73	48.0	545	22	AA85870	Human hippocampal
31	73	48.0	553	22	AA85871	Human hippocampal
32	73	48.0	553	22	AA85872	Human hippocampal
33	73	48.0	553	22	AA85873	Human hippocampal
34	73	48.0	559	20	AA85874	Human mammary sel-
35	73	48.0	559	22	AA85875	Human mammary sel-
36	73	48.0	589	20	AA85876	Human mammary sel-
37	73	48.0	589	21	AA85877	Human mammary sel-
38	73	48.0	589	22	AA85878	Human mammary sel-
39	73	48.0	592	20	AA85879	Human hippocampal
40	73	48.0	592	22	AA85880	Human hippocampal
41	73	48.0	626	22	AA85881	Human hippocampal
42	73	48.0	626	22	AA85882	Human hippocampal
43	73	48.0	627	22	AA85883	Human hippocampal
44	73	48.0	627	22	AA85884	Human hippocampal
45	73	48.0	666	20	AA85885	Human C-term mychi

ALIGNMENTS

RESULT 1	AA85852	13-SEP-1996 (first entry)	WD-40 domain-contg. beta-TRCP protein.
ID	AA85852	standard; peptide: 517 AA.	
XX	AA85852		
AC	AA85852		
XX	AA85852		
DE	13-SEP-1996 (first entry)		
XX	13-SEP-1996 (first entry)		
DE	WD-40 domain-contg. beta-TRCP protein.		
XX	WD-40 domain-contg. beta-TRCP protein.		
KW	WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.		
XX	WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.		
OS	Synthetic.		
XX	Synthetic.		
PN	WO9521252-A2.		
XX	WO9521252-A2.		
PD	10-AUG-1995.		
XX	10-AUG-1995.		
PF	31-JAN-1995: 95WO-US01210.		
XX	31-JAN-1995: 95WO-US01210.		
PR	01-FEB-1994: 94US-0190802.		
XX	01-FEB-1994: 94US-0190802.		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.		
XX	(STRD) UNIV LELAND STANFORD JUNIOR.		
PI	Mochly-Rosen D, Ron D;		
XX	Mochly-Rosen D, Ron D;		
DR	WPI: 1995-283772/37.		
XX	WPI: 1995-283772/37.		
XX	New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the activity of a protein, eg. protein kinase C, which interacts with a protein contg. a WD-40 region.		
PT	New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the activity of a protein, eg. protein kinase C, which interacts with a protein contg. a WD-40 region.		

XX	Example 5; Page 80-82; 351pp; English.
PS	
XX	Proteins AAR85851-92 are protein which contain at least one WD-40 (also
CC	called beta-transducin homologous) amino acid repeat motifs. The WD-40
CC	regions are involved in protein-protein interactions between proteins
CC	involved in intracellular signalling. An example of such an interaction
CC	is between protein kinase C and receptors of activated protein kinase
CC	(RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
CC	on homology with beta-transducin, whereas proteins AAR85882-92 were
CC	isolated based on homology with the WD-40 consensus sequence (AAR85893).
CC	The proteins were used to construct the peptides AAR84928-R85063 and
CC	AAR85786-R85842. The peptides can be used to identify target proteins
CC	congng. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC	proteins involved in protein-protein interaction and to screen for drugs
CC	that will affect protein-protein interaction involving WD-40 domains.
XX	
SQ	Sequence 517 AA;
	Query Match 100.0%; Score 152; DB 16; Length 517;
	Best Local Similarity 100.0%; Pred. No. 5,9e-15;
	Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 VEHSGRVFRLQDFEFQIVSSSHDDITLLW 29 Db 480 VEHSGRVFRLQDFEFQIVSSSHDDITLLW 508
RESULT 2	
AAV24054	
ID	AAV24054 standard; Protein: 569 AA.
XX	
AC	AAV24054;
XX	
DT	30-SEP-1999 (first entry)
XX	
DE	A human beta-transducin repeat containing protein.
XX	
Beta-transducin repeat containing protein; beta-Trcp; SKP1p; RW proteasome degradation pathway; Vpu protein; beta-catenin; KW human immune deficiency virus-1; HIV-1; cellular protein; IkappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; KW antiviral; antitumour; cell cycle regulation; protein degradation; KW and anti-inflammatory; osteo-articular inflammation; acute inflammation; tumour necrosis factor.	
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Region 147..191
FT	/note= "F box sequence"
FT	259..292
FT	/note= "WD motif"
FT	304..332
FT	/note= "WD motif"
FT	Region 343..372
FT	/note= "WD motif"
FT	Region 387..415
FT	/note= "WD motif"
FT	Region 427..455
FT	/note= "WD motif"
FT	Region 467..492
FT	/note= "WD motif"
FT	516..544
FT	/note= "WD motif"
XX	
PX	WO9338969-A1.
XX	
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99WO-FR00196.
XX	
R	09-DEC-1998; 98FR-0015545.

PR		30-JAN-1998;	98FR-0001100.
XX		(INRM) INSERM INST NAT SANTE & RECH MEDICALE.	
PA		(INSP) INST PASTEUR.	
XX			
PI		Arenzana Seisdedos F, Benarous R, Concordet J, Durand H;	
PI		Kroll M, Margollin F;	
XX			
DR		WP1; 1999-469329/39.	
N-PSDB; AAX86501.			
XX		New human beta-transducin repeat containing protein and its	
PT		fragments useful as, or to screen for, antiviral, antitumour,	
PI		anti-inflammatory and anti-Alzheimer's agents	
XX			
PS		Claim 1; Page 60-61; 71pp; French.	
XX			
CC		The present sequence represents a human beta-transducin repeat containing	
CC		protein (beta-Trcp). The protein directs proteins to the proteosome	
CC		degradation pathways. The protein is able to interact with the Vpu	
CC		protein of human immune deficiency virus-1 (HIV-1), cellular proteins	
CC		IkappaB or beta-catenin (bc) and/or protein skp1p. The protein controls	
CC		ubiquitylation of phosphorylated proteins and thus their targeting to	
CC		proteosomes for degradation. Depending on whether the process is	
CC		inhibited or promoted, the result may be delayed breakdown of CD4 (in	
CC		cases of HIV-1 infection); increased activity of Ikb (and thus reduced	
CC		activity of NFkappaB) and increased degradation of mutant bc in tumour	
CC		cells; or increased bc survival (and reduced apoptosis) in Alzheimer's	
CC		patients. The beta-Trcp protein, and its active peptide fragments, or its	
CC		nucleic acid, are used to screen for anti HIV-1 agents (antivirals),	
CC		antitumour agents that disrupt cell cycle regulation or protein	
CC		degradation in human tumour cells, and anti-inflammatory agents that	
CC		disrupt activation by NFkappaB. Fragments of the protein are also	
CC		useful for treating osteo-articular inflammation or acute inflammation	
CC		associated with release of tumour necrosis factor.	
XX			
SQ	Sequence	569 AA:	
Query Match		100.0%; Score 152; DB 20; Length 569;	
Best Local Similarity		100.0%; Pred. No. 6,7e-15;	
Matches 29; Conservative	0; Mismatches	0; Indels	0; Gaps 0
OY	1	VEHSGRVFRLQDFEFOIVSSSHDDITLLW 29	
Db	516	VEHSGRVFRLQDFEFOIVSSSHDDITLLW 544	
RESULT 3			
AAB12812	ID	AAB12812 standard; protein: 569 AA.	
XX	AC		
XX	AA	AAB12812;	
XX	XX		
XX	XX	27-NOV-2000 (first entry)	
DE	Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.		
XX	Ubiquitin ligase SCF complex; F-box protein; ubiquitylation; IkappaB;		
KW	beta-catenin; Skp1; Cull1; F-box motif; WDA0 repeat motif; FWD1;		
KM	gene therapy; colon cancer; beta-transducin repeat containing protein;		
XX	beta-Trcp.		
OS	Mus musculus.		
XX			
PJ	JF200016542-A.		
PN			
PD	20-JUN-2000.		
XX			
PF	02-DEC-1998; 98JP-0343437.		
XX			
PR	02-DEC-1998; 98JP-0343437.		
XX			
VA	(KAGA-) KAGAKU GIYUTSU SHINKO JIGYOJIAN.		

XX WPI: 2000-485550/43.
 DR N-PSDB; AAA73131.
 XX F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of IkappaB or beta-catenin
 PS Claim 2; Page 9-10; 19pp; Japanese.
 XX The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of IkappaB or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for
 CC the gene therapy of colon cancer by being recombined to a virus vector.
 XX Sequence 569 AA;
 SO
 Query Match 100.0%; Score 152; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 6,7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VEHSGRVRLQDFEFOIVSSSHDPTILIW 29
 DB 516 VEHSGRVRLQDFEFOIVSSSHDPTILIW 544
 RESULT 4
 AAB12813
 ID AAB12813 standard; protein; 569 AA.
 XX AAB12813;
 AC 27-NOV-2000 (first entry)
 XX Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
 DE Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FMD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-TrCP.
 XX Homo sapiens.
 OS JP200016542-A.
 XX 20-JUN-2000.
 PD 02-DEC-1998; 98JP-0343437.
 XX 02-DEC-1998; 98JP-0343437.
 PF 02-DEC-1998; 98JP-0343437.
 PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA WPI: 2000-485550/43.
 XX N-PSDB; AAA73132.
 DR F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of IkappaB or beta-catenin
 XX Claim 3; Page 10-12; 19pp; Japanese.
 PS The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of IkappaB or
 CC beta-catenin and is constituted by Skp1 protein, Cull1 protein and a
 CC complex (SCF complex) of F-box protein containing F-box motif and WD40
 CC repeat motif and has the amino acid sequence of 45 residues (AAB12811)
 CC or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin
 CC ligase FMD1 protein) and (AAB12813, which is human beta-transducin
 CC repeat containing protein (beta-TrCP)). The F-box protein can be used for

CC the gene therapy of colon cancer by being recombined to a virus vector.
 XX Sequence 569 AA;
 SO
 Query Match 100.0%; Score 152; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 6,7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VEHSGRVRLQDFEFOIVSSSHDPTILIW 29
 DB 516 VEHSGRVRLQDFEFOIVSSSHDPTILIW 544
 RESULT 5
 AAY96697
 ID AAY96697 standard; protein; 569 AA.
 XX AAY96697;
 AC 26-SEP-2000 (first entry)
 XX Human beta-TrCP.
 DE E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
 KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
 KW anti-inflammatory; immunosuppressive; cytostatic.
 XX Homo sapiens.
 OS WO200034447-A2.
 XX 15-JUN-2000.
 PD 10-DEC-1999; 99WO-US29371.
 PF 10-DEC-1998; 98US-0210060.
 PR 10-DEC-1998; 98US-0210060.
 XX (SIGN-) SIGNAL PHARM INC.
 PA (YISS) YISSUM RES & DEV CO.
 XX Menning AM, Mercurio F, Amlt S, Ben-eriah Y, Davis M, Hatzubai A;
 PI Lavon I, Yaron A;
 XX WPI: 2000-431294/37.
 DR N-PSDB; AAA51229.
 XX Polypeptide enhancing phosphorylated IkappaB ubiquitination useful for
 PT treating disorder associated with NF-kappaB activation e.g. cancer,
 PT comprising amino acid sequence of human E3 ubiquitin ligase or its
 PT variant
 PS Claim 21; Page 72-74; 77pp; English.
 XX Human beta-TrCP, an F-box/MD protein family member, has been shown to
 CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
 CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
 CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
 CC degradation via the ubiquitin pathway is useful for identifying
 CC modulators of this process for use in treating diseases associated with
 CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
 CC the F-box results in a protein that functions as a dominant negative
 CC molecule in vivo. Transient over-expression of endogenous I-kappa-B-alpha
 CC deletion mutant inhibited the degradation of phosphorylated
 CC in stimulated Jurkat cells, resulting in accumulation of NF-kappa-B
 CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
 CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
 CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
 XX Sequence 569 AA;
 SO
 Query Match 100.0%; Score 152; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 6,7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEQTIVSSSHDITLIM 29
 DB 516 VEHSGRVRLQDFEQTIVSSSHDITLIM 544

RESULT 6

ID AAY83041 standard; Protein; 569 AA.

AC AAY83041;

DT 16-AUG-2000 (first entry)

DE F-box protein FBP-1.

XX F-box protein; FBP; diagnosis; treatment; screening; agonist;
 KW antagonist; proliferative disorder; differentiative disorder;
 KW breast cancer; prostate cancer; ovarian cancer; cancer;
 KW small cell lung carcinoma; immune disorder; cardiovascular disorder;
 KW inflammatory disorder; human.

OS Homo sapiens.

PN W0200012679-A1.

PD 09-MAR-2000.

PF 27-AUG-1999; 99WO-US19560.

PR 28-AUG-1998; 98US-0098355.

PR 03-FEB-1999; 99US-0118568.

PR 15-MAR-1999; 99US-0124449.

PA (UYNX) UNIV NEW YORK STATE.

PI Chlaur DS, Pagano M, Latres E.

DR WPI; 2000-256635/22.

DR N-PSDB; AA293350.

XX Novel nucleic acid for screening compounds useful for treating

XX proliferative and differentiative disorders such as cancer and immune

XX disorders comprises sequences encoding ubiquitin ligases

PS Disclosure; Figure 3a; 245pp; English.

CC Nucleic acids encoding substrate-targeting subunits of ubiquitin
 CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 CC of proliferative and differentiated related disorders by measuring
 CC FBP gene expression. Cells expressing such proteins or
 CC their fragments are useful for screening compounds. The compounds
 CC are agonists or antagonists, which are useful for treating a
 CC proliferative or differentiative disorder in a mammal such as
 CC breast, ovarian and prostate cancer and small cell lung carcinoma
 CC and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein,
 CC analogs, derivatives and their subsequences, anti-FBP antibodies
 CC are also useful in diagnosis of the disorders.

XX Sequence 569 AA;

Query Match 100.0%; Score 152; DB 21; Length 569;

Best Local Similarity 100.0%; Pred. No. 6.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEQTIVSSSHDITLIM 29

DB 516 VEHSGRVRLQDFEQTIVSSSHDITLIM 544

RESULT 7
 AAY83250

ID AAY83250 standard; Protein; 569 AA.

AC AAY83250;

DT 16-AUG-2000 (first entry)

DE F-box protein hBetarCP.

XX Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human.

OS Homo sapiens.

PN W0200022110-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23705.

PR 09-OCT-1998; 98US-0103787.

PA (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR WPI; 2000-317970/27.

DR N-PSDB; AA293710.

XX Targeting degradation of polypeptide useful for treating cancer and
 XX other proliferative disorders. Involves conjugating polypeptide with
 XX ubiquitin protein ligase or inhibiting ubiquitination using organic
 XX compound

PS Claim 9; Page 171; 185pp; English.

CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

XX Sequence 569 AA;

Query Match 100.0%; Score 152; DB 21; Length 569;

Best Local Similarity 100.0%; Pred. No. 6.7e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEQTIVSSSHDITLIM 29

DB 516 VEHSGRVRLQDFEQTIVSSSHDITLIM 544

RESULT 8

ID AAY83254 standard; Protein; 569 AA.

AC AAY83254;

DT 16-AUG-2000 (first entry)

DR N-PSDB; AAZ29233.
 XX
 CC Human cell signaling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders
 PT
 PS Claim 1; Page 77-78; 90pp; English.
 XX
 CC The present sequence is cell signalling protein-12 (CSIGP-12) encoded
 CC by cDNA obtained from Incyte clone 3239149 of COLAUCP01 library. It is
 CC expressed in musculoskeletal, gastrointestinal and nervous tissues and is
 CC found to be homologous to beta-transducin repeats containing
 CC protein. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC them with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 CC
 SQ Sequence 569 AA;

Query Match 100.0%; Score 152; DB 21; Length 569;
 Best Local Similarity 100.0%; Pred. No. 6.7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQFDEFOIVSSSHDDTILW 29
 ||||||||||||||||||
 Db 516 VEHSGRVRLQFDEFOIVSSSHDDTILW 544

RESULT 10
 AAB48298

ID AAB48298 standard; protein; 569 AA.

XX AAB48298;

DT 02-APR-2001 (first entry)

XX Human ZF11 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytosolic.

XX Homo sapiens.

XX WO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15449.

XX 04-JUN-1999; 99US-0137494.

XX (UYVA) UNTV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

XX N-PSDB; AAC84610.

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -

XX Claim 3; Page 130-132; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the

CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell, SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 CC
 SQ Sequence 569 AA;

Query Match 100.0%; Score 152; DB 22; Length 569;
 Best Local Similarity 100.0%; Pred. No. 6.7e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQFDEFOIVSSSHDDTILW 29
 ||||||||||||||||||
 Db 516 VEHSGRVRLQFDEFOIVSSSHDDTILW 544

RESULT 11

ID AAM78583 standard; Protein; 579 AA.

XX AAM78583;

DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1245.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX 20-JUN-2000; 2000US-0598075.

XX 19-JUL-2000; 2000US-0620325.

XX 01-SEP-2000; 2000US-0654936.

XX 15-SEP-2000; 2000US-0663561.

XX 20-OCT-2000; 2000US-0693325.

XX 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX Xue AD, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.

XX N-PSDB; AAK51716.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -

XX Claim 20; Page 3504-3505; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC Inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM00020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 579 AA:

Query Match 100.0%; Score 152; DB 22; Length 579;
 Best Local Similarity 100.0%; Pred. No. 6,8e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQDFEQIVSSSHDITLW 29
 |||||||

DB 526 VEHSGRVRLQDFEQIVSSSHDITLW 554

RESULT 12
 AAM00847
 ID AAM00847 standard; Protein; 590 AA.

XX AAM00847;

DT 01-OCT-2001 (first entry)

DE Human bone marrow protein, SEQ ID NO: 210.

KW Human: bone marrow; antiinflammatory; cytosolic; neuroprotective;
 KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 KW immunosuppressive; gene therapy; cytokine cell proliferation;
 KW cell differentiation modulator; immune disorder; infection; cancer;
 KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

OS Homo sapiens.

PN WO200153453-A2.

PD 26-JUL-2001.

PF 23-DEC-2000; 2000WO-US34960.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 30-NOV-2000; 2000US-0250583.

PA (HYSE-) HYSEQ INC.

PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;

PI Ren F, Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Drmanac RT;

DR WPI: 2001-488707/53.

DR N-PSDB: AAK89966.

PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful

PT for treating e.g. cancer and immune deficiency disorders -

PS Claim 10; Page 354-355; 648pp; English.

CC encodes is useful for the diagnosis and/or prognosis of one
 CC or more types of cancer. The polynucleotide and polypeptide can be
 CC used as nutritional sources or supplements and in the screening of
 CC chemical compounds as potential drugs.

XX Sequence 590 AA:

Query Match 100.0%; Score 152; DB 22; Length 590;
 Best Local Similarity 100.0%; Pred. No. 6,9e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQDFEQIVSSSHDITLW 29
 |||||||

DB 537 VEHSGRVRLQDFEQIVSSSHDITLW 565

RESULT 13
 AAM78582
 ID AAM78582 standard; Protein; 605 AA.

XX AAM78582;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1244.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0596075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wehrman T, Goodrich R;

DR WPI: 2001-476283/51.

DR N-PSDB: AAK51715.

PT Nucleic acids encoding polypeptides with cytokine-like activities,

PT useful in diagnosis and gene therapy -

PS Claim 20; Page 3503-3504; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, hematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

XX Sequence 605 AA;

Query Match 100.0%; Score 152; DB 22; Length 605;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVFRLOPDEFQIVSSSHDDTLLW 29
Db 552 VEHSGRVFRLOPDEFQIVSSSHDDTLLW 580
|||||

RESULT 14
AAM00960
ID AAM00960 standard; Protein: 608 AA.

XX AAM00960;

DT 01-OCT-2001 (first entry)

DE Human bone marrow protein, SEQ ID NO: 436.

XX Human; bone marrow; antiinflammatory; cytosolic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.

XX Homo sapiens.

OS WO200153453-A2.

XX 26-JUL-2001.

PF 23-DEC-2000; 2000WO-US34960.

XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 30-NOV-2000; 2000US-0250583.

XX (HYSE-) HYSEQ INC.

XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Drmanac RT;

XX WPI: 2001-488707/53.

DR N-PSDB; AAM90079.

PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT for treating e.g. cancer and immune deficiency disorders -

PS Claim 10; Page 523-524; 648pp; English.

XX The present sequence is one of 251 novel human polypeptides encoded
CC by a bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one

CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.

XX Sequence 608 AA;

Query Match 100.0%; Score 152; DB 22; Length 608;
Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVFRLOPDEFQIVSSSHDDTLLW 29
Db 555 VEHSGRVFRLOPDEFQIVSSSHDDTLLW 583
|||||

RESULT 15
AAM78584
ID AAM78584 standard; Protein: 632 AA.

XX AAM78584;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1246.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

OS WO200157190-A2.

XX 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI: 2001-476283/51.

DR N-PSDB; AAK51717.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -

PS Claim 20; Page 3505-3507; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78123-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666

CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX
 SQ Sequence 632 AA;

Query Match 100.0%; Score 152; DB 22; Length 632;

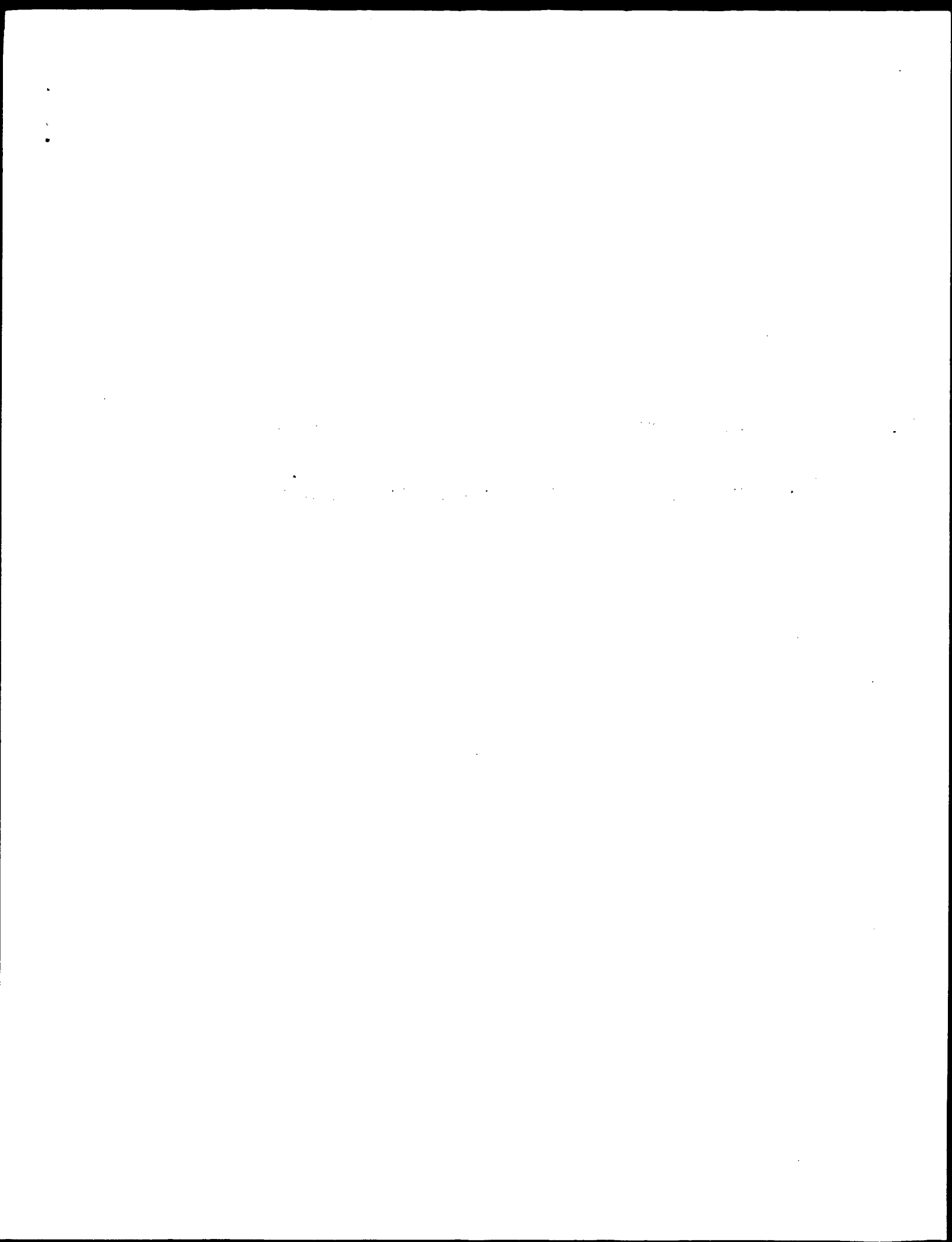
Best Local Similarity 100.0%; Pred. No. 7.5e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVFRQLQFDEFOIVSSHDDTLIW 29
 ||||||||||||||||||||||||||||

Db 579 VEHSGRVFRQLQFDEFOIVSSHDDTLIW 607

Search completed: April 11, 2003, 11:48:17
 Job time : 8.93666 secs



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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:41:55 ; Search time 3.00244 Seconds

(without alignments)
284.191 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544

Perfect score: 152

Sequence: 1 VEHSGRVFLQFDFQIVSSSHDITLIW 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	517	1 US-08-190-802A-30	Sequence 30, Appl
2	152	100.0	517	4 US-08-477-346-30	Sequence 30, Appl
3	152	100.0	517	4 US-08-473-089-30	Sequence 30, Appl
4	152	100.0	517	4 US-08-477-072A-30	Sequence 30, Appl
5	148	97.4	29	1 US-08-190-802A-89	Sequence 89, Appl
6	148	97.4	29	4 US-08-477-346-89	Sequence 89, Appl
7	148	97.4	29	4 US-08-473-089-89	Sequence 89, Appl
8	148	97.4	29	4 US-08-487-072A-89	Sequence 89, Appl
9	65.5	43.1	640	4 US-09-177-165A-30	Sequence 89, Appl
10	64	42.1	34	1 US-08-190-802A-83	Sequence 83, Appl
11	64	42.1	34	4 US-08-477-346-83	Sequence 83, Appl
12	64	42.1	34	4 US-08-473-089-83	Sequence 83, Appl
13	64	42.1	34	4 US-08-487-072A-83	Sequence 83, Appl
14	64	42.1	34	4 US-08-988-556A-21	Sequence 21, Appl
15	60.5	39.8	28	1 US-08-190-802A-84	Sequence 84, Appl
16	60.5	39.8	28	4 US-08-477-346-84	Sequence 84, Appl
17	60.5	39.8	28	4 US-08-473-089-84	Sequence 84, Appl
18	60.5	39.8	28	4 US-08-487-072A-84	Sequence 84, Appl
19	56	36.8	250	4 US-09-291-170A-12	Sequence 12, Appl
20	56	36.8	250	4 US-09-724-884-12	Sequence 12, Appl
21	56	36.8	704	1 US-08-188-582-18	Sequence 18, Appl
22	56	36.8	704	1 US-08-646-715-18	Sequence 18, Appl
23	56	36.8	798	1 US-08-190-802A-64	Sequence 64, Appl
24	56	36.8	798	1 US-08-190-802A-64	Sequence 64, Appl
25	56	36.8	798	2 US-08-308-818-2	Sequence 2, Appl
26	56	36.8	798	4 US-08-477-346-64	Sequence 64, Appl
27	56	36.8	798	4 US-08-477-346-64	Sequence 68, Appl

28	56	36.8	798	4 US-08-473-089-64	Sequence 64, Appl
29	56	36.8	798	4 US-08-473-089-68	Sequence 68, Appl
30	56	36.8	798	4 US-08-487-072A-64	Sequence 64, Appl
31	56	36.8	798	4 US-08-487-072A-68	Sequence 68, Appl
32	56	36.8	1194	4 US-09-092-508-2	Sequence 2, Appl
33	56	36.8	1194	4 US-09-435-115-2	Sequence 2, Appl
34	56	36.8	1194	4 US-09-069-023-26	Sequence 26, Appl
35	56	36.8	1194	4 US-09-092-310-2	Sequence 2, Appl
36	56	36.8	1205	4 US-09-092-508-16	Sequence 16, Appl
37	56	36.8	1205	4 US-09-435-115-16	Sequence 16, Appl
38	55	36.2	29	1 US-08-190-802A-86	Sequence 86, Appl
39	55	36.2	29	4 US-08-477-346-86	Sequence 86, Appl
40	55	36.2	29	4 US-08-473-089-86	Sequence 86, Appl
41	55	36.2	29	4 US-08-487-072A-86	Sequence 86, Appl
42	54	35.5	31	1 US-08-190-802A-239	Sequence 239, App
43	54	35.5	31	4 US-08-477-346-239	Sequence 239, App
44	54	35.5	31	4 US-08-473-089-239	Sequence 239, App
45	54	35.5	31	4 US-08-487-072A-239	Sequence 239, App

ALIGNMENTS

RESULT 1
US-08-190-802A-30
Sequence 30, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Therof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-190-802A-30
Query Match 100.0%; Score 152; DB 1; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VEHSGRVFLQFDFQIVSSSHDITLIW 29

DB 480 VEHSGRVRLQFDEFOIVSSSHDITLIM 508

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|||||
RESULT 2
US-08-477-346-30
; Sequence 30, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match 100.0%; Score 152; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQFDEFOIVSSSHDITLIM 29
DB 480 VEHSGRVRLQFDEFOIVSSSHDITLIM 508

RESULT 3
US-08-473-089-30
; Sequence 30, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster

```

```

; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 100.0%; Score 152; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQFDEFOIVSSSHDITLIM 29
DB 480 VEHSGRVRLQFDEFOIVSSSHDITLIM 508

RESULT 4
US-08-487-072A-30
; Sequence 30, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 100.0%; Score 152; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VHSGRVFRLODFEFOIVSSHDDTILIW 29
Db 480 VHSGRVFRLODFEFOIVSSHDDTILIW 508

RESULT 5
US-08-190-802A-89
Sequence 89, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190.802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP VII, Fig. 13
US-08-190-802A-89

Query Match 97.4%; Score 148; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EHSGRVFRLODFEFOIVSSHDDTILIW 29

Db 1 EHSGRVFRLODFEFOIVSSHDDTILIW 28

RESULT 6
US-08-477-346-89
Sequence 89, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP VII, Fig. 13
US-08-477-346-89

Query Match 97.4%; Score 148; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EHSGRVFRLODFEFOIVSSHDDTILIW 29
Db 1 EHSGRVFRLODFEFOIVSSHDDTILIW 28

RESULT 7
US-08-473-089-89
Sequence 89, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVII, Fig. 13
US-08-473-089-89

Query Match
Best Local Similarity 97.4%; Score 148; DB 4; Length 29;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHSGRVRLQFDFQIVSSSHDITLIW 29
DB 1 EHSGRVRLQFDFQIVSSSHDITLIW 28

RESULT 8
US-08-487-072A-89
Sequence 89, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morriston & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP rVII, Fig. 13
US-08-487-072A-89

Query Match
Best Local Similarity 97.4%; Score 148; DB 4; Length 29;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHSGRVRLQFDFQIVSSSHDITLIW 29
DB 1 EHSGRVRLQFDFQIVSSSHDITLIW 28

RESULT 9
US-09-177-165A-30
Sequence 30, Application US/09177165A
Patent No. 6426205
GENERAL INFORMATION:
APPLICANT: Tyers, Mike
APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.10USU1
CURRENT APPLICATION NUMBER: US/09/177,165A
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 640
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30

Query Match
Best Local Similarity 43.1%; Score 65.5; DB 4; Length 640;
Matches 13; Conservative 6; Mismatches 7; Indels 11; Gaps 1;

QY 4 SGRVRLQF-----DFQIVSSSHDITLIW 29
DB 541 TKGCIIRLQFGHGVWDIADNFRILSSSHGSIKIV 577

RESULT 10
US-08-190-802A-83
Sequence 83, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-190-802A-83

Query Match 42.1%; Score 64; DB 1; Length 34;
Best Local Similarity 50.0%; Pred. No. 0.0025;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 EHSGRVRLQDFEFOIVSSSHDITILW 29
| | | | | : | | | | | : | | | | |
Db 6 ETSKGVYCLQYDDOKIVSGLRDNITIKIW 33

RESULT 11
US-08-477-346-83
Sequence 83, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487, 072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-477-346-83

Query Match 42.1%; Score 64; DB 4; Length 34;
Best Local Similarity 50.0%; Pred. No. 0.0025;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 EHSGRVRLQDFEFOIVSSSHDITILW 29
| | | | | : | | | | | : | | | | |
Db 6 ETSKGVYCLQYDDOKIVSGLRDNITIKIW 33

RESULT 12
US-08-473-089-83
Sequence 83, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473, 089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP r1, Fig. 13
US-08-473-089-83

Query Match 42.1%; Score 64; DB 4; Length 34;
Best Local Similarity 50.0%; Pred. No. 0.0025;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 EHSGRVRLQDFEFOIVSSSHDITILW 29
| | | | | : | | | | | : | | | | |
Db 6 ETSKGVYCLQYDDOKIVSGLRDNITIKIW 33

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RESULT 13
US-08-487-072A-83
: Sequence 83, Application US/08487072A
: Patent No. 6423684
: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Darla
: APPLICANT: Ron, Dorit
: TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
: TITLE OF INVENTION: Thereof
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 2000 Pennsylvania Avenue, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,072A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 2550-0025.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 83:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 34 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: BETA TRCP R1, Fig. 13
US-08-487-072A-83

Query Match 42.1%; Score 64; DB 4; Length 34;
Best Local Similarity 50.0%; Pred. No. 0.0025;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0.

QY 2 EHSGRVRLQDFEQLVSSHDDTILW 29
| | | | | | | | | | | | | | | |
Db 6 ETSKGVYCIQYDQKIVSGIRNTIKIW 33

RESULT 14
US-08-988-856B-21
: Sequence 21, Application US/08988856B
: Patent No. 6291642
: GENERAL INFORMATION:
: APPLICANT: Weinstein, Jasmlinder
: TITLE OF INVENTION: No. 6291642el Mammalian Cell Cycle Protein
: FILE REFERENCE: 06843.0026-04; A 283 D
: CURRENT APPLICATION NUMBER: US/08/988,856B
: CURRENT FILING DATE: 1997-12-11
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 43
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-08-988-856B-21

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OY      2 EHSGRVRLQF--DEFQIVSSSHDDTLIIW 29
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Query Match          42.1%; Score 64; DB 4; Length 43;
Best Local Similarity 40.0%; Pred. No. 0.0033;
Matches 12; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

DB      13 EHTGEVCGLSKSDGLQLASGCGNDNTVMIM 42
RESULT 15
US-08-190-802A-84
; Sequence 84, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0650
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/Ms-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0860
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP rII, Fig. 13
US-08-190-802A-84

Query Match          39.8%; Score 60.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 0.0069;
Matches 12; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY      3 HSGRVRLQFDEFQIVSSSHDDTLIIW 29
       ||| | | : | | : | | : | |
DB      2 HTGSVLCLQDYDERVIITGS-DSTVKWM 27

Search completed: April 10, 2003, 12:51:20
Job time : 4.00244 secs
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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 12:49:06 ; Search time 2.96711 Seconds

(without alignments)
597.532 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544

Perfect score: 152
Sequence: 1 VEHSGRVFRLQDFEFOIVSSSHDDITLLIW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

ALIGNMENTS

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21 73 48.0 666 9 US-09-213-888-27 Sequence 27, Appl
22 73 48.0 666 9 US-09-328-877A-27 Sequence 27, Appl
23 73 48.0 669 9 US-09-213-888-25 Sequence 25, Appl
24 73 48.0 669 9 US-09-328-877A-25 Sequence 25, Appl
25 65.5 43.1 640 9 US-10-060-019-30 Sequence 30, Appl
26 64 42.1 43 10 US-09-843-845-21 Sequence 21, Appl
27 61 40.1 678 10 US-09-801-368-314 Sequence 314, App
28 56 36.8 1194 10 US-09-876-667-2 Sequence 16, Appl
29 56 36.8 1205 10 US-09-876-667-16 Sequence 145, Ap
30 54 35.5 114 9 US-09-796-692-1545 Sequence 1541, Ap
31 54 35.5 114 9 US-09-796-692-1541 Sequence 1895, Ap
32 54 35.5 114 9 US-09-796-692-1895 Sequence 9, Appl1
33 54 35.5 317 9 US-09-998-042-9 Sequence 9, Appl1
34 54 35.5 422 12 US-10-042-417-4 Sequence 12, Appl
35 53 34.9 375 10 US-09-828-310-12 Sequence 10, Appl
36 53 34.9 375 9 US-10-119-932-1 Sequence 10, Appl
37 53 34.9 1356 9 US-10-077-111-10 Sequence 76, Appl
38 52 34.2 178 9 US-09-798-889-76 Sequence 49, Appl
39 52 34.2 382 9 US-09-798-889-42 Sequence 2, Appl1
40 52 34.2 1121 8 US-08-915-048A-2 Sequence 6, Appl1
41 51 33.6 353 10 US-09-226-248B-6 Sequence 699, App
42 51 33.6 371 10 US-09-925-297-699 Sequence 2, Appl
43 50.5 33.2 340 10 US-09-226-248B-2 Sequence 11, Appl
44 50 32.9 422 10 US-09-168-474-11 Sequence 13, Appl
45 50 32.9 422 10 US-09-168-474-13
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Database : Published_Applications_AA:*

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- 12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	569	9 US-10-038-010-8	Sequence 8, Appl1
2	152	100.0	569	12 US-10-042-417-2	Sequence 2, Appl1
3	73	48.0	540	9 US-09-213-888-7	Sequence 7, Appl1
4	73	48.0	540	9 US-09-213-888-10	Sequence 10, Appl
5	73	48.0	540	9 US-09-328-877A-10	Sequence 7, Appl1
6	73	48.0	540	9 US-09-328-877A-10	Sequence 10, Appl
7	73	48.0	540	9 US-09-213-888-6	Sequence 6, Appl1
8	73	48.0	545	9 US-09-328-877A-6	Sequence 6, Appl1
9	73	48.0	553	9 US-09-213-888-5	Sequence 5, Appl1
10	73	48.0	553	9 US-09-328-877A-5	Sequence 5, Appl1
11	73	48.0	559	9 US-09-213-888-9	Sequence 9, Appl1
12	73	48.0	559	9 US-09-328-877A-9	Sequence 8, Appl1
13	73	48.0	589	9 US-09-213-888-8	Sequence 8, Appl1
14	73	48.0	589	9 US-09-328-877A-8	Sequence 8, Appl1
15	73	48.0	592	9 US-09-213-888-4	Sequence 4, Appl1
16	73	48.0	592	9 US-09-328-877A-4	Sequence 4, Appl1
17	73	48.0	626	9 US-09-213-888-21	Sequence 21, Appl
18	73	48.0	626	9 US-09-328-877A-21	Sequence 21, Appl
19	73	48.0	627	9 US-09-213-888-3	Sequence 3, Appl1

RESULT 1
US-10-038-010-8
; Sequence 8, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta-Trcpl
; LOCATION: (1)..(569)
; OTHER INFORMATION:
US-10-038-010-8

Query Match 100.0%; Score 152; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVFRLQDFEFOIVSSSHDDITLLIW 29
Db 516 VEHSGRVFRLQDFEFOIVSSSHDDITLLIW 544

RESULT 2
US-10-042-417-2
; Sequence 2, Application US/10042417
; Patent No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 569
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 152; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 3,9e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HSGRVFRLQDFEQIVSSSHDDTILIW 29
Db 516 VEHSGRVFRLQDFEQIVSSSHDDTILIW 544

RESULT 3
US-09-213-888-7
Sequence 7, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-7

Query Match 48.0%; Score 73; DB 9; Length 540;
Best Local Similarity 48.1%; Pred. No. 0.0037;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRVFRLQDFEQIVSSSHDDTILIW 29
Db 373 HTNRVYSLQDFGIHVSGSLDTSIRW 399

RESULT 4
US-09-213-888-10
Sequence 10, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens

US-09-213-888-10

Query Match 48.0%; Score 73; DB 9; Length 540;
Best Local Similarity 48.1%; Pred. No. 0.0037;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRVFRLQDFEQIVSSSHDDTILIW 29
Db 373 HTNRVYSLQDFGIHVSGSLDTSIRW 399

RESULT 5
US-09-328-877A-7
Sequence 7, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-7

Query Match 48.0%; Score 73; DB 9; Length 540;
Best Local Similarity 48.1%; Pred. No. 0.0037;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRVFRLQDFEQIVSSSHDDTILIW 29
Db 373 HTNRVYSLQDFGIHVSGSLDTSIRW 399

RESULT 6
US-09-328-877A-10
Sequence 10, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-328-877A-10

Query Match 48.0%; Score 73; DB 9; Length 540;
Best Local Similarity 48.1%; Pred. No. 0.0037;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRVFRLQDFEQIVSSSHDDTILIW 29
Db 373 HTNRVYSLQDFGIHVSGSLDTSIRW 399

RESULT 7
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6

Query Match 48.0%; Score 73; DB 9; Length 545;
Best Local Similarity 48.1%; Pred. No. 0.0038;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVFRLQDFQIVSSSHDITLIW 29
Db 378 HTNRVYSLQFDGIHVVGSLDTSIRW 404

RESULT 8
US-09-328-877A-6
; Sequence 6, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-6

Query Match 48.0%; Score 73; DB 9; Length 545;
Best Local Similarity 48.1%; Pred. No. 0.0038;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVFRLQDFQIVSSSHDITLIW 29
Db 378 HTNRVYSLQFDGIHVVGSLDTSIRW 404

RESULT 9
US-09-213-888-5
; Sequence 5, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-5

FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-5

Query Match 48.0%; Score 73; DB 9; Length 553;
Best Local Similarity 48.1%; Pred. No. 0.0038;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVFRLQDFQIVSSSHDITLIW 29
Db 386 HTNRVYSLQFDGIHVVGSLDTSIRW 412

RESULT 10
US-09-328-877A-5
; Sequence 5, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-5

Query Match 48.0%; Score 73; DB 9; Length 553;
Best Local Similarity 48.1%; Pred. No. 0.0038;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVFRLQDFQIVSSSHDITLIW 29
Db 386 HTNRVYSLQFDGIHVVGSLDTSIRW 412

RESULT 11
US-09-213-888-9
; Sequence 9, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-9

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RESULT 12
 US-09-328-877A-9
 Sequence 9, Application US/09328877A
 Patent No. US20020177187A1
 GENERAL INFORMATION:
 APPLICANT: Guiney, Mark E.
 APPLICANT: Li, Jinhe
 APPLICANT: Pauley, Adele M.
 APPLICANT: Pharmacia & Upjohn Company
 TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 TITLE OF INVENTION: Encode Them
 FILE REFERENCE: 6142
 CURRENT APPLICATION NUMBER: US/09/328,877A
 CURRENT FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 559
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-328-877A-9

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RESULT 13
US-09-213-888-8
: Sequence 8, Application US/09213888A
: Patent No. US20020164683A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: TITLE OF INVENTION: Encode Them
: FILE REFERENCE: 6142
: CURRENT APPLICATION NUMBER: US/09/213,888A
: CURRENT FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 589
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-213-888-8

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Query Match	48.0%;	Score 73;	DB 9;	Length 589;
Best Local Similarity	48.1%;	Pred. NO. 0.0041;		
Matches 13;	Conservative	5;	Mismatches	9;
			Indels	0;
			Gaps	0;
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RESULT 14
US-09-328-877A-8

? Sequence 8, Application US/09328877A
 ? Patent No. US20020177187A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Gurney, Mark E.
 ? APPLICANT: Li, Jinhe
 ? APPLICANT: Pauley, Adele M.
 ? APPLICANT: Pharmacia & Upjohn Company
 ? TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 ? TITLE OF INVENTION: Encode Them
 ? FILE REFERENCE: 6142
 ? CURRENT APPLICATION NUMBER: US/09/328,877A
 ? CURRENT FILING DATE: 1999-06-09
 ? NUMBER OF SEQ ID NOS: 27
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO 8
 ? LENGTH: 589
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 ? US-09-328-877A-8

	Query Match	48.0%;	Score 73;	DB 9;	Length 589;
	Best Local Similarity	48.1%;	Pred. No.	0.0041;	
	Matches 13; Conservative	5;	Mismatches	9;	Indels 0; Gaps 0;
Oy	3 HSGRVERLOPDEFQIVSSSHDDITLILM	29			
	: : :				
Db	422 HITNRVYISLPFDGIIHVYSGSLDLSIRVM	448			

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RESULT 15
US-09-213-888-4
: Sequence 4, Application US/09213888A
: Patent No. US20020164683A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: FILE REFERENCE: Encode them
: CURRENT APPLICATION NUMBER: US/09/213,888A
: CURRENT FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 4
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-213-888-4

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Query Match	48.0%	Score 73	DB 9	Length 592
Best Local Similarity	48.1%	Pred. No. 0.0041		
Matches 13	Conservative	5	Mismatches	9
			Indels	0
			Gaps	0
OY	3	HSGRVFRLQDFEQIVSSSDHTILIM	29	
		: :		
Db	425	HTNREYSLQDFGIHVVSGSLDTSIRKW	451	

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Search completed: April 10, 2003, 13:16:47
Job time : 2.96711 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:15:21 ; Search time 3.35566 Seconds
(without alignments)
830.804 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544

Perfect score: 152
Sequence: 1 VEHSGRVFRLQDFEFOIVSSSHDDTLILW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR:73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	518	2	B48088
2	143	94.1	701	2	TI6607
3	70	46.1	267	2	S62507
4	70	46.1	506	2	T50211
5	69	45.4	605	2	T38932
6	66	43.4	650	2	T46660
7	65.5	43.1	640	2	S49932
8	64	42.1	610	2	S64126
9	62	40.8	611	2	TI5410
10	61	40.1	651	2	T50289
11	57	37.5	330	2	T50127
12	57	37.5	375	2	T03256
13	57	37.5	377	2	TI6985
14	57	37.5	377	2	T07376
15	57	37.5	377	2	T04086
16	57	37.5	377	2	T04086
17	57	37.5	380	2	T02085
18	57	37.5	380	2	T03765
19	57	37.5	380	2	T08036
20	57	37.5	714	2	S56893
21	56.5	37.2	424	2	T05775
22	56.5	36.8	311	2	F90116
23	56	36.8	316	2	S57839
24	56	36.8	377	2	T05266
25	56	36.8	496	2	TI9776
26	56	36.8	715	2	S38051
27	56	36.8	798	2	S34023
28	56	36.8	1194	2	T03818
29	55.5	36.5	415	2	B84544

30	55.5	36.5	612	2	T08602	protein T1pD - s11
31	55	36.2	290	2	T02300	GTP-binding regula
32	55	36.2	325	2	T23309	hypothetical prote
33	55	36.2	600	2	T23457	hypothetical prote
34	55	36.2	1683	2	AF2071	WD-40 repeat prote
35	54.5	35.9	1008	2	T32986	hypothetical prote
36	54	35.5	317	2	A33928	GTP-binding protei
37	54	35.5	317	2	B33928	GTP-binding protei
38	54	35.5	317	2	S45054	GTP-binding regula
39	54	35.5	317	2	S38398	GTP-binding regula
40	54	35.5	317	2	A36986	activated protein
41	54	35.5	318	2	S11904	GTP-binding regula
42	54	35.5	325	2	T06784	GTP-binding protei
43	54	35.5	325	2	T09613	probable GTP-bindi
44	54	35.5	327	2	S48839	guanine nucleotide
45	54	35.5	356	2	T22478	hypothetical prote

ALIGNMENTS

RESULT 1
B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trcp
C:Species: Xenopus laevis (African clawed frog)
C>Date: 26-May-1994 #sequence-revision 26-May-1994 #text-change 21-Jul-2000
C/Accession: B48088
R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A>Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase
A:Reference number: A48088; MUID:93330289; PMID:8393141
A:Accession: B48088
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SPE>
A:Cross-references: GB:M98268; NID:9295542; PIDN:AAA02810.1; PID:9295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <WD1>

Query Match 100.0%; Score 152; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVFRLQDFEFOIVSSSHDDTLILW 29
DB 481 VEHSGRVFRLQDFEFOIVSSSHDDTLILW 509

RESULT 2
TI6607
hypothetical protein K10B2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 20-Sep-1999
C/Accession: TI6607
R:Miller, N.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: Z18545
A:Accession: TI6607
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-701 <MIU>
A:Cross-references: EMBL:U28730; NID:g660694; PID:g660695; PIDN:AAA6258.1; CESP:K10B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.1
A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
Query Match 94.1%; Score 143; DB 2; Length 701;
Best Local Similarity 89.7%; Pred. No. 3.9e-13;
Matches 26; Conservative 3; Mismatches 0; Indels 0; Gaps 0;


```

A:Residues: 1-60,'I','62-640<THO>
A:Cross-references: EMBL:IL26505; NID:g432493; PID:g432494
C:Genetics:
A:Gene: SGD:MET30
A:Cross-references: SGD:S0001308; MIPS:YII046w
A:Map position: 9L
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
F:298-329/Domain: WD repeat homology <WD1>
F:338-369/Domain: WD repeat homology <WD2>
F:374-409/Domain: WD repeat homology <WD3>
F:417-450/Domain: WD repeat homology <WD4>
Query Match      43.1%; Score 65.5; DB 2; Length 640;
Best Local Similarity 35.1%; Pred. No. 0.12;
Matches 13; Conservative 6; Mismatches 7; Indels 11; Gaps 1;
QY    4 SGRVFRLOF-----DEFOIVSSSHDDITLIW 29
Db     541 TGKCIPTGFHGVGWDIAADNFRIISGSHDSIKW 577
               ||| | | | | | | | | | | | | | | |
cell division control protein CDC20 - yeast (Saccharomyces cerevisiae)
S64126
N:Alternate names: protein G2939; protein YGL116w
C:Species: Saccharomyces cerevisiae
C>Date: 17-May-1996 #sequence.revision 17-May-1996 #text_change 26-May-2000
C:Accession: S64126; S18840; S48507
R:Laquin, G.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64122
A:Accession: S64126
A:Molecule type: DNA
A:Residues: 1-610 <LAU>
A:Cross-references: EMBL:L27638; NID:g1322668; PIDD:CAA96824.1; PID:e243344; PID:g1322668
Experimental source: strain S288C
R:Setuh, N.; Montanudo, M.C.; Koshland, D.; Hogan, E.; Burke, D.J.
Mol. Cell. Biol. 11, 5592-5602, 1991
A>Title: The CDC20 gene product of Saccharomyces cerevisiae, a beta-transducin homolog,
A:Reference number: S18840; MUID:92017840; PMID:1922065
A:Accession: S18840
A:Molecule type: DNA
A:Residues: 1-517,'MA',370-501,'QRMSLFITMKONS',514,'LOR'<SFT>
A:Cross-references: EMBL:X59428; NID:g3644; PIDD:CAA42058.1; PID:g3645
A>Note: the authors translated the codon TAT for residue 220 as Glu
R:Doi, A.; Doi, K.
submitted to the EMBL Data Library, June 1993
A>Description: Correct end of the ORF for the CDC20 gene of Saccharomyces cerevisiae.
A:Reference number: S48507
A:Accession: S48507
A:Molecule type: DNA
A:Residues: 50-610 <DOI>
A:Cross-references: EMBL:D16506; NID:9391938; PIDD:BAA03957.1; PID:I004473; PID:g416288B
C:Comment: This is a G-beta protein.
C:Genetics:
A:Gene: SGD:CDC20
A:Cross-references: SGD:S0003084; MIPS:YGI116w
A:Map position: 7L
C:Function:
A>Description: required for nuclear movements prior to anaphase; required for chromosome
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
F:381-414/Domain: WD repeat homology <WD1>
Query Match      42.1%; Score 64; DB 2; Length 610;
Best Local Similarity 40.0%; Pred. No. 0.19;
Matches 12; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
QY    2 EHSRVFRLOF--DEFOIVSSSHDDITLIW 29
Db     383 EHTEVCGLSTYSKDGLQLASGGNDNTVMIM 412

```

```

T15410
hypothetical protein C04F6.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 26-May-2000
C:Accession: T15410
R:Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C04F6.
A:Reference number: Z18346
A:Accession: T15410
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-611 <NHA>
A:Cross-references: EMBL:U42835; NID:g1125760; PID:g1125764; PIDN:AAA83588.1; CESP:CO
C:Genetics:
A:Gene: CESP:C04F6.4
A:Introns: 25/1; 184/3; 349/1; 514/3; 577/1
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match          40.8%; Score 62; DB 2; Length 611;
Best Local Similarity 51.6%; Pred. No. 0.37;
Matches 16; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

OY      1 VEHSGRVFRLOF--DEFOIVSSSHDDITLW 29
          ||||| | | | | | | | | | | | | | | | |
DB      236 VAHSGVFGLTWSPDGTRIASADKTIKW 266

RESULT 10
T50289
WD repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50289
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25054
A:Accession: T50289
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-651 <WOO>
A:Cross-references: EMBL:AL157993; PIDN:CAW6232.1; GSPDB:GN00066; SPDB:SPACUNK12.01
A:Experimental source: strain 972h(-); cosmid c25D11
C:Genetics:
A:Gene: SPDB:SPACUNK12.01
A:Map position: 1

Query Match          40.1%; Score 61; DB 2; Length 651;
Best Local Similarity 34.5%; Pred. No. 0.56;
Matches 10; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY      1 VEHSGRVFRLOFDEFOIVSSSHDDITLW 29
          ||||| | | | | | | | | | | | | | | | |
DB      533 IGH7APISLQFDNSNHLVSGSYDNSVRIM 561

RESULT 11
S70127
hypothetical protein YDR267c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D9954.11
C:Species: Saccharomyces cerevisiae
C:Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C:Accession: S70127
R:Le, T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of S. cerevisiae cosmid 9954.
A:Reference number: S70124
A:Accession: S70127
A:Molecule type: DNA
A:Residues: 1-330 <LEF>
A:Cross-references: EMBL:U51030; NID:g1332633; PID:g1230640; GSPDB:GN00004; MIPS:YDR2
C:Genetics:
A:Gene: MIPS:YDR267c

```

A:Cross-references: SGD:S0002675

A:Map position: 4R

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

F:54-87/Domain: WD repeat homology <WD1>

F:103-136/Domain: WD repeat homology <WD2>

F:149-182/Domain: WD repeat homology <WD3>

Query Match 37.5%; Score 57; DB 2; Length 330;

Best Local Similarity 35.5%; Pred. No. 1;

Matches 11; Conservative 6; Mismatches 10; Indels 4; Gaps 1;

OY 3 HSGRVFRLQF---DEFOYSSSHDDITLW 29

Db 196 HEGTVSSDFDKTEGVFRLCSGSDSTVRW 226

RESULT 12

T03256

GTP-binding protein beta chain - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000

C:Accession: T03256

R:Oelmeier, R.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z14864

A:Accession: T03256

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-375 <OEI>

A:Cross-references: EMBL:X8161; NID:q1360091; PIDN:CA66842.1

A:Experimental source: cultivar Samsun NN; tissue-type leaf

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:244-277/Domain: WD repeat homology <WDR>

Query Match 37.5%; Score 57; DB 2; Length 375;

Best Local Similarity 34.5%; Pred. No. 1.2;

Matches 10; Conservative 11; Mismatches 6; Indels 2; Gaps 1;

OY 3 HSGRVFRLQF---DEFOYSSSHDDITLW 29

Db 64 HTGKVSILDMWTPKRNIVSASODGRLIW 92

RESULT 13

T16985

GTP-binding protein beta chain - curled-leaved tobacco

N:Alternate names: G protein beta chain

C:Species: Nicotiana glauca (curled-leaved tobacco)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000

C:Accession: T16985

R:Kaydanov, C.; Tewes, A.; Mantouf, R.

submitted to the EMBL Data Library, November 1996

A:Description: Molecular cloning of a G protein alpha and beta subunit from somatic embryo

A:Reference number: Z18624

A:Accession: T16985

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-377 <KAY>

A:Cross-references: EMBL:Y09513

A:Experimental source: somatic embryo

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; signal transduction

F:244-277/Domain: WD repeat homology <WDR>

Query Match 37.5%; Score 57; DB 2; Length 377;

Best Local Similarity 34.5%; Pred. No. 1.2;

Matches 10; Conservative 11; Mismatches 6; Indels 2; Gaps 1;

OY 3 HSGRVFRLQF---DEFOYSSSHDDITLW 29

Db 64 HTGKVSILDMWTPKRNIVSASODGRLIW 92

RESULT 14

T07376

G-protein beta chain Gb1 - potato

N:Alternate names: Gb1 protein

C:Species: Solanum tuberosum (potato)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000

C:Accession: T07376

R:Provart, N.J.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z15997

A:Accession: T07376

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-377 <PKO>

A:Cross-references: EMBL:X87837

A:Experimental source: cv. Desiree; dev. stage 8 weeks; tissue type epidermal fragment

C:Genetics:

A:Note: gbl

C:Complex: heterotrimer

C:Function:

A:Description: belongs to a family of guanine nucleotide-binding proteins that relay

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:244-277/Domain: WD repeat homology <WDR>

Query Match 37.5%; Score 57; DB 2; Length 377;

Best Local Similarity 34.5%; Pred. No. 1.2;

Matches 10; Conservative 11; Mismatches 6; Indels 2; Gaps 1;

OY 3 HSGRVFRLQF---DEFOYSSSHDDITLW 29

Db 64 HTGKVSILDMWTPKRNIVSASODGRLIW 92

RESULT 15

T04086

GTP binding protein beta chain - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000

C:Accession: T04086

R:Lein, W.; Saalbach, G.

submitted to the EMBL Data Library, February 1997

A:Description: Characterization of G-protein function in plants.

A:Reference number: Z15198

A:Accession: T04086

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-377 <LEI>

A:Cross-references: EMBL:Z84820; PIDN:CAB0618.1

A:Experimental source: strain SRI; tissue-type leaf

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:244-277/Domain: WD repeat homology <WDR>

Query Match 37.5%; Score 57; DB 2; Length 377;

Best Local Similarity 34.5%; Pred. No. 1.2;

Matches 10; Conservative 11; Mismatches 6; Indels 2; Gaps 1;

OY 3 HSGRVFRLQF---DEFOYSSSHDDITLW 29

Db 64 HTGKVSILDMWTPKRNIVSASODGRLIW 92

Search completed: April 10, 2003, 13:23:06

Job time : 4.35566 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using SW model

Run on: April 10, 2003, 12:51:26 ; Search time 2.08404 Seconds
(without alignments)
577.154 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544

Sequence: 1 VEHSGRVFRLQDFEIVSSHDDTLIIW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	518	1 TRCB_XENLA	Q91854 xenopus lae
2	152	100.0	605	1 FW1A_HUMAN	Q9Y297 homo sapien
3	151	99.3	542	1 FW1B_HUMAN	Q9UKB1 homo sapien
4	143	94.1	665	1 L123_CAEEL	Q09990 caenorhabd
5	70	46.1	506	1 POFB_SCHPO	Q09855 schizosacch
6	69	45.4	605	1 POPI_SCHPO	P87053 schizosacch
7	66	43.4	650	1 SC02_NEUCR	Q01377 neurospora
8	65.5	43.1	640	1 MT30_YEAST	P39014 saccharomyc
9	64.5	42.4	525	1 CO2A_HUMAN	Q92828 homo sapien
10	64	42.1	610	1 CC20_YEAST	P26309 saccharomyc
11	62	40.8	611	1 WDRI_CAEEL	Q11176 caenorhabd
12	61	40.1	651	1 Y1X1_SCHPO	Q9P713 schizosacch
13	61	40.1	678	1 SC0B_EMENT	Q00659 emericella
14	57	37.5	375	1 GBB3_TOBAC	P40507 nicotiana t
15	57	37.5	377	1 GBB1_TOBAC	P93397 nicotiana t
16	57	37.5	377	1 GBB2_TOBAC	P93398 nicotiana t
17	57	37.5	377	1 GBB_NICPL	P93339 solanum tub
18	57	37.5	377	1 GBB_SOLTU	P49178 zea mays (m
19	57	37.5	380	1 GBB_MAIZE	Q40667 oryza sativ
20	57	37.5	380	1 GBB_ORYSA	P47025 saccharomyc
21	57	37.5	714	1 YJL2_YEAST	Q22469 arabidopsis
22	56.5	37.2	424	1 MS13_ARATH	Q02346 neurospora
23	56	36.8	316	1 GBLP_NEUCR	Q25189 hydra atten
24	56	36.8	317	1 GBLP_HYDAT	P49177 arabidopsis
25	56	36.8	377	1 GBB_ARATH	P36037 saccharomyc
26	56	36.8	715	1 DOAI_YEAST	P38129 saccharomyc
27	56	36.8	798	1 T2D4_YEAST	Q15542 homo sapien
28	56	36.8	800	1 APAF_HUMAN	O14727 homo sapien
29	55.5	36.8	1248	1 MS12_ARATH	Q22468 arabidopsis
30	55.5	36.5	415	1 T1PD_DICDI	O15736 dicystosell
31	55.5	36.5	612	1 WDR9_HUMAN	Q9NS16 homo sapien
32	55.5	36.5	2295	1 GBLP_CAEEL	Q21215 caenorhabd
33	55	36.2	324	1 GBLP_CAEEL	Q21215 caenorhabd

34	55	36.2	1683	1 YL24_ANASP	Q8YV57 anabaena sp
35	54	35.5	316	1 GBLP_BIOGL	Q93134 biophthalari
36	54	35.5	317	1 GBLP_BRARE	O42248 brachydanio
37	54	35.5	317	1 GBLP_HUMAN	P25388 homo sapien
38	54	35.5	317	1 GBLP_ORYZ	O42249 oreochromis
39	54	35.5	318	1 GBLP_CHLRE	P25387 chlamydomon
40	54	35.5	325	1 GBLP_MEDSA	O24076 medicago sa
41	54	35.5	325	1 GBLP_SOYBN	Q39836 glycine max
42	54	35.5	327	1 GBLP_ARATH	O24456 arabidopsis
43	54	35.5	327	1 GBLP_BRANA	Q39336 brassica na
44	54	35.5	356	1 GBB2_CAEEL	Q20636 caenorhabd
45	54	35.5	422	1 FBW2_HUMAN	Q9UKT8 homo sapien

ALIGNMENTS

```

RESULT 1
TRCB_XENLA          STANDARD:      PRT:      518 AA.
ID                  TRCB_XENLA          PRT:      518 AA.
AC 091854: P70037: P70038:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-TripC (Beta-transducin repeat-containing protein).
GN FBXW1 OR BTFCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=9330289; PubMed=8393141;
RX Sevak W., Keiper B.D., Stratowa C., Castanon M.J.;
"Saccharomyces cerevisiae dccl5 mutants arrested at a late stage in
anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein
with beta-transducin repeats.";
RT Mol. Cell. Biol. 13:4953-4966(1993).
RL [2]
RN SEQUENCE OF 302-518 FROM N.A.
RP MEDLINE=97109804; PubMed=8952061;
RX Hudson J.W., Alarcon V.B., Rinson R.P.;
"Identification of new localized RNAs in the Xenopus oocyte by
RT differential display PCR.";
RL Dev. Genet. 19:190-196(1996).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: PART OF A SCF (SKP1-CUL1IN-F-BOX) PROTEIN LIGASE COMPLEX
CC (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
CC MAURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
CC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
CC NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD, OR
CC TADPOLE EMBRYO.
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M98268; AAA02810.1; -
CC EMBL: U63921; AAA49671.1; -
CC EMBL: U63922; AAA49672.1; -
CC InterPro: IPR001810; F-box.
CC InterPro: IPR001880; WD40.
CC Pfam: PF00400; WD40; 7.

```

DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ubl conjugation pathway; Repeat; WD repeat.
 FT DOMAIN 119 157 F-BOX.
 FT REPEAT 230 258 WD 1.
 FT REPEAT 270 298 WD 2.
 FT REPEAT 310 338 WD 3.
 FT REPEAT 353 381 WD 4.
 FT REPEAT 393 421 WD 5.
 FT REPEAT 433 461 WD 6.
 FT REPEAT 482 510 WD 7.
 FT CONFLICT 302 304 GEM -> EFR (IN REF. 2).
 FT CONFLICT 516 518 GLA -> AAH (IN REF. 2).
 SQ SEQUENCE 518 AA; 59507 MW; 2A52EC19028127F3 CRC64;

Query Match 100.0%; Score 152; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEQIVSSSHDITLILW 29
 DB 481 VEHSGRVRLQDFEQIVSSSHDITLILW 509

RESULT 2

FW1A_HUMAN STANDARD; PRT; 605 AA.
 AC Q9Y297; Q9Y213;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-Trcp)
 DE (E3R8IKppab) (pIkappabalpha-E3 receptor subunit).
 GN FBXW1A OR FBW1A OR BTCP OR BTCP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99075339; PubMed=9859996;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RT Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the ikappabalpha-
 RT ubiquitin ligase";
 RL Nature 396:590-594(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lymphoid;
 RX MEDLINE=98325370; PubMed=9660940;
 RA Margolin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
 RA Thomas D., Strebel K., Benarous R.,
 RT "A novel human WD protein, h-beta TrCP, that interacts with HIV-1 Vpu
 RT connects CD4 to the ER degradation pathway through an F-box motif";
 RL Mol. Cell 1:565-574(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20003060; PubMed=10531035;
 RA Cenciarelli C., Chaur D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Komero P., Chu C.Y., Ellledge S.J.,

RA Harper J.W.;
 RT "The SCF(beta-Trcp)-ubiquitin ligase complex associates specifically
 RT with phosphorylated destruction motifs in F-box proteins and
 RT beta-catenin and stimulates F-box ubiquitination in vitro";
 RL Genes Dev. 13:270-283(1999).
 CC -1- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKK ALPHA
 CC (IKKAPPAALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR
 CC UBIQUITINATION AND DEGRADATION.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CUL1-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
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CC EMBL: AF101784; AAD08702.1; -
 CC EMBL: Y14153; CA74572.1; -
 CC EMBL: AF129530; AAF04464.1; -
 CC DR GeneW: HGNC:1144; BTCP.
 CC DR MIM: 603482; -
 CC DR InterPro: IPR001810; F-box.
 CC DR InterPro: IPR001680; WD40.
 CC DR Pfam: PF00400; WD40; 7.
 CC DR Pfam: PF00646; F-box; 1.
 CC DR PRINTS: PR00320; GPROTEINBRPT.
 CC DR PRODOM: PD000018; WD40; 4.
 CC DR SMART: SM00256; FBOX; 1.
 CC DR SMART: SM00320; WD40; 7.
 CC DR PROSITE: PS50181; FBOX; 1.
 CC DR PROSITE: PS00678; WD_REPEATS_1; 6.
 CC DR PROSITE: PS50082; WD_REPEATS_2; 7.
 CC DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 CC KW Ubl conjugation pathway; Repeat; Alternative splicing.
 FT DOMAIN 190 228 F-BOX.
 FT REPEAT 301 338 WD 1.
 FT REPEAT 341 378 WD 2.
 FT REPEAT 381 418 WD 3.
 FT REPEAT 424 461 WD 4.
 FT REPEAT 464 503 WD 5.
 FT REPEAT 505 541 WD 6.
 FT REPEAT 553 590 WD 7.
 FT VARSPLIC 17 52 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 605 AA; 68866 MW; 4C67F3B7E400ED37 CRC64;

Query Match 100.0%; Score 152; DB 1; Length 605;
 Best Local Similarity 100.0%; Pred. No. 2.2e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEQIVSSSHDITLILW 29
 DB 552 VEHSGRVRLQDFEQIVSSSHDITLILW 580

RESULT 3

FW1B_HUMAN STANDARD; PRT; 542 AA.
 AC Q9UKB1; Q9Y4C6; Q9P2S8; Q9P2S9;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-Trcp2).
 GN FBXW1B OR FBW1B OR BTCP2 OR KIAA0696.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20003060; PubMed=10531035;
 RA Genciarelli C., Chlaud D.S., Guardavaccaro D., Parks W., Vidal M.,
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP TISSUE=Petal lung;
 RX MEDLINE=20160458; PubMed=10694485;
 RA Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katoh M.;
 RT "Molecular cloning and genomic structure of the betatropin gene on
 RT chromosome 5q35.1.";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation.
 CC -1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AND C (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 CC
 DR EMBL: AF176022; AAF04528.1; -;
 DR EMBL: AB033279; BAA92329.1; -;
 DR EMBL: AB033280; BAA92330.1; -;
 DR EMBL: AB033281; BAA92331.1; -;
 DR EMBL: AB014596; BAA31671.1; ALT_INIT.
 DR Genew: HGNC:13607; FBXW1B.
 DR MIM: 605651; -;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00440; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS0181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 5.
 DR PROSITE: PS00082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ub1 conjugation pathway; Repeat; WD repeat; Alternative splicing.
 FT DOMAIN 129 167 F-BOX.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPLIC 16 49 MISSING (IN ISOFORM A).

FT VARSPLIC 16 48 CSVPSLMLGCAVLVESGALSLQSMPSVRL -> NRSV
 FT SEQUENCE 542 AA: 62090 MW: 7CD40087EFAA5C8A CRC64;
 SQ
 Query Match 99.3%; Score 151; DB 1; Length 542;
 Best Local Similarity 96.6%; Pred. No. 2.8e-15;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VEHSGRVFLRQDFEFOIIVSSHDDITLIM 29
 DB 489 VEHSGRVFLRQDFEFOIIVSSHDDITLIM 517
 RESULT 4
 ID L123 CAEFL STANDARD; PRT: 665 AA.
 AC 009950; Q9GNN6;
 DT 15-JUN-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE F-box/WD-repeat protein lin-23.
 GN LIN-23 OR K10B2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STAGE, AND MUTAGENESIS.
 RX MEDLINE=20515608; PubMed=11060233;
 RA Kipreos E.T., Gohei S.P., Hedgecock E.M.;
 RT "The Caenorhabditis elegans F-box/WD-repeat protein lin-23 functions
 RT to limit cell division during development.";
 RL Development 127:5071-5082(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Functions cell autonomously to negatively regulate cell
 CC cycle progression. Required to restrain cell proliferation in
 CC response to developmental cues. Probably recognizes and binds to
 CC some proteins and promotes their ubiquitination and degradation
 CC (By similarity).
 CC -1- SUBUNIT: Part of a SCF (SKP1-CULLIN-F-BOX) protein ligase complex
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- DEVELOPMENTAL STAGE: Highest levels in embryos and adults, lowest
 CC levels in larvae. Maternal expression results in high zygotic
 CC levels.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
 CC
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 CC
 DR EMBL: AF275253; AAG28037.1; -;
 DR EMBL: U28730; AAA68258.2; -;
 DR WormRep: K10B2.1; CE28600.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00440; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.

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DR Prodom: PD000018; WD40: 4.
DR SMART: SM00256; FBOX: 1.
DR SMART: SM00320; WD40: 7.
DR PROSITE: PS0181; FBOX: 1.
DR PROSITE: PS00678; WD_REPEATS_1: 5.
DR PROSITE: PS00082; WD_REPEATS_2: 7.
DR PROSITE: PS0294; WD_REPEATS_REGION: 1.
KW Developmental protein; Cell cycle; Cell division;
KW Ubl conjugation pathway; Repeat; WD repeat.
FT DOMAIN 81 127
FT REPEAT 220 257 WD 1.
FT REPEAT 260 299 WD 2.
FT REPEAT 301 337 WD 3.
FT REPEAT 343 380 WD 4.
FT REPEAT 383 420 WD 5.
FT REPEAT 423 460 WD 6.
FT REPEAT 472 509 WD 7.
FT DOMAIN 525 582 WD 7.
FT MOTIF 441 441 ALA-RICH.
SQ SEQUENCE 665 AA; 75916 MW; BF3E9AF51F12ECCC CRC64;

Query Match 94.1%; Score 143; DB 1; Length 665;
Best Local Similarity 89.7%; Pred. No. 5,8e-14;
Matches 26; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFDEQIVSSSHDITLIW 29
DB 471 VQHTGRVRLQDFDEQIVSSSHDITLIW 499

RESULT 5
POF1_SCHPO STANDARD; PRT; 506 AA.
AC 009855; Q9P7V1.
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof1.
GN POF1 OR SPAC39E6.01 OR SPAC30.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison C.L., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RT fission yeast."
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Glynnoprez B.,
RA Weltens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lemnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Weiler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

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RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Bartell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD_REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: AB061694; BAB5543.1; -
DR EMBL: AL136538; CAB66464.1; -
DR EMBL: Z66525; CA91423.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR Pfam: PF00646; F-box; 1.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 3.
DR SMART: SM00256; FBOX: 1.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS0181; FBOX: 1.
DR PROSITE: PS00678; WD_REPEATS_1: 3.
DR PROSITE: PS00082; WD_REPEATS_2: 6.
DR PROSITE: PS0294; WD_REPEATS_REGION: 1.
KM Repeat; WD repeat.
FT DOMAIN 70 116 F-BOX.
FT REPEAT 219 256 WD 1.
FT REPEAT 259 298 WD 2.
FT REPEAT 301 338 WD 3.
FT REPEAT 345 386 WD 4.
FT REPEAT 388 426 WD 5.
FT REPEAT 427 464 WD 6.
FT REPEAT 468 505 WD 7.
SQ SEQUENCE 506 AA; 58257 MW; CEF34DAEFFC2E10 CRC64;

Query Match 46.1%; Score 70; DB 1; Length 506;
Best Local Similarity 46.2%; Pred. No. 0.0051;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 4 SGRVRLQDFDEQIVSSSHDITLIW 29
DB 470 NSRVEGLQDFHRIITACTHSEILIW 495

RESULT 6
POF1_SCHPO STANDARD; PRT; 605 AA.
AC P87053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE F-box/WD-repeat protein pof1 (Skp1-binding protein 1).
GN POF1 OR SBI1 OR SPAC37A10.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Katayama S., Kitamura K., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in
RT fission yeast."

```

Submitted (SEP-1999) to the EMBL/GenBank/DBU databases.

Sequence from N.A.

STRAIN-972;

W004V, Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Scours J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Godle A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jajals K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., O'Neill C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Stimmings M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymonprez B., Wellens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hillbert H., Borzym K., Langer T., Beck A., Lehnach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambolt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.

"The genome sequence of *Schizosaccharomyces pombe*."

Nature 415:871-880(2002).

FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

SBUTIT: PART OF A SCF (SKP1-CULIN-F-BOX) PROTEIN LIGASE COMPLEX (BY SIMILARITY).

1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.

1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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EMBL: AB032410; BAA84528.1; -

EMBL: Z94864; CAB08168.1; -

InterPro: IPR001810; F-box.

InterPro: IPR001680; WD40.

Pfam: PF00400; WD40; 7.

Pfam: PF00646; F-box; 1.

PRINTS: PR00320; GPROTEINRPT.

ProDom: PD000018; WD40; 5.

SMART: SM00256; FBOX; 1.

SMART: SM00320; WD40; 7.

PROSITE: PS50181; FBOX; 1.

PROSITE: PS50678; WD_REPEATS_1; 2.

PROSITE: PS50082; WD_REPEATS_2; 7.

PROSITE: PS50294; WD_REPEATS_REGION; 1.

Ubl conjugation: Repeat; WD repeat.

DOMAIN 107 153

REPEAT 271 299 WD 1.

REPEAT 311 339 WD 2.

REPEAT 350 379 WD 3.

REPEAT 390 420 WD 4.

REPEAT 432 460 WD 5.

REPEAT 472 500 WD 6.

REPEAT 510 538 WD 7.

SEQUENCE 605 AA; 67110 MW; 711809379E5C5C1F0 CRC64;

Query Match 45.4%; Score 69; DB 1; Length 605;

Best Local Similarity 51.9%; Pred. No. 0.0089;

Matches 14; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 3 HSGRVERLQDFEFOIVSSSHDDTLITW 29

DB 312 HSGGVICLQDFQCKILSGSMXTIRIW 338

RESULT 7

SC02_NEUCR STANDARD; PRT; 650 AA.

AC 001277;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Sulfur controller-2 (SCON2).

GN SCON-2.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=74-OR23-1A; PubMed=7724564;

RX MEDLINE=95241499; PubMed=7724564;

RT Kumar A., Paletta J.V.

"The sulfur controller-2 negative regulatory gene of *Neurospora crassa* encodes a protein with beta-transducin repeats."

Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).

CC 1- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.

CC 1- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR CONDITIONS.

CC 1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).

CC 1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.

CC 1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT PROTEINS.

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EMBL: U17251; AAA68968.1; -

InterPro: IPR001810; F-box.

InterPro: IPR001680; WD40.

Pfam: PF00400; WD40; 7.

Pfam: PF00646; F-box; 1.

PRINTS: PR00320; GPROTEINRPT.

ProDom: PD000018; WD40; 4.

SMART: SM00256; FBOX; 1.

SMART: SM00320; WD40; 7.

PROSITE: PS50181; FBOX; 1.

PROSITE: PS00678; WD_REPEATS_1; 2.

PROSITE: PS50082; WD_REPEATS_2; 6.

PROSITE: PS50294; WD_REPEATS_REGION; 1.

KW Transcription regulation; Repeat; WD repeat.

DOMAIN 124 170

REPEAT 292 320 WD 1.

REPEAT 332 360 WD 2.

REPEAT 372 400 WD 3.

REPEAT 411 441 WD 4.

REPEAT 453 488 WD 5.

REPEAT 528 564 WD 6.

REPEAT 576 604 WD 7.

REPEAT 616 644 WD 8.

SEQUENCE 650 AA; 72189 MW; 7473859C99F1B028 CRC64;

Query Match 43.4%; Score 66; DB 1; Length 650;

Best Local Similarity 41.4%; Pred. No. 0.028;

Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 VHSGRVERLQDFEFOIVSSSHDDTLITW 29

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DB      331 VCHTAGIRALOPDDSKLISGSLDHTIKW 359

RESULT 8
MT30_YEAST
ID      MT30_YEAST      STANDARD:      PRT:      640 AA.
AC      P39014:
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      MET30 protein.
GN      MET30 OR Y11046W.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX      NCBI_TaxID=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=X2180-1A;
RX      MEDLINE=96069360; PubMed=8524217;
RA      Thomas D., Kuras L., Barbey R., Charest H., Blaiseau P.L.,
RA      Sardin-Kejarian Y.,
RT      "Met30p, a yeast transcriptional inhibitor that responds to S-
RT      adenosylmethionine, is an essential protein with WD40 repeats.";
RL      Mol. Cell. Biol. 15:6526-6534(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=S288c / AB972;
RA      Bartell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA      Churrier C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA      Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA      Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA      Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA      Walsh S.V., Whitehead S.;
RL      Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC      -1 FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BIOSYNTHESIS
CC      -1 GENE EXPRESSION.
CC      -1 SUBUNIT: SEEMS TO INTERACT WITH MET4.
CC      -1 SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC      -1 SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC      -1 SIMILARITY: BELONGS TO THE MET30/SCON/SCON-2 FAMILY OF WD-REPEAT
CC      PROTEINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Z46861; CAAB6905.1; -
DR      EMBL; L26505; AAA96717.1; -
DR      SGD; S0001308; MET30.
DR      InterPro; IPR001810; F-box.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00400; WD40; 7.
DR      Pfam; PF00646; F-box; 1.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      PRODOM; PD000018; WD40; 4.
DR      SMART; SM00256; FBOX; 1.
DR      SMART; SM00320; WD40; 6.
DR      PROSITE; PS50181; FBOX; 1.
DR      PROSITE; PS00678; WD_REPEATS_1; 4.
DR      PROSITE; PS50082; WD_REPEATS_2; 6.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM      Transcription regulation: Methionine biosynthesis;
KW      Cysteine biosynthesis; Repeat; WD repeat.
FT      DOMAIN 181 227
FT      REPEAT 300 328 WD 1.
FT      REPEAT 340 368 WD 2.
FT      REPEAT 380 408 WD 3.

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FT      REPEAT 419 449 WD 4.
FT      REPEAT 461 499 WD 5.
FT      REPEAT 509 538 WD 6.
FT      REPEAT 550 578 WD 7.
FT      REPEAT 607 635 WD 8 (POTENTIAL).
FT      CONFLICT 61 61 M -> I (IN REF. 1).
SQ      SEQUENCE 640 AA; 72835 MW; 5135D4C4ZELB97 CRC64;

Query Match
Best local Similarity 43.1%; Score 65.5; DB 1; Length 640;
Matches 13; Conservative 35.1%; Pred. No. 0.032; Mismatches 7; Indels 11; Gaps 1.

OY      4 SGKVFRLQF-----DEQIVSSSHDITLIW 29
DB      541 TGKCFRQFGHGVWDIADNFRILISGSDSIKW 577

RESULT 9
CO2A_HUMAN
ID      CO2A_HUMAN      STANDARD:      PRT:      525 AA.
AC      Q92828; Q92829;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Coronin 2A (WD-repeat protein 2) (IR10).
GN      CO2A OR WDR2 OR IR10.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Epidermis;
RX      MEDLINE=97138092; PubMed=8985118;
RA      Zaphropoulos P.G., Toltgard R.;
RT      "cDNA cloning of a novel WD repeat protein mapping to the 9q22.3
RT      chromosomal region.";
RL      DNA Cell Biol. 15:1049-1056(1996).
CC      -1 SUBUNIT: BINDS ACTIN (BY SIMILARITY).
CC      -1 SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
CC      -1 SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U57057; AAB47807.1; -
DR      EMBL; U57058; AAB47808.1; -
DR      Genew; HGNC:2255; CORO2A.
DR      MIM; 602159;
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00400; WD40; 3.
DR      PRINTS; PR00320; GPROTEINBRPT.
DR      PRODOM; PD000018; WD40; 1.
DR      SMART; SM00320; WD40; 3.
DR      PROSITE; PS00678; WD_REPEATS_1; 1.
DR      PROSITE; PS50082; WD_REPEATS_2; 3.
DR      PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW      Actin-binding; Repeat; WD repeat; Coiled coil.
FT      REPEAT 80 120 WD 1.
FT      REPEAT 130 170 WD 2.
FT      REPEAT 178 217 WD 3.
FT      REPEAT 220 263 WD 4.
FT      REPEAT 269 308 WD 5.
FT      DOMAIN 485 524
FT      CONFLICT 88 88 COILED COIL (POTENTIAL).
SQ      SEQUENCE 525 AA; 59636 MW; 8D065270A5C28BC7 CRC64;

Query Match
42.4%; Score 64.5; DB 1; Length 525;

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FT REPEAT 145 185 WD 2.
 FT REPEAT 188 227 WD 3.
 FT REPEAT 237 276 WD 4.
 FT REPEAT 322 361 WD 5.
 FT REPEAT 446 485 WD 6.
 FT REPEAT 489 528 WD 7.
 FT REPEAT 534 573 WD 8.
 FT REPEAT 579 610 WD 9.
 SQ SEQUENCE 611 AA; 65323 MW; 821452C61B5D27A CRC64;

Query Match 40.8%; Score 62; DB 1; Length 611;
 Best Local Similarity 51.6%; Pred. No. 0.1;
 Matches 16; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

OY 1 VEHSGRVFRLQF--DEFOIVSSHDDTLLW 29
 Db 236 VAHSGSVFGLTWPDPGKIASADKTIKILW 266

RESULT 12

YIX1_SCHPO STANDARD; PRT; 651 AA.

AC Q9P713;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical WD-repeat protein C25D11.01 in chromosome I.
 GN SPAC25D11.01
 OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC SPRAIN-972:

RA MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicaket G., Aert R., Robben J., Grymoprez B.,
 RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Gerton A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002).

-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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DR EMBL: AL157993; CAB76232.1;
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein Repeat; WD repeat.
 FT REPEAT 350 369 WD 1.
 FT REPEAT 372 409 WD 2.
 FT REPEAT 433 473 WD 3.
 FT REPEAT 492 531 WD 4.
 FT REPEAT 534 573 WD 5.
 FT REPEAT 575 610 WD 6.
 FT REPEAT 620 650 WD 7.
 SQ SEQUENCE 651 AA; 72372 MW; 4F59D1104A650DBA CRC64;

Query Match 40.1%; Score 61; DB 1; Length 651;
 Best Local Similarity 34.5%; Pred. No. 0.16;
 Matches 10; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 1 VEHSGRVFRLQFDEFOIVSSHDDTLLW 29
 Db 533 IGHVAPISLQFDSNHLGSGYDNSVRLW 561

RESULT 13

SCOB_EMENT STANDARD; PRT; 678 AA.

AC Q00659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sulfur metabolite repression control protein.
 GN SCONB OR MAPBI.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Natoff R.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
 CC REPRESSION.
 CC -1- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).

CC -1- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
 CC PROTEINS.

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DR EMBL: U21220; AAC15905.1;
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR Pfam: PF00646; F-box; 1.
 DR PRINTS: PRO0320; GPROTEINBRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00326; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; 4.
 DR PROSITE: PS00682; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.

Transcription regulation; Repeat; WD repeat.
 KM DOMAIN 178 224 F-BOX.
 FT REPEAT 178 224 F-BOX.
 FT REPEAT 375 375 WD 1.
 FT REPEAT 387 415 WD 2.
 FT REPEAT 427 455 WD 3.
 FT REPEAT 466 496 WD 4.
 FT REPEAT 508 543 WD 5.
 FT REPEAT 553 595 WD 6.
 FT REPEAT 607 635 WD 7.
 FT REPEAT 647 675 WD 8.
 SQ SEQUENCE 678 AA; 76070 MW; D840D452E37B4C53 CRC64;
 Query Match 40.1%; Score 61; DB 1; Length 678;
 Best Local Similarity 40.7%; Pred. No. 0.17;
 Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 3 HSGRVFLQFDEFQIVSSSHDTILIM 29
 Db 388 HESGIRCLQFDPTKLISGMDRTIKW 414
 RESULT 14
 GBB3_TOBAC STANDARD; PRT; 375 AA.
 AC Q40507;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Guanine nucleotide-binding protein beta subunit.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Samsun NN; TISSUE=leaf;
 RA Kustretsov V.V., Oelmueller R.;
 RT "Isolation and characterization of cDNAs encoding the subunit beta of
 heterotrimeric G proteins from N. tabacum.";
 RT (In) Plant Gene Register PGR96-048.
 RL
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
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 CC
 CC EMBL: X98161; CAA66842.1; -.
 DR HSSP: P04901; ITRG.
 DR InterPro: IPR001632; Gprotein_B.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PRODOM: PD000018; WD40; 5.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 63 93 WD 1.
 FT REPEAT 105 135 WD 2.
 FT REPEAT 154 185 WD 3.

FT REPEAT 202 233 WD 4.
 FT REPEAT 246 276 WD 5.
 FT REPEAT 293 323 WD 6.
 FT REPEAT 339 369 WD 7.
 SQ SEQUENCE 375 AA; 40812 MW; 72D53D1DFC5CF598 CRC64;
 Query Match 37.5%; Score 57; DB 1; Length 375;
 Best Local Similarity 34.5%; Pred. No. 0.34;
 Matches 10; Conservative 11; Mismatches 6; Indels 2; Gaps 1;
 QY 3 HSGRVFLQF--DEFQIVSSSHDTILIM 29
 Db 64 HTGKVSILDWTPKRNIVSASODGRLTW 92
 RESULT 15
 GBB1_TOBAC STANDARD; PRT; 377 AA.
 AC P93397;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Guanine nucleotide-binding protein beta subunit 1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. SRL; TISSUE=Leaf;
 RA Lein W., Saalbach G.;
 RT Submitted (FE8-1997) to the EMBL/GenBank/DBJ databases.
 RL
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL: Z84820; CAB06618.1; -.
 DR HSSP: P04901; ITRG.
 DR InterPro: IPR001632; Gprotein_B.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PRODOM: PD000018; WD40; 5.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 2.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KM Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 63 93 WD 1.
 FT REPEAT 105 135 WD 2.
 FT REPEAT 154 185 WD 3.
 FT REPEAT 202 233 WD 4.
 FT REPEAT 246 276 WD 5.
 FT REPEAT 293 323 WD 6.
 FT REPEAT 339 369 WD 7.
 SQ SEQUENCE 377 AA; 41145 MW; 23351986467A079B CRC64;
 Query Match 37.5%; Score 57; DB 1; Length 377;
 Best Local Similarity 34.5%; Pred. No. 0.34;

Fri Apr 11 13:31:14 2003

us-09-601-168b-2_copy_516_544.rsp

Page 10

	Matches	10;	Conservative	11;	Mismatches	6;	Indels	2;	Gaps	1;
QY	3	HSGRYERLQF--DEFOIVSSHDILLILW	29	:	:	:	:	:	:	:
Dd	64	HTGKTVSLDWTPEKNRIIVASQDGRLIIV	92							

Search completed: April 10, 2003, 13:19:38
Job time : 2.08404 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 11:23:10 ; Search time 6.85262 Seconds
(without alignments)
871.983 Million cell updates/sec

Title: US-09-601-168b-2_COPY_516_544

Sequence: 1 VEHSGRVRLQDFEFQIVSSSHDTILW 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	100.0	569	11 09R1G7	09R1G7 mus musculus
2	152	100.0	569	11 09R2159	09R2159 mus musculus
3	152	100.0	569	11 09Q015	09Q015 mus musculus
4	151	99.3	562	11 09R22C7	09R22C7 mus musculus
5	151	99.3	563	11 09R23H0	09R23H0 mus musculus
6	149	98.0	510	5 044382	044382 drosophila
7	149	98.0	510	5 09VDE3	09VDE3 drosophila
8	141	92.8	430	5 09R154	09R154 heterodera
9	116	76.3	47	13 08UUN2	08UUN2 xenopus lae
10	73	48.0	553	4 09MDX6	09MDX6 homo sapien
11	73	48.0	561	4 096R12	096R12 homo sapien
12	73	48.0	589	4 096LE0	096LE0 homo sapien
13	73	48.0	627	4 096A16	096A16 homo sapien
14	73	48.0	629	11 08VHP4	08VHP4 mus musculus
15	73	48.0	629	11 08VBV4	08VBV4 mus musculus
16	73	48.0	707	4 0969H0	0969H0 homo sapien

17	73	48.0	1326	5 09VZP4	09VZP4 drosophila
18	69	45.4	293	4 08TC14	08TC14 homo sapien
19	69	45.4	468	11 09DB63	09DB63 mus musculus
20	69	45.4	472	4 096D26	096D26 homo sapien
21	69	45.4	472	4 09BR11	09BR11 homo sapien
22	69	45.4	504	4 096JVS	096JVS homo sapien
23	65	42.8	391	5 09VU65	09VU65 drosophila
24	64.5	42.4	525	4 09BWS5	09BWS5 homo sapien
25	62	40.8	992	16 098GJ0	098GJ0 rhizobium
26	61	40.1	220	5 09VAG1	09VAG1 drosophila
27	61	40.1	419	5 09FTJ1	09FTJ1 enccephalito
28	61	40.1	556	5 08SC04	08SC04 enccephalito
29	59	38.8	727	5 08SS07	08SS07 xenopus lae
30	57	37.5	122	13 08UUN3	08UUN3 seccaromyc
31	57	37.5	330	3 005583	08Y22 phytophthor
32	57	37.5	344	10 08RYB2	08RYB2 nicotiana t
33	57	37.5	377	10 09FV61	09FV61 plasm sativ
34	57	37.5	377	10 09XFK0	09XFK0 plasm sativ
35	57	37.5	377	10 09SW94	09SW94 solanum tub
36	57	37.5	380	10 0945H7	0945H7 solanum tub
37	57	37.5	380	10 064944	064944 avena fatua
38	57	37.5	423	5 08SSJ1	08SSJ1 enccephalito
39	57	37.5	1221	4 09Y2K9	09Y2K9 homo sapien
40	56	36.8	311	10 09AVW0	09AVW0 guillardia
41	56	36.8	316	3 09HGV7	09HGV7 emericella
42	56	36.8	375	10 094AR3	094AR3 arabidopsis
43	56	36.8	496	5 093339	093339 caenorhabdi
44	56	36.8	505	4 08WUD8	08WUD8 homo sapien
45	56	36.8	513	11 055039	055039 mus musculus

ALIGNMENTS

RESULT 1
ID 09R1G7 PRELIMINARY: PRT: 569 AA.

AC 09R1G7; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-transducin repeat-containing protein.
GN BTRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
CC Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF110396; AADA1025.1; .
DR MGD; MGI:138871; BTRC.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR01680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
DR PROSITE; PS00862; WD_REPEATS_2; 7.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SO SEQUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;

Query Match: 100.0%; Score 152; DB 11; Length 569;
Best Local Similarity: 100.0%; Pred. No. 7.8e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VEHSGRVRLQDFEFOIVSSSHDDTILIW 29
 DB 516 VEHSGRVRLQDFEFOIVSSSHDDTILIW 544

RESULT 2

ID 092159 PRELIMINARY; PRT; 569 AA.
 AC 092159;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Beta-transducin repeat containing protein.
 GN BTRC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=9145465; PubMed=9990853;
 RA Spencer E., Jiang J., Chen Z.J.;
 RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
 RT Slimb/beta-Trcp.";
 RL Genes Dev. 13:284-294 (1999).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF112979; AAD04181.1; -;
 DR MGD; MGI:1338871; Btrc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00236; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat: WD repeat.
 SQ SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;

Query Match 100.0%; Score 152; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7.8e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VEHSGRVRLQDFEFOIVSSSHDDTILIW 29
 DB 516 VEHSGRVRLQDFEFOIVSSSHDDTILIW 544

RESULT 3

ID 090015 PRELIMINARY; PRT; 569 AA.
 AC 090015;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ubiquitin ligase FMD1 (Beta-transducin repeat containing protein)
 DE (F-box-WD40 repeat protein 1).
 GN BTRC OR FBXW1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=919275; PubMed=10097128;
 RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,
 RA Hattori K., Hishashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
 RA Nakayama K.-i.;
 RT "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a

RT ubiquitin ligase Skp1/Cul 1/F-box protein FMD1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863 (1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99075339; PubMed=9859996;
 RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
 RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
 RT "Identification of the receptor component of the IkappaBalpha-
 RT ubiquitin ligase.";
 RL Nature 396:590-594 (1998).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=129/5V;
 RX MEDLINE=21601157; PubMed=11735228;
 RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
 RA Nakayama K.-i.;
 RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
 RT Caenorhabditis elegans SEL-10.";
 RL Genomics 78:214-222 (2001).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF081887; AAD17755.1; -;
 DR EMBL: AF099932; AAD08701.1; -;
 DR EMBL: BC003989; AAH03989.1; -;
 DR EMBL: AF391190; AAL40929.1; -;
 DR EMBL: AF391178; AAL40929.1; JOINED.
 DR EMBL: AF391179; AAL40929.1; JOINED.
 DR EMBL: AF391180; AAL40929.1; JOINED.
 DR EMBL: AF391181; AAL40929.1; JOINED.
 DR EMBL: AF391182; AAL40929.1; JOINED.
 DR EMBL: AF391183; AAL40929.1; JOINED.
 DR EMBL: AF391184; AAL40929.1; JOINED.
 DR EMBL: AF391185; AAL40929.1; JOINED.
 DR EMBL: AF391186; AAL40929.1; JOINED.
 DR EMBL: AF391187; AAL40929.1; JOINED.
 DR EMBL: AF391188; AAL40929.1; JOINED.
 DR EMBL: AF391189; AAL40929.1; JOINED.
 DR MGD; MGI:1338871; Btrc.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR ProDom: PD000018; WD40; 4.
 DR SMART: SM00236; FBOX; 1.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS50181; FBOX; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE: PS50082; WD_REPEATS_2; 7.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Ligase; Repeat: WD repeat.

SQ SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match 100.0%; Score 152; DB 11; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7.8e-15;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VEHSGRVRLQDFEFOIVSSSHDDTILIW 29
 DB 516 VEHSGRVRLQDFEFOIVSSSHDDTILIW 544

RESULT 4

ID 0922C7 PRELIMINARY; PRT; 252 AA.
 AC 0922C7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to f-box and WD-40 domain protein 1B (Fragment).

```

GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: BC008552; AAC08552.1; -.
DR MGI: 2144023; Fbxw1b.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 3.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 6.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KM Repeat: WD repeat.
FT NON_TER
SQ SEQUENCE 252 AA; 28424 MW; F71737CBD7A9F75F CRC64;

Query Match 99.3%; Score 151; DB 11; Length 252;
Best Local Similarity 96.6%; Pred. No. 4.6e-15;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQFDEFQIVSSSHDITLIW 29
Db 199 VEHSGRVRLQFDEFQIVSSSHDITLIW 227
|||||
ID Q923H0 PRELIMINARY; PRT; 563 AA.
AC Q923H0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F-box/WD40 repeat-containing protein HOS.
GN FBXW1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FB/N;
RA Bhatia N., Hertler J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
RT "Mouse homolog of HOS (MHOS) is overexpressed in skin tumors and
RT implicated in constitutive activation of NF-kappaB."
CC Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY038079; AAK72095.1; -.
DR MGI: 2144023; Fbxw1b.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRODOM: PD000018; WD40; 4.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KM Repeat: WD repeat.
SQ SEQUENCE 563 AA; 64741 MW; 9A8562F3FF5E3496 CRC64;

Query Match 99.3%; Score 151; DB 11; Length 563;
Best Local Similarity 96.6%; Pred. No. 1.1e-14;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQFDEFQIVSSSHDITLIW 29
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Db 510 VEHSGRVRLQFDEFQIVSSSHDITLIW 538

RESULT 6
QYVDE3 PRELIMINARY; PRT; 510 AA.
ID 044382
AC 044382;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SLMB.
GN SLMB OR SLMB OR CG3412.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98121115; PubMed=9461217;
RX Jiang J., Struhl G.;
RT "Regulation of the Hedgehog and WINGLESS signalling pathways by the F-
RT box/WD40-repeat protein SLMB."
RL Nature 391:493-496(1998).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF032878; AAC38852.1; -.
DR FLYBASE: FBgn0023423; slmb.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KM Repeat: WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;

Query Match 98.0%; Score 149; DB 5; Length 510;
Best Local Similarity 96.6%; Pred. No. 2e-14;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VEHSGRVRLQFDEFQIVSSSHDITLIW 29
Db 459 VEHSGRVRLQFDEFQIVSSSHDITLIW 487
|||||

RESULT 7
QYVDE3 PRELIMINARY; PRT; 510 AA.
ID 09VDE3
AC 09VDE3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SLMB protein (SLMB).
GN SLMB OR CG3412.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

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Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 April J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 Glorides A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshireli A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-OVARY, AND IMAGINAL DISC;
 RX MEDLINE=20245299; PubMed=10781936;
 RA Miletich I., Limbourg-Bouchon B.;
 RT "Drosophila null limb clones transiently deregulate Hedgehog-
 independent transcription of wingless in all limb discs, and induce
 RT decapentaplegic transcription linked to imaginal disc regeneration.";
 RL Mech. Dev. 93:15-26(2000).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AF003733; AAF5853.1; -;
 DR EMBL: AF222924; AAF63214.1; -;
 DR EMBL: AF222923; AAF63213.1; -;
 DR FlyBase; FBgn0023423; limb.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 510 AA; 58952 MW; FAD5DF126F58A012 CRC64;

Query Match 98.0%; Score 149; DB 5; Length 510;
 Best Local Similarity 96.6%; Pred. No. 2e-14;
 Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VHSGRVRLQDFEFOIVSSSHDITLIM 29
 DB 459 VHTGRVRLQDFEFOIVSSSHDITLIM 487

RESULT 8
 09B5J4

ID 09B5J4 PRELIMINARY; PRT; 430 AA.
 AC 09B5J4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Beta-transducin repeat-containing protein (Fragment).
 OS Heterodera glycines (Soybean cyst nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
 OX NCBI_TaxID=51029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kovaleva E.S., Yakovlev A.G., Masler E.P.;
 RT "Plant parasitic nematode b-TRCP.";
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL; AF339101; AAK26376.1; -;
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER 1
 SQ SEQUENCE 430 AA; 47916 MW; 4ABC3F2DFE3A50B CRC64;

Query Match 92.8%; Score 141; DB 5; Length 430;
 Best Local Similarity 89.3%; Pred. No. 2.8e-13;
 Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 EHSGRVRLQDFEFOIVSSSHDITLIM 29
 DB 341 QHTGRVRLQDFEFOIVSSSHDITLIM 368

RESULT 9
 ID 080UN2 PRELIMINARY; PRT; 47 AA.
 AC 080UN2;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Beta-TRCP protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carnevali F.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA "Analisi strutturale e funzionale del gene beta-TRCP in *Xenopus*
 RT laevis".
 RT Thesis (2001).
 RL Department of Genetics and Molecular Biology "Charles Darwin",
 RL University of Rome La Sapienza, Rome, Italy.
 DR EMBL; AJ428939; CAD21936.1; -;
 DR InterPro; IPR001680; WD40.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 47 AA; 5521 MW; FD0A221906DC70B9 CRC64;

Query Match 76.3%; Score 116; DB 13; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 8 FRQGFDEFQIVSSSHDITLW 29
    1 FRQGFDEFQIVSSSHDITLW 22
Db
RESULT 10
O9N0X6 PRELIMINARY: PRT: 553 AA.
AC O9N0X6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDNA FJ11071 f15, clone PLACE1004937, moderately similar to SEL-10
DE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Itoga T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuno Y., Sasaki N.;
RT "MEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AK001933; BAA91986.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Repeat: WD repeat.
KW SEQUENCE 553 AA; 62280 MW; CA829C221986A3F2 CRC64;
SQ
Query Match 48.0%; Score 73; DB 4; Length 553;
Best Local Similarity 48.1%; Pred. No. 0.01;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRFRLOFDEFQIVSSSHDITLW 29
    1 HSGRFRLOFDEFQIVSSSHDITLW 412
Db 386 HTRNRYSLQFDGIHVVGSLDTSIRW 412
RESULT 11
O96R12 PRELIMINARY: PRT: 561 AA.
AC O96R12;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F-box protein FBX30 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20003061; PubMed=10531037;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins."
RL Curr. Biol. 9:1180-1182(1999).
RN [2]

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RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper J.W., Elledge S.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF383178; AAK60269.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat: WD repeat.
FT NON_TER 1
SQ SEQUENCE 561 AA; 63165 MW; B81CC1E2206B0D88 CRC64;
SQ
Query Match 48.0%; Score 73; DB 4; Length 561;
Best Local Similarity 48.1%; Pred. No. 0.01;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRFRLOFDEFQIVSSSHDITLW 29
    1 HSGRFRLOFDEFQIVSSSHDITLW 420
Db 394 HTRNRYSLQFDGIHVVGSLDTSIRW 420
RESULT 12
O96LE0 PRELIMINARY: PRT: 589 AA.
AC O96LE0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F-box protein SEL10.
CN SEL10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R.,
RA Buhl A.E., Gurney M.E.;
RT "SEL-10 Interacts with Presenilin 1, Facilitates Its Ubiquitination,
RT and Alters A-beta Production."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AY008274; AAC16640.1; -
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR ProDom: PD000018; WD40; 2.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat: WD repeat.
SQ SEQUENCE 589 AA; 66120 MW; 2AFB6BA36E6E8DE CRC64;
SQ
Query Match 48.0%; Score 73; DB 4; Length 589;
Best Local Similarity 48.1%; Pred. No. 0.01;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 HSGRFRLOFDEFQIVSSSHDITLW 29
    1 HSGRFRLOFDEFQIVSSSHDITLW 448
Db 422 HTRNRYSLQFDGIHVVGSLDTSIRW 448
RESULT 13
O96A16 PRELIMINARY: PRT: 627 AA.

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AC 096A16;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Archipelago beta form (F-box protein FBW7).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21449047; PubMed=11565033;
RX Moberg K.H., Bell D.W., Maher D.C., Haber D.A., Hariharan I.K.;
RT "Archipelago regulates Cyclin E levels in Drosophila and is mutated in
RL human cancer cell lines.";
RL Nature 413:311-316(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20003061; PubMed=10531037;
RX Winston J.T., Koepf D.M., Zhu C., Ellledge S.J., Harper J.W.;
RT "A family of mammalian F-box proteins.";
RL Curr. Biol. 9:1180-1182(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Koepf D.M., Winston J.T., Harper W., Ellledge S.J.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: AF411972; AAL06291.1; -;
DR EMBL: AY033553; AKS7547.1; -;
DR InterPro: IPR001810; F-box.
DR Pfam: PF00646; F-box; 1.
DR ProDom: PD000018; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 627 AA; 70324 MW; 3D4107C053381BED CRC64;
Query Match 48.0%; Score 73; DB 4; Length 627;
Best Local Similarity 48.1%; Pred. No. 0.012;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVRLQDFEFOIVSSSHDITLIM 29
DB 460 HTNRVYSLQFDGIHVYSGSLDTSIRW 486
RESULT 14
ID 08VBV4 PRELIMINARY; PRT; 629 AA.
AC 08VBV4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F-box protein.
GN FBWD6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ilyin G.P.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF427101; AAL50052.1; -;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINRPT.
SQ SEQUENCE 629 AA; 70547 MW; 80483A7C2ED61FE7 CRC64;
Query Match 48.0%; Score 73; DB 11; Length 629;
Best Local Similarity 48.1%; Pred. No. 0.012;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVRLQDFEFOIVSSSHDITLIM 29
DB 462 HTNRVYSLQFDGIHVYSGSLDTSIRW 488

DR ProDom: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 629 AA; 70562 MW; BE916405A3490A3E CRC64;
Query Match 48.0%; Score 73; DB 11; Length 629;
Best Local Similarity 48.1%; Pred. No. 0.012;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVRLQDFEFOIVSSSHDITLIM 29
DB 462 HTNRVYSLQFDGIHVYSGSLDTSIRW 488
RESULT 15
ID 08VBV4 PRELIMINARY; PRT; 629 AA.
AC 08VBV4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F-box-WD40 repeat protein 6.
GN FBXW6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21601157; PubMed=11735228;
RA Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA Nakayama K.-I.;
RT "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue of
RL Genomics 78:214-222(2001).
DR EMBL: AF391202; AAL40930.1; -;
DR EMBL: AF391193; AAL40930.1; JOINED.
DR EMBL: AF391194; AAL40930.1; JOINED.
DR EMBL: AF391195; AAL40930.1; JOINED.
DR EMBL: AF391196; AAL40930.1; JOINED.
DR EMBL: AF391197; AAL40930.1; JOINED.
DR EMBL: AF391198; AAL40930.1; JOINED.
DR EMBL: AF391199; AAL40930.1; JOINED.
DR EMBL: AF391200; AAL40930.1; JOINED.
DR EMBL: AF391201; AAL40930.1; JOINED.
DR EMBL: AF391192; AAL40928.1; -;
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINRPT.
DR ProDom: PD000018; WD40; 2.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS50181; FBOX; 1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_5.
DR PROSITE: PS50082; WD_REPEATS_2; 7.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 629 AA; 70547 MW; 80483A7C2ED61FE7 CRC64;
Query Match 48.0%; Score 73; DB 11; Length 629;
Best Local Similarity 48.1%; Pred. No. 0.012;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 3 HSGRVRLQDFEFOIVSSSHDITLIM 29
DB 462 HTNRVYSLQFDGIHVYSGSLDTSIRW 488

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